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Description

BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND USES THEREOF

Cross Reference to Related Applications

[0001] The present invention is a continuation of application 10/293,338 incorporated herein, now abandoned.

Appendix Data

[0002] Computer Disk OBJECT_ID Sequence listing part

[0003] Computer Disk 2 OBJECT_ID #2 Sequence listing (copy 2)

Background of Invention

FIELD OF THE INVENTION

[0004] The present invention relates to a group of bioinformatically detectable novel genes, here identified as "genomic address messenger"or "GAM"genes, which are believed to be related to the micro RNA (miRNA) group of genes.

Description of Prior Art

[0005] Over 300 small noncoding RNA"s, termed Micro RNA"s (miRNA"s), have been identified to date in animals and plants (1-8). The MIR genes, code for ~70-120nt long non-protein-coding RNA sequences, that are the precursors of the ~22 nt miRNA sequences, which in some cases, specifically inhibit translation of target genes, by complementary binding to their untranslated regions (UTR) (9-13). The first two MIR genes discovered, Lin-4 and Let-7, were found in the nematode Ceanorhabditis elegans, and shown to be involved in developmental timing (14, 15), hence originally called Short Temporal RNA (stRNA) (16). The ~22 nt sequences inhibit translation of two respective target genes, Lin-14 and Lin-41, by complementary binding to their 3" untranslated regions (UTR) (14, 17). Later studies by three separate groups (1-3) identified several precursor and mature miRNA"s, some of them in clusters (1), expressed as sequences found in size fractionated (<80nt) total RNA, in a wide spectrum of species, including C. elegans, Drosophila melanogaster, Homo sapiens, as well as plants. More recently, additional miRNA"s from human (mir-91 to mir-121 (6)), mouse (mir-122 to mir-155 (4)) and plants (mir-156 to mir-171 (5)), have been reported. Furthermore, Llave et al identi-

fied in Arabidopsis thaliana 125 sequences, 21-24 nucleotides in length and presumably miRNAs (8). Each of the MIR genes is transcribed and processed to an ~80 nt-long hairpin shaped miRNA precursor, which is then processed by an enzyme called Dicer, to yield the mature ~22 nt-long single stranded miRNA. Such small RNAs will inhibit translation of target genes by complementary binding to sites in the 3" or 5" untranslated regions (18). Their structural similarity to the two well-studied miRNA"s in C. elegans, Lin-4 and Let-7, supports the belief that MIR genes code for specific translation inhibitors of target genes. However, determining the targets of the miRNAs is more complicated than just searching for antisense complementarity, because bulges and loops, disrupting perfect complementarity, are not only tolerated, but seem to be the rule in the postulated binding between the miRNA"s and their target UTR"s(19). Target-gene binding sites of most reported miRNA"s, except of Lin-4 and Let-7, have not been found, and therefore the specific functionality of these genes is still unknown. Using a computational approach, Rhoades et al (19), predicted targets for 14 A. thaliana miRNA"s by identifying their near complementarity to the predicted targets. However, using the

same approach was not helpful in identifying miRNA targets in C. elegans and D. melanogaster, raising the possibility that the near-perfect complementarity appears to be specific to plants (19).

[0006] The ability to detect novel RNA genes is limited by the methodologies used to detect such genes. All RNA genes identified so far either present a visibly discernable whole body phenotype, as do Lin-4 and Let-7 (Wightman et. al., Cell 75, 855 (1993); Reinhart et al., Nature 403, 901 (2000)), or produce significant enough quantities of RNA so as to be detected by the standard biochemical genomic techniques, as do the 93 recently detected miRNA genes. Since a limited number clones were sequenced by the researchers discovering these genes, 300 by Bartel and 100 by Tuschl (Bartel et. al., Science 294 ,858 (2001); Tuschl et. al., Science 294 ,853 (2001)), the RNA genes found can not be much rarer than 1% of all RNA genes. The recently detected miRNA genes therefore represent the more prevalent among the miRNA gene family.

[0007] Current methodology has therefore been unable to detect RNA genes which either do not present a visually discernable whole body phenotype, or are rare (e.g. rarer than 0.1% of all RNA genes), and therefore do not produce sig-

nificant enough quantities of RNA so as to be detected by standard biochemical technique.

SUMMARY OF INVENTION

[0008] The present invention relates to a novel group of regulatory, non-protein coding genes, which are functional in specifically inhibiting translation of other genes, some of which are known to be involved in various diseases. Each gene in this novel group of genes, here identified as "GAM"or "Genomic Address Messengers", specifically inhibits translation of one of more other "target" genes by means of complimentary hybridization of a segment of the RNA transcript encoded by GAM2, to an inhibitor site located in the 3"untranslated region of the mRNA of the one or more "target" genes.

[0009] In various preferred embodiments, the present invention seeks to provide improved method and system for specific modulation of expression of specific known "target" genes involved in significant human diseases, and improved method and system for detection of expression of these target genes.

[0010] Accordingly, the invention provides several substantially pure DNAs (e.g., genomic DNA, cDNA or synthetic DNA) each encoding a novel gene of the GAM group of gene,

vectors comprising the DNAs, probes comprising the DNAs, a method and system for selectively modulating translation of known "target" genes utilizing the vectors, and a method and system for detecting expression of known "target" genes utilizing the probe.

[0011] By "substantially pure DNA" is meant DNA that is free of the genes which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the genes discovered and isolated by the present invention. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote at a site other than its natural site; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

[0012] "Inhibiting translation" is defined as the ability to prevent synthesis of a specific protein encoded by a respective gene, by means of inhibiting the translation of the mRNA of this gene. "Translation inhibiter site" is defined as the

minimal DNA sequence sufficient to inhibit translation.

[0013] There is thus provided in accordance with a preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioinformatically detectable novel gene is about 18 to about 24 nucleotides in length, and originates from an RNA precursor, which RNA precursor is about 50 to about 120 nucleotides in length, a nucleotide sequence of a first half of the RNA precursor is a partial inversed-reversed sequence of a nucleotide sequence of a second half thereof, a nucleotide sequence of the RNA encoded by the novel gene is a partial inversed-reversed sequence of a nucleotide sequence of a binding site associated with at least one target gene, the novel gene cannot be detected by either of the following: a visually discernable whole body phenotype, and detection of 99.9% of RNA species shorter than 25 nucleotides expressed in a tissue sample, and a function of the novel gene is bioinformatically deducible.

[0014] There is further provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioninformatically

detectable novel gene includes a plurality of RNA sections, each of the RNA sections being about 50 to about 120 nucleotides in length, and including an RNA segment, which RNA segment is about 18 to about 24 nucleotides in length, a nucleotide sequence of a first half of each of the RNA sections encoded by the novel gene is a partial inversed-reversed sequence of nucleotide sequence of a second half thereof, a nucleotide sequence of each of the RNA segments encoded by the novel gene is a partial inversed-reversed sequence of the nucleotide sequence of a binding site associated with at least one target gene, and a function of the novel gene is bioinformatically deducible from the following data elements: the nucleotide sequence of the RNA encoded by the novel gene, a nucleotide sequence of the at least one target gene, and function of the at least one target gene.

[0015] There is still further provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioinformatically detectable novel gene is about 18 to about 24 nucleotides in length, and originates from an RNA precursor, which RNA precursor is about 50 to about 120 nucleotides in

length, a nucleotide sequence of a first half of the RNA precursor is a partial inversed-reversed sequence of a nucleotide sequence of a second half thereof, a nucleotide sequence of the RNA encoded by the novel gene is a partial inversed-reversed sequence of a nucleotide sequence of a binding site associated with at least one target gene, a function of the novel gene is modulation of expression of the at least one target gene, and the at least one target gene does not encode a protein.

[0016] There is additionally provided in accordance with another preferred embodiment of the present invention A bioinformatically detectable novel gene encoding substantially pure DNA wherein: the bioinformatically detectable novel gene does not encode a protein, RNA encoded by the bioinformatically detectable novel gene is maternally transferred by a cell to at least one daughter cell of the cell, a function of the novel gene includes modulation of a cell type of the daughter cell, and the modulation is bioinformatically deducible.

[0017] There is moreover provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: the bioinformatically detectable novel

gene does not encode a protein, a function of the novel gene is promotion of expression of the at lease one target gene, and the at least one target gene is bioinformatically deducible.

[0018] Further in accordance with a preferred embodiment of the present invention the function of the novel gene is bioinformatically deducible from the following data elements: the nucleotide sequence of the RNA encoded by the bioinformatically detectable novel gene, a nucleotide sequence of the at least one target gene, and a function of the at least one target gene.

[0019] Still further in accordance with a preferred embodiment of the present invention the RNA encoded by the novel gene complementarily binds the binding site associated with the at least one target gene, thereby modulating expression of the at least one target gene.

[0020] Additionally in accordance with a preferred embodiment of the present invention the binding site associated with at least one target gene is located in an untranslated region of RNA encoded by the at least one target gene.

[0021] Moreover in accordance with a preferred embodiment of the present invention the function of the novel gene is selective inhibition of translation of the at least one target

gene, which selective inhibition includes complementary hybridization of the RNA encoded by the novel gene to the binding site.

[0022] Further in accordance with a preferred embodiment of the present invention the invention includes a vector including the DNA.

[0023] Still further in accordance with a preferred embodiment of the present invention the invention includes a method of selectively inhibiting translation of at least one gene, including introducing the vector.

[0024] Moreover in accordance with a preferred embodiment of the present invention the introducing includes utilizing RNAi pathway.

[0025] Additionally in accordance with a preferred embodiment of the present invention the invention includes a gene expression inhibition system including: the vector, and a vector inserter, functional to insert the vector into a cell, thereby selectively inhibiting translation of at least one gene.

[0026] Further in accordance with a preferred embodiment of the present invention the invention includes a probe including the DNA.

[0027] Still further in accordance with a preferred embodiment of

the present invention the invention includes a method of selectively detecting expression of at least one gene, including using the probe.

[0028] Additionally in accordance with a preferred embodiment of the present invention the invention includes a gene expression detection system including: the probe, and a gene expression detector functional to selectively detect expression of at least one gene.

Brief Description of Drawings

[0029] Fig.1 is a simplified diagram illustrating the genomic differentiation enigma that the present invention addresses;

[0030] Figs. 2 through 4 are schematic diagrams which when taken together provide an analogy that illustrates a conceptual model of the present invention, addressing the genomic differentiation enigma;

[0031] Figs. 5A and 5B are schematic diagrams, which when taken together illustrate a "genomic records" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0032] Fig. 6 is a schematic diagram illustrating a "genomically programmed cell differentiation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0033] Fig. 7 is a schematic diagram illustrating a "genomically programmed cell-specific protein expression modulation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0034] Fig. 8 is a simplified diagram illustrating a mode by which genes of a novel group of genes of the present invention, modulate expression of known target genes;

[0035] Fig. 9 is a simplified block diagram illustrating a bioinformatic gene detection system capable of detecting genes of the novel group of genes of the present invention, which system is constructed and operative in accordance with a preferred embodiment of the present invention;

[0036] Fig. 10 is a simplified flowchart illustrating operation of a mechanism for training of a computer system to recognize the novel genes of the present invention, which mechanism is constructed and operative in accordance with a preferred embodiment of the present invention;

[0037] Fig. 11A is a simplified block diagram of a non-coding genomic sequence detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0038] Fig. 11B is a simplified flowchart illustrating operation of a non-coding genomic sequence detector constructed and

operative in accordance with a preferred embodiment of the present invention;

[0039] Fig. 12A is a simplified block diagram of a hairpin detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0040] Fig. 12B is a simplified flowchart illustrating operation of a hairpin detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0041] Fig. 13A is a simplified block diagram of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0042] Fig. 13 B is a simplified flowchart illustrating training of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0043] Fig. 14A is a simplified block diagram of a target-gene binding-site detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0044] Fig. 14B is a simplified flowchart illustrating operation of a target-gene binding-site detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0045] Fig. 15 is a simplified flowchart illustrating operation of a function & utility analyzer constructed and operative in accordance with a preferred embodiment of the present invention;

[0046] Fig. 16 is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention;

[0047] Figs. 17A and 17B are pictures of laboratory results, which when taken together demonstrate laboratory confirmation of expression of the bioinformatically detected novel gene of Fig. 16;

[0048] Fig. 18

[0049] Fig. 19

[0050] Fig. 20

[0051] Figs. 21A through 28020D are schematic diagrams illustrating sequences, functions and utilities of 28,000 specific genes of the novel group of genes of the present invention, detected using the bioinformatic gene detection system described hereinabove with reference to Figs. 8 through 15;

[0052] and Figs. 28021A through 3121B are schematic diagrams illustrating sequences, functions and utilities of 3,000

specific genes of a second group of novel genes of the present invention, detected using the bioinformatic gene detection system described hereinabove with reference to Figs. 8 through 15.

Brief Description of Sequences

[0053] A Sequence Listing of genomic sequences of the present invention is attached to this application, enclosed in computer readable form.

Detailed Description

[0054] Reference is now made to Fig. 1 which is a simplified diagram providing a conceptual explanation of a genomic differentiation enigma, which the present invention addresses.

[0055] Referring to Fig. 1, it is appreciated that different cell types in an organism, such as CARTILAGE CELL, LIVER CELL, FIBROBLAST CELL and BONE CELL all contain identical DNA, and derive from the initial FERTILIZED EGG CELL, and yet each of these cells expresses different proteins, and hence acquires different shape and function.

[0056] The present invention proposes that the inevitable conclusion from this constraint is, however, strikingly simple: the coding system used must be modular. It must com-

prise multiple modules, or records, one for each cell-type, and a mechanism whereby each cell at its inception is instructed which record to open, and behaves according to instructions in that record.

[0057] This modular code concept is somewhat difficult to grasp, since we are strongly habituated to viewing things from an external viewpoint. An architect, for example, looks at a blueprint of a building, which details exactly where each element (block, window, door, electrical switch, etc.) is to be placed relative to all other elements, and then instructs builders to place these elements in their designated places. This is an external viewpoint: the architect is external to the blueprint, which itself is external to the physical building, and its different elements. The architect may therefore act as an "external organizing agent": seeing the full picture and the relationships between all elements, and being able to instruct from the outside where to place each of them.

[0058] Genomics differentiation coding evidently works differently, without any such external organizing agent: It comprises only one smart block (the first cell), which is the architect and the blueprint, and which continuously duplicates itself, somehow knowing when to manifest itself as

a block and when as a window, door, or electrical switch.

[0059] Reference is now made to Figs. 2 through 4 which are schematic diagrams which when taken together provide an analogy that illustrates a conceptual model of the present invention, addressing the genomic differentiation enigma.

[0060] Referring to Fig. 2A, imagine a very talented chef, capable of preparing any meal provided he is given specific written cooking instructions. This chef is equipped with two items: (a) a thick recipe book, and (b) a small note with a number scribbled on it. The book comprises multiple pages, each page detailing how to prepare a specific meal. The small note indicates the page to be opened, and therefore the meal to be prepared. The chef looks at the page-number written on the note, opens the recipe book at the appropriate page, and prepares the meal according to the written instructions on this page. As an example, Fig. 2A depicts a CHEF holding a note with the number 12 written on it, he opens the book on page 12, and since that page contains the recipe for preparing BREAD, the CHEF prepares a loaf of BREAD.

[0061] Referring now to Fig. 2B, which depicts two identical chefs, CHEF A and CHEF B, holding an identical recipe

book. Despite their identity, and the identity of their recipe book, since CHEF A holds a note numbered 12, and therefore opens the book on page 12 and prepares BREAD, whereas CHEF B holds a note numbered 34 and therefore opens the book on page 34 and prepares a PIE.

[0062] Referring now to Fig. 3. Imagine the chef of the analogy is also capable of duplicating himself once he has finished preparing the specified meal. The format of the book is such that at the bottom of each page, two numbers are written. When he has finished preparing the meal specified on that page, the chef is trained to do the following: (i) divide himself into two identical duplicate chefs, (ii) duplicate the recipe book and hand a copy to each of his duplicate chefs, and (iii) write down the two numbers found at the bottom of the page of the meal he prepared, on two small notes, handing one note to each of his two duplicate chefs.

[0063] Each of the two resulting duplicate chefs are now equipped with the same book, and have the same talent to prepare any meal, but since each of them received a different note, they will now prepare different meals.

[0064] Fig. 3 depicts CHEF A holding a recipe book and receiving a note numbered 12. CHEF A therefore opens the book on

page 12 and prepares BREAD. When he is finished making bread, CHEF A performs the following actions: (i) divides himself into two duplicate chefs, designated CHEF B and CHEF C, (ii) duplicates his recipe book handing a copy to each of CHEF B and CHEF C, (iii) writes down the numbers found at the bottom of page 12, numbers 34 and 57, on two notes, handing note numbered 34 to CHEF B and note numbered 57 to CHEF C.

[0065] Accordingly, CHEF B receives a note numbered 34 and therefore opens the recipe book on page 34 and prepares PIE, whereas CHEF C receives a note numbered 57 and therefore opens the book on page 57 and therefore prepares RICE.

[0066] It is appreciated that while CHEF A, CHEF B & CHEF C are identical and hold identical recipe books, they each prepare a different meal. It is also appreciated that the meals prepared by CHEF B and CHEF C are determined CHEF A, and are mediated by the differently numbered notes passed on from CHEF A to CHEF B and CHEF C.

[0067] It is further appreciated that the mechanism illustrated by Fig. 3 enables an unlimited lineage of chefs to divide into duplicate, identical chefs and to determine the meals those duplicate chefs would prepare. For example, having

been directed to page 34, when CHEF B divides into duplicate chefs (not shown), he will instruct its two duplicate chefs to prepare meals specified on pages 14 and 93 respectively, according to the numbers at the bottom of page 34 to which he was directed. Similarly, CHEF C will instruct its duplicate chefs to prepare meals specified on pages 21 and 46 respectively, etc.

[0068] Referring now to Fig. 4. Imagine that the cooking instructions on each page of the recipe book are written in shorthand format: The main meal-page to which the chef was directed by the scribbled note, merely contains a list of numbers which direct him to multiple successive pages, each specifying how to prepare an ingredient of that meal.

[0069] As an example, Fig. 4 depicts CHEF A of FIGS 2 and 3, holding a recipe book and a note numbered 12. Accordingly, CHEF A opens the recipe book on page 12, which details the instructions for preparing BREAD. However, the "instructions" on making BREAD found on page 12 comprise only of 3 numbers, 18, 7 and 83, which "refer" CHEF A to pages detailing preparation of the ingredients of BREAD FLOUR, MILK and SALT, respectively.

[0070] As illustrated in Fig. 4, turning from the main "meal page" (e.g. 12) to respective "ingredients pages" (e.g. pages 18,

7 & 83) is mediated by scribbled notes with the page-numbers written on them. In this analogy, the scribbled notes are required for seeking the target pages to be turned to both when turning to main "meal pages" (e.g. page 12), as well as when turning to "ingredient pages" (e.g. pages 18, 7 & 83).

[0071] The chef in the given analogy, schematically depicted in FIGS 2 through 4, represents a cell; the thick recipe book represents the DNA; preparing a meal in the given analogy represents the cell manifesting itself as a specific cell-type; and ingredients of a meal represent proteins expressed by that cell-type. Like the chef equipped with the thick recipe book in the given analogy, all cells in an organism contain the same DNA and are therefore each potentially capable of manifesting itself as any cell-type, expressing proteins typical of that cell type.

[0072] Reference is now made to Figs. 5A and 5B which are schematic diagrams, which when taken together illustrate a "genomic records" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0073] The Genomic Records concept asserts that the DNA (the thick recipe book in the illustration) comprises a very

large number of Genomic Records (analogous to pages in the recipe book), each containing the instructions for differentiation of a different cell-type, or developmental process. Each Genomic Record is headed by a very short genomic sequence which functions as a "Genomic Address" of that Genomic Record (analogous to the page number in the recipe book). At its inception, in addition to the DNA, each cell also receives a short RNA segment (the scribbled note in the illustration). This short RNA segment binds complementarily to a "Genomic Address" sequence of one of the Genomic Records, thereby activating that Genomic Record, and accordingly determining the cell"s-fate (analogous to opening the book on the page corresponding to the number on the scribbled note, thereby determining the meal to be prepared).

[0074] Referring to Fig. 5A, a CELL is illustrated which comprises a GENOME. The GENOME comprises a plurality of GENOMIC RECORDS, each of which correlates to a specific cell type (for clarity only 6 sample genomic records are shown). Each genomic record comprises genomic instructions on differentiation into a specific cell-type, as further elaborated below with reference to Fig. 7. At cell inception, the CELL receives a maternal short RNA segment,

which activates one of the GENOMIC RECORDS, causing the cell to differentiate according to the instructions comprised in that genomic record. As an example, Fig. 5A illustrates reception of a maternal short RNA segment designated A" and outlined by a broken line, which activates the FIBRO genomic record, causing the cell to differentiate into a FIBROBLAST CELL.

[0075] Referring now to Fig. 5B, which is a simplified schematic diagram, illustrating cellular differentiation mediated by the "Genomic Records" concept. Fig. 5B depicts 2 cells in an organism, designated CELL A and CELL B, each having a GENOME. It is appreciated that since CELL A and CELL B are cells in the same organism, the GENOME of CELL A is identical to that of CELL B. Despite having an identical GENOME, CELL A differentiates differently from CELL B, due to activation of different genomic records in these two cells. In CELL A the FIBRO GENOMIC RECORD is activated, causing CELL A to differentiate into a FIBROBLAST CELL, whereas in CELL B the BONE GENOMIC RECORD is activated, causing the CELL B to differentiate into a BONE CELL. The cause for activation of different genomic records in these two cells is the different maternal short RNA which they both received: CELL A received a maternal

short RNA segment designated A" which activated genomic record FIBRO, whereas CELL B received a maternal short RNA segment designated B" which activated genomic record BONE.

[0076] Reference is now made to Fig. 6 which is a schematic diagram illustrating a "genomically programmed cell differentiation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0077] A cell designated CELL A divides into 2 cells designated CELL B and CELL C. CELL A, CELL B and CELL C each comprise a GENOME, which GENOME comprises a plurality of GENOMIC RECORDS. It is appreciated that since CELL A, CELL B and CELL C are cells in the same organism, the GENOME of these cells, and the GENOMIC RECORDS comprised therein, are identical.

[0078] As described above with reference to Fig. 5B, at its inception, CELL A receives a maternal short RNA segment, designated A" and marked by a broken line, which activates the FIBRO genomic record, thereby causing CELL A to differentiate into a FIBROBLAST CELL. However, Fig. 6 shows further details of the genomic records: each cell genomic record also comprises two short genomic sequences, referred to here as Daughter Cell Genomic Addresses.

Blocks designated B and C are Daughter Cell Genomic Addresses of the FIBRO Genomic Record. At cell division, each parent cell transcribes two short RNA segments, corresponding to the two Daughter Cell Genomic Addresses of the Genomic Record of that parent cell, and transfers one to each of its two daughter cells. CELL A of Fig. 6 transcribes and transfers to its two respective daughter cells, two short RNA segments, outlined by a broken line and designated B" and C", corresponding to daughter cell genomic addresses designated B and C comprised in the FIBRO genomic record.

[0079] CELL B therefore receives the above mentioned maternal short RNA segment designated B", which binds complementarily to genomic address designated B of genomic record BONE, thereby activating this genomic record, which in turn causes CELL B to differentiate into a BONE CELL. Similarly, CELL C receives the above mentioned maternal short RNA segment designated C", which binds complementarily to genomic address designated C of genomic record CARTIL., thereby activating this genomic record, which in turn causes CELL C to differentiate into a CARTILAGE CELL.

[0080] It is appreciated that the mechanism illustrated by Fig. 6

enables an unlimited lineage of cells to divide into daughter cells containing the same DNA, and to determine the cell-fate of these daughter cells. For example, when CELL B and CELL C divide into their respective daughter cells (not shown), they will transfer short RNA segments designated D" & E", and F" & G" respectively, to their respective daughter cells. The cell fate of each of these daughter cells would be determined by the identity of the maternal short RNA segment they receive, which would determine the genomic record activated.

[0081] Reference is now made to Fig. 7 which is a schematic diagram illustrating a "genomically programmed cell-specific protein expression modulation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0082] Cell A receives a maternal short RNA segment designated A", which activates a genomic record designated FIBRO, by anti-sense binding to a binding site "header" of this genomic record, designated A. Genomic record FIBRO encodes 3 short RNA segments, designated 1, 2 and 4 respectively, which modulate expression of target genes designated GENE1, GENE2 and GENE4 respectively. Modulation of expression of these genes results in CELL A dif-

ferentiating into a FIBROBLAST CELL.

[0083] Reference is now made to Fig. 8 which is a simplified diagram illustrating a mode by which genes of a novel group of genes of the present invention, modulate expression of known target genes.

[0084] The novel genes of the present invention are micro RNA (miRNA)-like, regulatory RNA genes, modulating expression of known target genes. This mode of modulation is common to other known miRNA genes, as described hereinabove with reference to the background of the invention section.

[0085] GAM GENE and TARGET GENE are two human genes contained in the DNA of the human genome.

[0086] GAM GENE encodes a GAM PRECURSOR RNA. However, similar to other miRNA genes, and unlike most ordinary genes, its RNA, GAM PRECURSOR RNA, does not encode a protein.

[0087] GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA. As Fig.8 illustrates, GAM FOLDED PRECURSOR RNA forms a "hairpin structure", folding onto itself. As is well known in the art, this "hairpin structure", is typical genes of the miRNA genes, and is due to the fact that nucleotide sequence of the first half of

the RNA of a gene in this group is an accurate or partial inversed-reversed sequence of the nucleotide sequence of its second half. By "inversed-reversed"is meant a sequence which is reversed and wherein each nucleotide is replaced by a complimentary nucleotide, as is well known in the art (e.g. ATGGC is the inversed-reversed sequence of GCCAT).

[0088] An enzyme complex, designated DICER COMPLEX, "dices" the GAM FOLDED PRECURSOR RNA into a single stranded RNA segment, about 22 nucleotides long, designated GAM RNA. As is known in the art, "dicing" of the hairpin structured RNA precursor into shorter RNA segments about 22 nucleotides long by a Dicer type enzyme is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins.

[0089] TARGET GENE encodes a corresponding messenger RNA, designated TARGET RNA. This TARGET RNA comprises 3 regions: a 5" untranslated region, a protein coding region and a 3" untranslated region, designated 5"UTR, PROTEIN CODING and 3"UTR respectively.

[0090] GAM RNA binds complimentarily a BINDING SITE, located on the 3"UTR segment of TARGET RNA. This complimentarily binding is due to the fact that the nucleotide se-

quence of GAM RNA is an accurate or partial inversed-reversed sequence of the nucleotide sequence of BINDING SITE.

[0091] The complimentary binding of GAM RNA to BINDING SITE inhibits translation of TARGET RNA into TARGET PROTEIN. TARGET PROTEIN is therefore outlined by a broken line.

[0092] It is appreciated by one skilled in the art that the mode of transcriptional inhibition illustrated by Fig. 1 with specific reference to GAM genes of the present invention, is in fact common to all other miRNA genes. A specific complimentary binding site has been demonstrated only for Lin-4 and Let-7. All the other 93 newly discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complimentary binding, although specific complimentary binding sites for these genes have not yet been found (Ruvkun G., "Perspective: Glimpses of a tiny RNA world", Science 294 ,779 (2001)). The present invention discloses a novel group of genes, the GAM genes, belonging to the miRNA genes group, and for which a specific an complimentary binding has been determined.

[0093] Reference is now made to Fig. 9 which is a simplified block diagram illustrating a bioinformatic gene detection

system capable of detecting genes of the novel group of genes of the present invention, which system is constructed and operative in accordance with a preferred embodiment of the present invention.

[0094] A bioinformatic gene detection engine 100, is a preferred implementation of a mechanism capable of detecting genes of the novel group of genes of the present invention.

[0095] The function of the bioinformatic gene detection engine 100 is as follows: it receives three types of input, expressed RNA data 102, sequenced DNA data 104, and protein function data 106, performs a complex process of analysis of this data as elaborated below, and based on this analysis produces output of a bioinformatically detected group of novel genes designated 108.

[0096] Expressed RNA data 102 comprises published expressed sequence tags (EST) data, , published mRNA data, as well as other sources of published RNA data. Sequenced DNA data 104 comprises alphanumeric data describing sequenced genomic data, which preferably includes annotation data such as location of known protein coding regions relative to the sequenced data. Protein function data 106 comprises scientific publications reporting studies

which elucidated physiological function known proteins, and their connection, involvement and possible utility in treatment and diagnosis of various diseases. Expressed RNA data 102, sequenced DNA data 104 may preferably be obtained from data published by the National Center for Bioinformatics (NCBI) at the National Institute of Health (NIH), as well as from various other published data sources. Protein function data 106 may preferably be obtained from any one of numerous relevant published data sources, such as the Online Mendelian Inherited Disease In Man (OMIM) database developed by John Hopkins University, and also published by NCBI.

[0097] Prior to actual detection of bioinformatically detected novel genes 108 by the bioinformatic gene detection engine 100, a process of bioinformatic gene detection engine training & validation designated 110 takes place. This process uses the known miRNA genes as a training set (some 200 such genes have been found to date using biological laboratory means), to train the bioinformatic gene detection engine 100 to bioinformatically recognize miRNA-like genes, and their respective potential target binding sites. Bioinformatic gene detection engine training & validation 110 is further describe hereinbelow with ref-

erence to Fig. 10.

[0098] The bioinformatic gene detection engine 100 comprises several modules which are preferably activated sequentially, and are described as follows:A non-coding genomic sequence detector 112 operative to screen for and identify non-protein coding genomic sequences. The non-coding genomic sequence detector 112 is further described hereinbelow with reference to Figs. 11A and 11B.

[0099] A hairpin detector 114 operative to locate genomic "hairpin-shaped" sequences, similar to GAM FOLDED PRECURSOR of Fig. 8. The hairpin detector 114 is further described hereinbelow with reference to Figs. 12A and 12B.

[0100] A dicer-cut location detector 116 operative to detect the location on a hairpin shaped sequence which is enzymatically cut by DICER COMPLEX of Fig. 8. The dicer-cut location detector 116 is further described hereinbelow with reference to Fig. 13A.

[0101] A target-gene binding-site detector 118 operative to detect In these ESTs, the system locates "hairpin-shaped" (i.e. hairpin) sequences, which resemble known miRNA sequences. RNA 2D folding is calculated based on free-energy, using the Zucker algorithm (used throughout the process) [reference]. The 2D structure is then evaluated to

locate hairpin structures, and meticulously compared to that of known miRNA genes.

[0102] A combined neural and Bayesian networks system is used to detect location in which the Dicer enzyme-complex is predicted to cut the final novel miRNA gene from the hairpin shaped gene-precursor. Nucleotide sequence, and "Bulges" (i.e. mismatches) on the hairpin shaped precursor, are represented as the input and output layers of several neural networks, and hidden layer/s are designed for these neural networks accordingly. The networks are trained, evaluated and validated based on the "training set" of 120 known miRNA genes, using accepted neural networks methodology; prediction is further optimized by integrating results of multiple networks [reference].

[0103] Potential target-gene binding-sites are detected, by comparison of the final-gene sequence, calculated above, to untranslated regions of known genes, followed by a comparison of the 2D structure and free-energy of the binding site to that of known miRNA binding sites.

[0104] Lastly, biological and clinical function of target genes, utilizing reference databases such as Johns Hopkins" OMIM [reference] is manually reviewed, and is compared to tissue-data of EST in which novel gene was detected.

[0105] Referring to Fig. 9, the following is a technical description of the computer hardware configuration which was used:Hardware and Software SetupComputing power presented a major challenge. Initial time estimates indicated that over 30 months (!) of computing time would be required to detect all miRNA genes in human EST data, and their respective binding sites, using a powerful 8-processor machine.

[0106] In order to address this challenge at reasonable cost, a system has been built which, comprises a cluster of one hundred PCs (Pentium IV, 1.7GHz, with 40GB storage each), connected by Ethernet to 4 servers (2-CPU, Xeon 2.2GHz, with 200GB storage each), combined with an 8-processor server (8-CPU, Xeon 550Mhz w/ 8GB RAM) connected via 2 HBA fiber-channels to an EMC Clariion 100-disks, 3.6 Terabyte storage device. Figure 2 provides an overview of this hardware configuration.

[0107] Using this configuration, a database comprising 30 billion records was created, using Microsoft"s SQL-Server database software, demonstrating remarkable performance results, including bulk insert of 1 million records in 0.8 seconds. To the best of our knowledge, this is the largest number-of-records database ever built on an In-

tel-machine, achieving unprecedented record-insert performance. The system has further been optimized such that all one hundred PCs run at 100% CPU usage continually. Using this configuration reduced the calculation time from 30 months to 20 days.

[0108] Reference is now made to Fig. 10 which is a simplified flowchart illustrating operation of a mechanism for training of a computer system to recognize the novel genes of the present invention. This mechanism is a preferred implementation of the bioinformatic gene detection engine training & validation 110 described hereinabove with reference to Fig. 9.

[0109] Reference is now made to Fig. 11A which is a simplified block diagram of a preferred implementation of the non-coding genomic sequence detector 112 described hereinabove with reference to Fig. 9.

[0110] *The system uses as input published genomic data, including expressed RNA data (EST data and mRNA data), sequenced DNA data, and protein function data, from NCBI. EST data is blast-compared [reference] to known protein coding sequences; only non-protein-coding ESTs are searched for novel RNA genes.* Reference is now made to Fig. 11B which is a simplified flowchart illustrating a preferred operation of the non-coding ge-

nomic sequence detector 112 of Fig. 9.

[0111] Reference is now made to Fig. 12A which is a simplified block diagram of a preferred implementation of the hairpin detector 114 described hereinabove with reference to Fig. 9.

[0112] Reference is now made to Fig. 12B which is a simplified flowchart illustrating a preferred operation of the hairpin detector 114 of Fig. 9.

[0113] Reference is now made to Fig. 13A which is a simplified block diagram of a preferred implementation of the dicer-cut location detector 116 described hereinabove with reference to Fig. 9.

[0114] Reference is now made to Fig. 13 B which is a simplified flowchart illustrating a preferred implementation of dicer-cut location detector training & validation 126 of Fig. 10.

[0115] Reference is now made to Fig. 14A which is a simplified block diagram of a preferred implementation of the target-gene binding-site detector 118 described hereinabove with reference to Fig. 9.

[0116] Reference is now made to Fig. 14B which is a simplified flowchart illustrating a preferred operation of the target-gene binding-site detector 118 of Fig. 9.

[0117] Reference is now made to Fig. 15 which is a simplified

flowchart illustrating a preferred operation of the function & utility analyzer 120 described hereinabove with reference to Fig. 9.

[0118] Reference is now made to Fig. 16 which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. Fig. 16 shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST72223. It is appreciated that the sequence of this EST comprises sequences of one known miRNA gene, identified as MIR98, and of one novel GAM gene, referred to here as GAM-4, detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to Fig. 9.

[0119] Reference is now made to Figs. 17A and 17B that are pictures of laboratory results, which when taken together demonstrate laboratory confirmation of expression of the bioinformatically detected novel gene of Fig. 16.

[0120] Referring to Fig. 17A which is a Northern blot analysis of MIR-98 and EST72223 transcripts. MIR-98 and EST72223 were reacted with MIR-98 and GAM-4 probes as indicated in the figure. It is appreciated that the probes of both MIR-98 and GAM-4 reacted with EST72223, indicating

that EST72223 contains the sequences of MIR-98 and of GAM-4. It is further appreciated that the probe of GAM-4 did not cross-react with MIR-98.

[0121] With reference to Fig. 17B, a Northern blot analysis of EST72223 and MIR-98 transfections were performed, subsequently marking RNA by the MIR-98 and GAM-4 probes . Left, Northern reacted with MIR-98, Right, Northern reacted with GAM-4. The molecular Sizes of EST72223, MIR-98 and GAM-4 are indicated by arrows. Hela are control cells that have not been introduced to exogenous RNA. EST and MIR-98 Transfections are RNA obtained from Hela transfected with EST72223 and MIR-98, respectively. MIR-98 and EST are the transcripts used for the transfection experiment. The results indicate that EST72223, when transfected into Hela cells, is cut yielding known miRNA gene MIR-98 and novel miRNA gene GAM-4.

[0122] Referring to Figs. 17A and 17B, the following technical methods used are specified as follows: Transcript preparations: Digoxigenin (DIG) labeled transcripts were prepared from EST72223 (TIGER), MIR98 and predicted precursor hairpins by using a DIG RNA labeling kit (Roche Molecular Biochemicals) according to the manufacture"s

protocol. Briefly, PCR products with T7 promoter at the 5" end or T3 promoter at the 3"end were prepared from each DNA in order to use it as a template to prepare sense and antisense transcripts, respectively.

[0123] MIR-98 was amplified using EST72223 as a templet with T7miR98 forward primer: 5-"TAATACGACTCACTATAGGGTGAGGTAGTAAGTTGTATTGTT-3"and T3miR98 revse primer: 5"-AATTAACCCTCACTAAAGGGAAAGTAGTAAGTTGTATAGTT-3"EST72223 was amplified with T7-EST 72223 forward primer:5"-TAATACGACTCACTATAGGCCCTTATTAGAGGATTCTGCT-3"and T3-EST72223 reverse primer:5"-AATTAACCCTCACTAAAGGTTTTTTTTTCCTGAGACAGAGT-3" Bet-4 was amplified using EST72223 as a templet with Bet-4 forward primer: 5"-GAGGCAGGAGAATTGCTTGA- 3" and T3-EST72223 reverse primer:5"-AATTAACCCTCACTAAAGGCCTGAGACAGAGTCTTGCTC-3"The PCR products were cleaned and used for DIG-labeled or unlabeled transcription reactions with the appropriate polymerase. For transfection experiments, CAP reaction was performed by using a mMassage mMachine kit (Ambion).

[0124] Transfection procedure: Transfection of Hela cells was performed by using TransMessenger reagent (Qiagen) according to the manufacture"s protocol. Briefly, Hela cells were seeded to 1-2x 10^6 cells per plate a day before transfection. Two µg RNA transcripts were mixed with 8µl Enhancer in a final volume of 100µl, mixed and incubated at room temperature for 5 min. 16µl TransMessenger reagent was added to the RNA-Enhancer, mixed and incubated for additional 10 min. Cell plates were washed with sterile PBS twice and then incubated with the transfection mix diluted with 2.5 ml DMEM medium without serum. Cells were incubated with transfection mix for three hours under their normal growth condition (370C and 5% CO2) before the transfection mix was removed and a fresh DMEM medium containing serum was added to the cells. Cells were left to grow 48 hours before harvesting.

[0125] *Northern analysis:*RNAs were extracted from cells by using Tri-reagent according to the manufacture"s protocol. The RNAs were dissolved in water and heated to 650C to disrupt any association of the 25nt RNA with larger RNA molecules. RNA were placed on ice and incubated for 30 min with PEG (MW=8000) in a final concentration of 5% and NaCl in a final concentration of 0.5M to precipitate

high molecular weight nucleic acid. The RNAs were centrifuged at 10,000xg for 10 min to pellet the high molecular weight nucleic acid. The supernatant containing the low molecular weight RNAs was collected and three volumes of ethanol was added. The RNAs were placed at -200C for at least two hours and then centrifuged at 10,000xg for 10 min. The pellets were dissolved in Urea-TBE buffer (1Xtbe, 7M urea) for further analysis by a Northern blot.

[0126] RNA samples were boiled for 5 min before loading on 15%-8% polyacrylamide (19:1) gels containing 7M urea and 1xTBE. Gels were run in 1xTBE at a constant voltage of 300V and then transferred into a nylon membrane. The membrane was exposed to 3min ultraviolet light to cross link the RNAs to the membrane. Hybridization was performed overnight with DIG-labeled probes at 420C. Membranes were washed twice with SSCx2 and 0.2% SDS for 10 min. at 420C and then washed twice with SSCx0.5 for 5 min at room temperature. The membrane was then developed by using a DIG luminescent detection kit (Roche) using anti DIG and CSPD reaction, according to the manufacture"s protocol.

[0127] Reference is now made to Fig. 8, which is a simplified dia-

gram describing each of a plurality of novel bioinformatically detected genes of the present invention, referred to here as Genomic Address Messenger (GAM) genes, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0128] GAM is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM was detected is described hereinabove with reference to Figs. 2-8.

[0129] GAM GENE and GAM TARGET GENE are human genes contained in the human genome.

[0130] GAM GENE encodes a GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM PRECURSOR RNA does not encode a protein.

[0131] GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof. By inversed-reversed

is meant a sequence which is reversed and wherein each nucleotide is replaced by a complementary nucleotide, as is well known in the art (e.g. ATGGC is the inversed-reversed sequence of GCCAT).

[0132] An enzyme complex designated DICER COMPLEX, dices the GAM FOLDED PRECURSOR RNA into GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins.

[0133] GAM TARGET GENE encodes a corresponding messenger RNA, GAM TARGET RNA. GAM TARGET RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0134] GAM RNA binds complementarily to one or more target binding sites located in untranslated regions of GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illus-

tration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM RNA may have a different number of target binding sites in untranslated regions of a GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0135] The complementary binding of GAM RNA to target binding sites on GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM TARGET RNA into GAM TARGET PROTEIN. GAM TARGET PROTEIN is therefore outlined by a broken line.

[0136] It is appreciated that GAM TARGET GENE in fact represents a plurality of GAM target genes. The mRNA of each one of this plurality of GAM target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM RNA, and which when bound by GAM RNA causes inhibition of translation of respective one or more GAM target proteins.

[0137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM GENE on one or more GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0138] It is yet further appreciated that specific functions, and accordingly utilities, of GAM correlate with, and may be deduced from, the identity of the target genes which GAM binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0139] Nucleotide sequences of the GAM PRECURSOR RNA, and of the diced GAM RNA, and a schematic representation of the secondary folding of GAM FOLDED PRECURSOR RNA of

each of the plurality of GAM GENEs described by Fig. 8 are further described hereinbelow with reference to Table.

[0140] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM RNA are described hereinbelow with reference to Table.

[0141]

[0142] Fig. 8 further provides a conceptual description of a novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 24 (GAM24) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0143] GAM24 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM24 was detected is described hereinabove with reference to Figs. 2-8.

[0144] GAM24 gene, herein designated GAM GENE, and GAM24 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0145] GAM24 gene, herein designated GAM GENE, encodes a

GAM24 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM24 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM24 precursor RNA is designated SEQ ID:1, and is provided hereinbelow with reference to the sequence listing part.

[0146] GAM24 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM24 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0147] An enzyme complex designated DICER COMPLEX, dices the GAM24 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM24 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM24 RNA is designated SEQ ID:2, and is provided hereinbelow with reference to the sequence listing part.

[0148] GAM24 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM24 target RNA, herein designated GAM TARGET RNA. GAM24 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0149] GAM24 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM24 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM24 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM24 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM24 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0150] The complementary binding of GAM24 RNA, herein designated GAM RNA, to target binding sites on GAM24 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM24 target RNA, herein designated GAM TARGET RNA, into GAM24 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0151] It is appreciated that GAM24 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM24 target genes. The mRNA of each one of this plurality of GAM24 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM24 RNA, herein designated GAM RNA, and which when bound by GAM24 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM24 target proteins.

[0152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM24 gene, herein designated GAM GENE, on one or more GAM24 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0153] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM24 correlate with, and may be deduced from, the identity of the target genes which GAM24 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0154] Nucleotide sequences of the GAM24 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM24 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM24 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM24 are further described hereinbelow with reference to Table Table1.

[0155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM24 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0156]

[0157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 25 (GAM25) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[0158] GAM25 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM25 was detected is described hereinabove with reference to Figs. 2-8.

[0159] GAM25 gene, herein designated GAM GENE, and GAM25 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0160] GAM25 gene, herein designated GAM GENE, encodes a GAM25 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM25 precursor RNA is designated SEQ ID:11, and is provided hereinbelow with reference to the sequence listing part.

[0161] GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0162] An enzyme complex designated DICER COMPLEX, dices the GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM25 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM25 RNA is designated SEQ ID:12, and is provided hereinbelow with reference to the sequence listing part.

[0163] GAM25 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM25 target RNA, herein designated GAM TARGET RNA. GAM25 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0164] GAM25 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM25 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM25 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM25 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM25 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0165] The complementary binding of GAM25 RNA, herein designated GAM RNA, to target binding sites on GAM25 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM25 target RNA, herein designated GAM TARGET RNA, into GAM25 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0166] It is appreciated that GAM25 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM25 target genes. The mRNA of each one of this plurality of GAM25 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM25 RNA, herein designated GAM RNA, and which when bound by GAM25 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM25 target proteins.

[0167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM25 gene, herein designated GAM GENE, on one or more GAM25 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0168] It is yet further appreciated that specific functions, and accordingly utilities, of GAM25 correlate with, and may be deduced from, the identity of the target genes which GAM25 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0169] Nucleotide sequences of the GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM25 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM25 are further described hereinbelow with reference to Table Table1.

[0170] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM25 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0171]

[0172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 26 (GAM26) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0173] GAM26 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM26 was detected is described hereinabove with reference to Figs. 2-8.

[0174] GAM26 gene, herein designated GAM GENE, and GAM26 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0175] GAM26 gene, herein designated GAM GENE, encodes a GAM26 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM26 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM26 precursor RNA is designated SEQ ID:36, and is provided hereinbelow with reference to the sequence listing part.

[0176] GAM26 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM26 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0177] An enzyme complex designated DICER COMPLEX, dices the GAM26 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM26 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM26 RNA is designated SEQ ID:37, and is provided hereinbelow with

reference to the sequence listing part.

[0178] GAM26 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM26 target RNA, herein designated GAM TARGET RNA. GAM26 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0179] GAM26 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM26 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM26 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM26 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM26 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0180] The complementary binding of GAM26 RNA, herein designated GAM RNA, to target binding sites on GAM26 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM26 target RNA, herein designated GAM TARGET RNA, into GAM26 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0181] It is appreciated that GAM26 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM26 target genes. The mRNA of each one of this plurality of GAM26 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM26 RNA, herein designated GAM RNA, and which when bound by GAM26 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM26 tar-

get proteins.

[0182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM26 gene, herein designated GAM GENE, on one or more GAM26 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM26 correlate with, and may be deduced from, the identity of the target genes which GAM26 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0184] Nucleotide sequences of the GAM26 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM26 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM26 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM26 are further described hereinbelow with reference to Table Table1.

[0185] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM26 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0186]

[0187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 27 (GAM27) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0188] GAM27 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM27 was detected is described hereinabove with reference to Figs. 2-8.

[0189] GAM27 gene, herein designated GAM GENE, and GAM27 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0190] GAM27 gene, herein designated GAM GENE, encodes a GAM27 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM27 precursor RNA is designated SEQ ID:46, and is provided hereinbelow with reference to the sequence listing part.

[0191] GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0192] An enzyme complex designated DICER COMPLEX, dices

the GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM27 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM27 RNA is designated SEQ ID:47, and is provided hereinbelow with reference to the sequence listing part.

[0193] GAM27 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM27 target RNA, herein designated GAM TARGET RNA. GAM27 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0194] GAM27 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM27 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM27

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM27 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM27 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0195] The complementary binding of GAM27 RNA, herein designated GAM RNA, to target binding sites on GAM27 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM27 target RNA, herein designated GAM TARGET RNA, into GAM27 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0196] It is appreciated that GAM27 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM27 target genes. The mRNA of each one of this plurality of GAM27 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM27 RNA, herein designated GAM RNA, and which when bound by GAM27 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM27 target proteins.

[0197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM27 gene, herein designated GAM GENE, on one or more GAM27 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complemen-

tary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM27 correlate with, and may be deduced from, the identity of the target genes which GAM27 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0199] Nucleotide sequences of the GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM27 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM27 are further described hereinbelow with reference to Table Table1.

[0200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM27 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0201]

[0202] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 28 (GAM28) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0203] GAM28 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM28 was detected is described hereinabove with reference to Figs. 2-8.

[0204] GAM28 gene, herein designated GAM GENE, and GAM28 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0205] GAM28 gene, herein designated GAM GENE, encodes a GAM28 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM28 precursor RNA is designated SEQ ID:54, and is provided hereinbelow with reference to the sequence listing part.

[0206] GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM28 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0207] An enzyme complex designated DICER COMPLEX, dices the GAM28 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM28 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM28 RNA is designated SEQ ID:55, and is provided hereinbelow with reference to the sequence listing part.

[0208] GAM28 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM28 target RNA, herein designated GAM TARGET RNA. GAM28 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0209] GAM28 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM28 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM28 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM28 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM28 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[0210] The complementary binding of GAM28 RNA, herein designated GAM RNA, to target binding sites on GAM28 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM28 target RNA, herein designated GAM TARGET RNA, into GAM28 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0211] It is appreciated that GAM28 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM28 target genes. The mRNA of each one of this plurality of GAM28 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM28 RNA, herein designated GAM RNA, and which when bound by GAM28 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM28 target proteins.

[0212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM28 gene, herein designated GAM GENE, on one or

more GAM28 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0213] It is yet further appreciated that specific functions, and accordingly utilities, of GAM28 correlate with, and may be deduced from, the identity of the target genes which GAM28 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0214] Nucleotide sequences of the GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM28 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM28 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM28 are further described

hereinbelow with reference to Table Table1.

[0215] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM28 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0216]

[0217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 29 (GAM29) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0218] GAM29 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM29 was detected is described hereinabove with reference to Figs. 2-8.

[0219] GAM29 gene, herein designated GAM GENE, and GAM29 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0220] GAM29 gene, herein designated GAM GENE, encodes a GAM29 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM29 precursor RNA is designated SEQ ID:67, and is provided hereinbelow with reference to the sequence listing part.

[0221] GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0222] An enzyme complex designated DICER COMPLEX, dices the GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM29 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM29 RNA is designated SEQ ID:68, and is provided hereinbelow with reference to the sequence listing part.

[0223] GAM29 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM29 target RNA, herein designated GAM TARGET RNA. GAM29 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0224] GAM29 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM29 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM29 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM29 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM29 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0225] The complementary binding of GAM29 RNA, herein designated GAM RNA, to target binding sites on GAM29 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM29 target RNA, herein designated GAM TARGET RNA, into GAM29 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0226] It is appreciated that GAM29 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM29 target genes. The mRNA of each one of this plurality of GAM29 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM29 RNA, herein designated GAM RNA, and which when bound by GAM29 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM29 target proteins.

[0227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM29 gene, herein designated GAM GENE, on one or more GAM29 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0228] It is yet further appreciated that specific functions, and accordingly utilities, of GAM29 correlate with, and may be

deduced from, the identity of the target genes which GAM29 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0229] Nucleotide sequences of the GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM29 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM29 are further described hereinbelow with reference to Table Table1.

[0230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM29 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0231]

[0232] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 30 (GAM30) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0233] GAM30 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM30 was detected is described hereinabove with reference to Figs. 2-8.

[0234] GAM30 gene, herein designated GAM GENE, and GAM30 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0235] GAM30 gene, herein designated GAM GENE, encodes a GAM30 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM30 precursor RNA is designated SEQ ID:97, and is provided hereinbelow with reference to the sequence listing part.

[0236] GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0237] An enzyme complex designated DICER COMPLEX, dices the GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM30 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM30 RNA is designated SEQ ID:98, and is provided hereinbelow with reference to the sequence listing part.

[0238] GAM30 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM30 target RNA, herein designated GAM TARGET RNA. GAM30 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0239] GAM30 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM30 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM30 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM30 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM30 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0240] The complementary binding of GAM30 RNA, herein designated GAM RNA, to target binding sites on GAM30 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM30 target RNA, herein designated GAM TARGET RNA, into GAM30 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0241] It is appreciated that GAM30 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM30 target genes. The mRNA of each one of this plurality of GAM30 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM30 RNA, herein designated GAM RNA, and which when bound by GAM30 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM30 target proteins.

[0242] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM30 gene, herein designated GAM GENE, on one or more GAM30 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0243] It is yet further appreciated that specific functions, and accordingly utilities, of GAM30 correlate with, and may be deduced from, the identity of the target genes which GAM30 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0244] Nucleotide sequences of the GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM30 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM30 are further described hereinbelow with reference to Table Table1.

[0245] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM30 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0246]

[0247] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 31 (GAM31) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0248] GAM31 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM31 was detected is described hereinabove with reference to Figs. 2-8.

[0249] GAM31 gene, herein designated GAM GENE, and GAM31 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0250] GAM31 gene, herein designated GAM GENE, encodes a GAM31 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM31 precursor RNA is designated

SEQ ID:119, and is provided hereinbelow with reference to the sequence listing part.

[0251] GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0252] An enzyme complex designated DICER COMPLEX, dices the GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM31 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM31 RNA is designated SEQ ID:120, and is provided hereinbelow with reference to the sequence listing part.

[0253] GAM31 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM31 target RNA, herein designated GAM TARGET RNA. GAM31 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0254] GAM31 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM31 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM31 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM31 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM31 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0255] The complementary binding of GAM31 RNA, herein designated GAM RNA, to target binding sites on GAM31 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM31 target RNA, herein designated GAM TARGET RNA, into GAM31 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0256] It is appreciated that GAM31 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM31 target genes. The mRNA of each one of this plurality of GAM31 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM31 RNA, herein designated GAM RNA, and which when bound by GAM31 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM31 target proteins.

[0257] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM31 gene, herein designated GAM GENE, on one or more GAM31 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0258] It is yet further appreciated that specific functions, and accordingly utilities, of GAM31 correlate with, and may be deduced from, the identity of the target genes which GAM31 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0259] Nucleotide sequences of the GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM31 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM31 are further described hereinbelow with reference to Table Table1.

[0260] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM31 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0261]

[0262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 32 (GAM32) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0263] GAM32 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM32 was detected is described hereinabove with reference to Figs. 2-8.

[0264] GAM32 gene, herein designated GAM GENE, and GAM32

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0265] GAM32 gene, herein designated GAM GENE, encodes a GAM32 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM32 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM32 precursor RNA is designated SEQ ID:134, and is provided hereinbelow with reference to the sequence listing part.

[0266] GAM32 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM32 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0267] An enzyme complex designated DICER COMPLEX, dices the GAM32 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM32 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM32 RNA is designated SEQ ID:135, and is provided hereinbelow with reference to the sequence listing part.

[0268] GAM32 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM32 target RNA, herein designated GAM TARGET RNA. GAM32 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0269] GAM32 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM32 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM32 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM32 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM32 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0270] The complementary binding of GAM32 RNA, herein designated GAM RNA, to target binding sites on GAM32 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM32 target RNA, herein designated GAM TARGET RNA, into GAM32 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0271] It is appreciated that GAM32 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM32 target genes. The mRNA of each one of this plurality of GAM32 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM32 RNA, herein designated GAM RNA, and which when bound by GAM32 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM32 target proteins.

[0272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM32 gene, herein designated GAM GENE, on one or more GAM32 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM32 correlate with, and may be deduced from, the identity of the target genes which GAM32 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0274] Nucleotide sequences of the GAM32 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM32 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM32 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM32 are further described hereinbelow with reference to Table Table1.

[0275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM32 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0276]

[0277] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 33 (GAM33) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0278] GAM33 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM33 was detected is described hereinabove with reference to Figs. 2-8.

[0279] GAM33 gene, herein designated GAM GENE, and GAM33 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0280] GAM33 gene, herein designated GAM GENE, encodes a GAM33 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM33 precursor RNA is designated SEQ ID:160, and is provided hereinbelow with reference to the sequence listing part.

[0281] GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM33 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0282] An enzyme complex designated DICER COMPLEX, dices the GAM33 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM33 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM33 RNA is designated SEQ ID:161, and is provided hereinbelow with reference to the sequence listing part.

[0283] GAM33 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM33 target RNA, herein designated GAM TARGET RNA. GAM33 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein

coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0284] GAM33 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM33 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM33 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM33 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM33 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0285] The complementary binding of GAM33 RNA, herein designated GAM RNA, to target binding sites on GAM33 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM33 target RNA, herein designated GAM TARGET RNA, into GAM33 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0286] It is appreciated that GAM33 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM33 target genes. The mRNA of each one of this plurality of GAM33 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM33 RNA, herein designated GAM RNA, and which when bound by GAM33 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM33 target proteins.

[0287] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM33 gene, herein designated GAM GENE, on one or more GAM33 target gene, herein designated GAM TARGET

GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0288] It is yet further appreciated that specific functions, and accordingly utilities, of GAM33 correlate with, and may be deduced from, the identity of the target genes which GAM33 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0289] Nucleotide sequences of the GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM33 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM33 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM33 are further described hereinbelow with reference to Table Table1.

[0290] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM33 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0291]

[0292] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 34 (GAM34) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0293] GAM34 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM34 was detected is described hereinabove with reference to Figs. 2-8.

[0294] GAM34 gene, herein designated GAM GENE, and GAM34 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0295] GAM34 gene, herein designated GAM GENE, encodes a GAM34 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM34 precursor RNA is designated SEQ ID:177, and is provided hereinbelow with reference to the sequence listing part.

[0296] GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0297] An enzyme complex designated DICER COMPLEX, dices the GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM34 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM34 RNA is designated SEQ ID:178, and is provided hereinbelow with reference to the sequence listing part.

[0298] GAM34 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM34 target RNA, herein designated GAM TARGET RNA. GAM34 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0299] GAM34 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM34 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM34 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM34 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM34 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0300] The complementary binding of GAM34 RNA, herein designated GAM RNA, to target binding sites on GAM34 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM34 target RNA, herein designated GAM TARGET RNA, into GAM34 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0301] It is appreciated that GAM34 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM34 target genes. The mRNA of each one of this plurality of GAM34 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM34 RNA,

herein designated GAM RNA, and which when bound by GAM34 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM34 target proteins.

[0302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM34 gene, herein designated GAM GENE, on one or more GAM34 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0303] It is yet further appreciated that specific functions, and accordingly utilities, of GAM34 correlate with, and may be deduced from, the identity of the target genes which

GAM34 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0304] Nucleotide sequences of the GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM34 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM34 are further described hereinbelow with reference to Table Table1.

[0305] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM34 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0306]

[0307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 35 (GAM35) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0308] GAM35 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM35 was detected is described hereinabove with reference to Figs. 2-8.

[0309] GAM35 gene, herein designated GAM GENE, and GAM35 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0310] GAM35 gene, herein designated GAM GENE, encodes a GAM35 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM35 precursor RNA is designated SEQ ID:188, and is provided hereinbelow with reference to the sequence listing part.

[0311] GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[0312] An enzyme complex designated DICER COMPLEX, dices the GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM35 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 27%) nucleotide sequence of GAM35 RNA is designated SEQ ID:189, and is provided hereinbelow with reference to the sequence listing part.

[0313] GAM35 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM35 target RNA, herein designated GAM TARGET RNA. GAM35 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0314] GAM35 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM35 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM35 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM35 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM35 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0315] The complementary binding of GAM35 RNA, herein designated GAM RNA, to target binding sites on GAM35 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM35 target RNA, herein designated GAM

TARGET RNA, into GAM35 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0316] It is appreciated that GAM35 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM35 target genes. The mRNA of each one of this plurality of GAM35 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM35 RNA, herein designated GAM RNA, and which when bound by GAM35 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM35 target proteins.

[0317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM35 gene, herein designated GAM GENE, on one or more GAM35 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM35 correlate with, and may be deduced from, the identity of the target genes which GAM35 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0319] Nucleotide sequences of the GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM35 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM35 are further described hereinbelow with reference to Table Table1.

[0320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM35 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[0321]

[0322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 36 (GAM36) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0323] GAM36 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM36 was detected is described hereinabove with reference to Figs. 2-8.

[0324] GAM36 gene, herein designated GAM GENE, and GAM36 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0325] GAM36 gene, herein designated GAM GENE, encodes a GAM36 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM36 precursor RNA is designated SEQ ID:208, and is provided hereinbelow with reference to

the sequence listing part.

[0326] GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0327] An enzyme complex designated DICER COMPLEX, dices the GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM36 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 39%) nucleotide sequence of GAM36 RNA is designated SEQ ID:209, and is provided hereinbelow with reference to the sequence listing part.

[0328] GAM36 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM36 target RNA, herein designated GAM TARGET RNA. GAM36 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0329] GAM36 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM36 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM36 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM36 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM36 target RNA, herein designated GAM TARGET RNA. It is further

appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0330] The complementary binding of GAM36 RNA, herein designated GAM RNA, to target binding sites on GAM36 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM36 target RNA, herein designated GAM TARGET RNA, into GAM36 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0331] It is appreciated that GAM36 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM36 target genes. The mRNA of each one of this plurality of GAM36 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM36 RNA, herein designated GAM RNA, and which when bound by GAM36 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM36 target proteins.

[0332] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM36 gene, herein designated GAM GENE, on one or more GAM36 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM36 correlate with, and may be deduced from, the identity of the target genes which GAM36 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0334] Nucleotide sequences of the GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM36 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM36 are further described hereinbelow with reference to Table Table1.

[0335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM36 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0336]

[0337] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 37 (GAM37) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0338] GAM37 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM37 was detected is described hereinabove with reference to Figs. 2-8.

[0339] GAM37 gene, herein designated GAM GENE, and GAM37 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[0340] GAM37 gene, herein designated GAM GENE, encodes a GAM37 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM37 precursor RNA is designated SEQ ID:214, and is provided hereinbelow with reference to the sequence listing part.

[0341] GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0342] An enzyme complex designated DICER COMPLEX, dices the GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM37 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM37 RNA is designated SEQ ID:215, and is provided hereinbelow with reference to the sequence listing part.

[0343] GAM37 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM37 target RNA, herein designated GAM TARGET RNA. GAM37 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0344] GAM37 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM37 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM37 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM37 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM37 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0345] The complementary binding of GAM37 RNA, herein designated GAM RNA, to target binding sites on GAM37 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM37 target RNA, herein designated GAM TARGET RNA, into GAM37 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0346] It is appreciated that GAM37 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM37 target genes. The mRNA of each one of this plurality of GAM37 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM37 RNA, herein designated GAM RNA, and which when bound by GAM37 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM37 target proteins.

[0347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM37 gene, herein designated GAM GENE, on one or more GAM37 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[0348] It is yet further appreciated that specific functions, and accordingly utilities, of GAM37 correlate with, and may be deduced from, the identity of the target genes which GAM37 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0349] Nucleotide sequences of the GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM37 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM37 are further described hereinbelow with reference to Table Table1.

[0350] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM37 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0351]

[0352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

38 (GAM38) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0353] GAM38 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM38 was detected is described hereinabove with reference to Figs. 2-8.

[0354] GAM38 gene, herein designated GAM GENE, and GAM38 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0355] GAM38 gene, herein designated GAM GENE, encodes a GAM38 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM38 precursor RNA is designated SEQ ID:235, and is provided hereinbelow with reference to the sequence listing part.

[0356] GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0357] An enzyme complex designated DICER COMPLEX, dices the GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM38 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM38 RNA is designated SEQ ID:236, and is provided hereinbelow with reference to the sequence listing part.

[0358] GAM38 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM38 target RNA, herein designated GAM TARGET RNA. GAM38 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0359] GAM38 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM38 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM38 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM38 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM38 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0360] The complementary binding of GAM38 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM38 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM38 target RNA, herein designated GAM TARGET RNA, into GAM38 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0361] It is appreciated that GAM38 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM38 target genes. The mRNA of each one of this plurality of GAM38 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM38 RNA, herein designated GAM RNA, and which when bound by GAM38 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM38 target proteins.

[0362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM38 gene, herein designated GAM GENE, on one or more GAM38 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM38 correlate with, and may be deduced from, the identity of the target genes which GAM38 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0364] Nucleotide sequences of the GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM38 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM38 are further described hereinbelow with reference to Table Table1.

[0365] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM38 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0366]

[0367] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 39 (GAM39) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0368] GAM39 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM39 was detected is described hereinabove with reference to Figs. 2-8.

[0369] GAM39 gene, herein designated GAM GENE, and GAM39 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0370] GAM39 gene, herein designated GAM GENE, encodes a GAM39 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM39 precursor RNA, herein designated

GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM39 precursor RNA is designated SEQ ID:245, and is provided hereinbelow with reference to the sequence listing part.

[0371] GAM39 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0372] An enzyme complex designated DICER COMPLEX, dices the GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM39 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A

probable (over 64%) nucleotide sequence of GAM39 RNA is designated SEQ ID:246, and is provided hereinbelow with reference to the sequence listing part.

[0373] GAM39 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM39 target RNA, herein designated GAM TARGET RNA. GAM39 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0374] GAM39 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM39 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM39 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM39 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM39 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0375] The complementary binding of GAM39 RNA, herein designated GAM RNA, to target binding sites on GAM39 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM39 target RNA, herein designated GAM TARGET RNA, into GAM39 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0376] It is appreciated that GAM39 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM39 target genes. The mRNA of each one of this plurality of GAM39 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM39 RNA, herein designated GAM RNA, and which when bound by

GAM39 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM39 target proteins.

[0377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM39 gene, herein designated GAM GENE, on one or more GAM39 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0378] It is yet further appreciated that specific functions, and accordingly utilities, of GAM39 correlate with, and may be deduced from, the identity of the target genes which GAM39 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[0379] Nucleotide sequences of the GAM39 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM39 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM39 are further described hereinbelow with reference to Table Table1.

[0380] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM39 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0381]

[0382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 40 (GAM40) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0383] GAM40 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM40 was detected is described hereinabove with reference to Figs. 2-8.

[0384] GAM40 gene, herein designated GAM GENE, and GAM40 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0385] GAM40 gene, herein designated GAM GENE, encodes a GAM40 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM40 precursor RNA is designated SEQ ID:259, and is provided hereinbelow with reference to the sequence listing part.

[0386] GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[0387] An enzyme complex designated DICER COMPLEX, dices the GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM40 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM40 RNA is designated SEQ ID:260, and is provided hereinbelow with reference to the sequence listing part.

[0388] GAM40 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM40 target RNA, herein designated GAM TARGET RNA. GAM40 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0389] GAM40 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM40 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM40 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM40 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM40 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0390] The complementary binding of GAM40 RNA, herein designated GAM RNA, to target binding sites on GAM40 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM40 target RNA, herein designated GAM TARGET RNA, into GAM40 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0391] It is appreciated that GAM40 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM40 target genes. The mRNA of each one of this plurality of GAM40 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM40 RNA, herein designated GAM RNA, and which when bound by GAM40 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM40 target proteins.

[0392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM40 gene, herein designated GAM GENE, on one or more GAM40 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM40 correlate with, and may be deduced from, the identity of the target genes which GAM40 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0394] Nucleotide sequences of the GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM40 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM40 are further described hereinbelow with reference to Table Table1.

[0395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM40 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0396]

[0397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 41 (GAM41) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0398] GAM41 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM41 was detected is described hereinabove with reference to Figs. 2-8.

[0399] GAM41 gene, herein designated GAM GENE, and GAM41 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0400] GAM41 gene, herein designated GAM GENE, encodes a GAM41 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM41 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM41 precursor RNA is designated SEQ ID:263, and is provided hereinbelow with reference to the sequence listing part.

[0401] GAM41 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0402] An enzyme complex designated DICER COMPLEX, dices the GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM41 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM41 RNA is designated SEQ ID:264, and is provided hereinbelow with reference to the sequence listing part.

[0403] GAM41 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM41

target RNA, herein designated GAM TARGET RNA. GAM41 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0404] GAM41 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM41 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM41 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM41 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM41 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites

in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0405] The complementary binding of GAM41 RNA, herein designated GAM RNA, to target binding sites on GAM41 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM41 target RNA, herein designated GAM TARGET RNA, into GAM41 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0406] It is appreciated that GAM41 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM41 target genes. The mRNA of each one of this plurality of GAM41 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM41 RNA, herein designated GAM RNA, and which when bound by GAM41 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM41 target proteins.

[0407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM41 gene, herein designated GAM GENE, on one or more GAM41 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM41 correlate with, and may be deduced from, the identity of the target genes which GAM41 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0409] Nucleotide sequences of the GAM41 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM41 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM41 are further described hereinbelow with reference to Table Table1.

[0410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM41 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0411]

[0412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 42 (GAM42) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0413] GAM42 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM42 was detected is described hereinabove with reference to Figs. 2-8.

[0414] GAM42 gene, herein designated GAM GENE, and GAM42 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0415] GAM42 gene, herein designated GAM GENE, encodes a GAM42 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM42 precursor RNA is designated SEQ ID:283, and is provided hereinbelow with reference to the sequence listing part.

[0416] GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0417] An enzyme complex designated DICER COMPLEX, dices the GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM42 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM42 RNA is designated SEQ ID:284, and is provided hereinbelow with reference to the sequence listing part.

[0418] GAM42 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM42 target RNA, herein designated GAM TARGET RNA. GAM42 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0419] GAM42 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM42 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM42 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM42 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM42 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0420] The complementary binding of GAM42 RNA, herein designated GAM RNA, to target binding sites on GAM42 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM42 target RNA, herein designated GAM TARGET RNA, into GAM42 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0421] It is appreciated that GAM42 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM42 target genes. The mRNA of each one of this plu-

rality of GAM42 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM42 RNA, herein designated GAM RNA, and which when bound by GAM42 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM42 target proteins.

[0422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM42 gene, herein designated GAM GENE, on one or more GAM42 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM42 correlate with, and may be deduced from, the identity of the target genes which GAM42 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0424] Nucleotide sequences of the GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM42 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM42 are further described hereinbelow with reference to Table Table1.

[0425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM42 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0426]

[0427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 43 (GAM43) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[0428] GAM43 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM43 was detected is described hereinabove with reference to Figs. 2-8.

[0429] GAM43 gene, herein designated GAM GENE, and GAM43 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0430] GAM43 gene, herein designated GAM GENE, encodes a GAM43 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM43 precursor RNA is designated SEQ ID:300, and is provided hereinbelow with reference to the sequence listing part.

[0431] GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0432] An enzyme complex designated DICER COMPLEX, dices the GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM43 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM43 RNA is designated SEQ ID:301, and is provided hereinbelow with reference to the sequence listing part.

[0433] GAM43 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM43 target RNA, herein designated GAM TARGET RNA. GAM43 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[0434] GAM43 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM43 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM43 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM43 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM43 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0435] The complementary binding of GAM43 RNA, herein designated GAM RNA, to target binding sites on GAM43 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM43 target RNA, herein designated GAM TARGET RNA, into GAM43 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0436] It is appreciated that GAM43 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM43 target genes. The mRNA of each one of this plurality of GAM43 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM43 RNA, herein designated GAM RNA, and which when bound by GAM43 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM43 target proteins.

[0437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM43 gene, herein designated GAM GENE, on one or more GAM43 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM43 correlate with, and may be deduced from, the identity of the target genes which GAM43 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0439] Nucleotide sequences of the GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM43 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM43 are further described hereinbelow with reference to Table Table1.

[0440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM43 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0441]

[0442] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 44 (GAM44) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0443] GAM44 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM44 was detected is described hereinabove with reference to Figs. 2-8.

[0444] GAM44 gene, herein designated GAM GENE, and GAM44 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0445] GAM44 gene, herein designated GAM GENE, encodes a GAM44 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM44 precursor RNA is designated SEQ ID:309, and is provided hereinbelow with reference to the sequence listing part.

[0446] GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0447] An enzyme complex designated DICER COMPLEX, dices the GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM44 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM44 RNA is

designated SEQ ID:310, and is provided hereinbelow with reference to the sequence listing part.

[0448] GAM44 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM44 target RNA, herein designated GAM TARGET RNA. GAM44 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0449] GAM44 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM44 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM44 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM44 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM44 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0450] The complementary binding of GAM44 RNA, herein designated GAM RNA, to target binding sites on GAM44 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM44 target RNA, herein designated GAM TARGET RNA, into GAM44 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0451] It is appreciated that GAM44 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM44 target genes. The mRNA of each one of this plurality of GAM44 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM44 RNA, herein designated GAM RNA, and which when bound by GAM44 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM44 target proteins.

[0452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM44 gene, herein designated GAM GENE, on one or more GAM44 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0453] It is yet further appreciated that specific functions, and accordingly utilities, of GAM44 correlate with, and may be deduced from, the identity of the target genes which GAM44 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0454] Nucleotide sequences of the GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM44 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM44 are further described hereinbelow with reference to Table Table1.

[0455] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM44 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0456]

[0457] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 45 (GAM45) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0458] GAM45 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM45 was detected is described hereinabove

with reference to Figs. 2-8.

[0459] GAM45 gene, herein designated GAM GENE, and GAM45 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0460] GAM45 gene, herein designated GAM GENE, encodes a GAM45 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM45 precursor RNA is designated SEQ ID:337, and is provided hereinbelow with reference to the sequence listing part.

[0461] GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0462] An enzyme complex designated DICER COMPLEX, dices the GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM45 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 17%) nucleotide sequence of GAM45 RNA is designated SEQ ID:338, and is provided hereinbelow with reference to the sequence listing part.

[0463] GAM45 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM45 target RNA, herein designated GAM TARGET RNA. GAM45 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0464] GAM45 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM45 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM45 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM45 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM45 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0465] The complementary binding of GAM45 RNA, herein designated GAM RNA, to target binding sites on GAM45 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM45 target RNA, herein designated GAM TARGET RNA, into GAM45 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[0466] It is appreciated that GAM45 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM45 target genes. The mRNA of each one of this plurality of GAM45 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM45 RNA, herein designated GAM RNA, and which when bound by GAM45 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM45 target proteins.

[0467] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM45 gene, herein designated GAM GENE, on one or more GAM45 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0468] It is yet further appreciated that specific functions, and accordingly utilities, of GAM45 correlate with, and may be deduced from, the identity of the target genes which GAM45 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0469] Nucleotide sequences of the GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM45 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM45 are further described hereinbelow with reference to Table Table1.

[0470] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM45 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0471]

[0472] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 46 (GAM46) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0473] GAM46 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM46 was detected is described hereinabove with reference to Figs. 2-8.

[0474] GAM46 gene, herein designated GAM GENE, and GAM46 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0475] GAM46 gene, herein designated GAM GENE, encodes a GAM46 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM46 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM46 precursor RNA is designated SEQ ID:365, and is provided hereinbelow with reference to the sequence listing part.

[0476] GAM46 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM46 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0477] An enzyme complex designated DICER COMPLEX, dices the GAM46 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM46 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM46 RNA is designated SEQ ID:366, and is provided hereinbelow with reference to the sequence listing part.

[0478] GAM46 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM46 target RNA, herein designated GAM TARGET RNA. GAM46

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0479] GAM46 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM46 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM46 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM46 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM46 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0480] The complementary binding of GAM46 RNA, herein designated GAM RNA, to target binding sites on GAM46 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM46 target RNA, herein designated GAM TARGET RNA, into GAM46 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0481] It is appreciated that GAM46 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM46 target genes. The mRNA of each one of this plurality of GAM46 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM46 RNA, herein designated GAM RNA, and which when bound by GAM46 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM46 target proteins.

[0482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM46 gene, herein designated GAM GENE, on one or more GAM46 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0483] It is yet further appreciated that specific functions, and accordingly utilities, of GAM46 correlate with, and may be deduced from, the identity of the target genes which GAM46 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0484] Nucleotide sequences of the GAM46 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM46 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM46 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM46 are further described hereinbelow with reference to Table Table1.

[0485] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM46 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0486]

[0487] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 47 (GAM47) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0488] GAM47 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM47 was detected is described hereinabove with reference to Figs. 2-8.

[0489] GAM47 gene, herein designated GAM GENE, and GAM47 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0490] GAM47 gene, herein designated GAM GENE, encodes a

GAM47 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM47 precursor RNA is designated SEQ ID:387, and is provided hereinbelow with reference to the sequence listing part.

[0491] GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0492] An enzyme complex designated DICER COMPLEX, dices the GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM47 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of GAM47 RNA is designated SEQ ID:388, and is provided hereinbelow with reference to the sequence listing part.

[0493] GAM47 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM47 target RNA, herein designated GAM TARGET RNA. GAM47 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0494] GAM47 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM47 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM47 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM47 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM47 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0495] The complementary binding of GAM47 RNA, herein designated GAM RNA, to target binding sites on GAM47 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM47 target RNA, herein designated GAM TARGET RNA, into GAM47 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0496] It is appreciated that GAM47 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM47 target genes. The mRNA of each one of this plurality of GAM47 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM47 RNA, herein designated GAM RNA, and which when bound by GAM47 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM47 target proteins.

[0497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM47 gene, herein designated GAM GENE, on one or more GAM47 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0498] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM47 correlate with, and may be deduced from, the identity of the target genes which GAM47 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0499] Nucleotide sequences of the GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM47 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM47 are further described hereinbelow with reference to Table Table1.

[0500] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM47 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0501]

[0502] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 48 (GAM48) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[0503] GAM48 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM48 was detected is described hereinabove with reference to Figs. 2-8.

[0504] GAM48 gene, herein designated GAM GENE, and GAM48 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0505] GAM48 gene, herein designated GAM GENE, encodes a GAM48 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM48 precursor RNA is designated SEQ ID:422, and is provided hereinbelow with reference to the sequence listing part.

[0506] GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0507] An enzyme complex designated DICER COMPLEX, dices the GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM48 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM48 RNA is designated SEQ ID:423, and is provided hereinbelow with reference to the sequence listing part.

[0508] GAM48 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM48 target RNA, herein designated GAM TARGET RNA. GAM48 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0509] GAM48 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM48 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM48 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM48 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM48 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0510] The complementary binding of GAM48 RNA, herein designated GAM RNA, to target binding sites on GAM48 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM48 target RNA, herein designated GAM TARGET RNA, into GAM48 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0511] It is appreciated that GAM48 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM48 target genes. The mRNA of each one of this plurality of GAM48 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM48 RNA, herein designated GAM RNA, and which when bound by GAM48 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM48 target proteins.

[0512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM48 gene, herein designated GAM GENE, on one or more GAM48 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0513] It is yet further appreciated that specific functions, and accordingly utilities, of GAM48 correlate with, and may be deduced from, the identity of the target genes which GAM48 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0514] Nucleotide sequences of the GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM48 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM48 are further described hereinbelow with reference to Table Table1.

[0515] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM48 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0516]

[0517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 49 (GAM49) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0518] GAM49 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM49 was detected is described hereinabove with reference to Figs. 2-8.

[0519] GAM49 gene, herein designated GAM GENE, and GAM49 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0520] GAM49 gene, herein designated GAM GENE, encodes a GAM49 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM49 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM49 precursor RNA is designated SEQ ID:429, and is provided hereinbelow with reference to the sequence listing part.

[0521] GAM49 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0522] An enzyme complex designated DICER COMPLEX, dices the GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM49 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM49 RNA is designated SEQ ID:430, and is provided hereinbelow with

reference to the sequence listing part.

[0523] GAM49 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM49 target RNA, herein designated GAM TARGET RNA. GAM49 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0524] GAM49 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM49 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM49 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM49 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM49 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0525] The complementary binding of GAM49 RNA, herein designated GAM RNA, to target binding sites on GAM49 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM49 target RNA, herein designated GAM TARGET RNA, into GAM49 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0526] It is appreciated that GAM49 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM49 target genes. The mRNA of each one of this plurality of GAM49 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM49 RNA, herein designated GAM RNA, and which when bound by GAM49 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM49 tar-

get proteins.

[0527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM49 gene, herein designated GAM GENE, on one or more GAM49 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0528] It is yet further appreciated that specific functions, and accordingly utilities, of GAM49 correlate with, and may be deduced from, the identity of the target genes which GAM49 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0529] Nucleotide sequences of the GAM49 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM49 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM49 are further described hereinbelow with reference to Table Table1.

[0530] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM49 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0531]

[0532] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 50 (GAM50) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0533] GAM50 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM50 was detected is described hereinabove with reference to Figs. 2-8.

[0534] GAM50 gene, herein designated GAM GENE, and GAM50 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0535] GAM50 gene, herein designated GAM GENE, encodes a GAM50 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM50 precursor RNA is designated SEQ ID:453, and is provided hereinbelow with reference to the sequence listing part.

[0536] GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0537] An enzyme complex designated DICER COMPLEX, dices

the GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM50 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM50 RNA is designated SEQ ID:454, and is provided hereinbelow with reference to the sequence listing part.

[0538] GAM50 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM50 target RNA, herein designated GAM TARGET RNA. GAM50 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0539] GAM50 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM50 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM50

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM50 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM50 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0540] The complementary binding of GAM50 RNA, herein designated GAM RNA, to target binding sites on GAM50 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM50 target RNA, herein designated GAM TARGET RNA, into GAM50 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0541] It is appreciated that GAM50 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM50 target genes. The mRNA of each one of this plurality of GAM50 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM50 RNA, herein designated GAM RNA, and which when bound by GAM50 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM50 target proteins.

[0542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM50 gene, herein designated GAM GENE, on one or more GAM50 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complemen-

tary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0543] It is yet further appreciated that specific functions, and accordingly utilities, of GAM50 correlate with, and may be deduced from, the identity of the target genes which GAM50 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0544] Nucleotide sequences of the GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM50 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM50 are further described hereinbelow with reference to Table Table1.

[0545] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM50 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0546]

[0547] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 51 (GAM51) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0548] GAM51 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM51 was detected is described hereinabove with reference to Figs. 2-8.

[0549] GAM51 gene, herein designated GAM GENE, and GAM51 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0550] GAM51 gene, herein designated GAM GENE, encodes a GAM51 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM51 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM51 precursor RNA is designated SEQ ID:459, and is provided hereinbelow with reference to the sequence listing part.

[0551] GAM51 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM51 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0552] An enzyme complex designated DICER COMPLEX, dices the GAM51 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM51 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 26%) nucleotide sequence of GAM51 RNA is designated SEQ ID:460, and is provided hereinbelow with reference to the sequence listing part.

[0553] GAM51 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM51 target RNA, herein designated GAM TARGET RNA. GAM51 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0554] GAM51 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM51 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM51 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM51 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM51 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[0555] The complementary binding of GAM51 RNA, herein designated GAM RNA, to target binding sites on GAM51 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM51 target RNA, herein designated GAM TARGET RNA, into GAM51 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0556] It is appreciated that GAM51 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM51 target genes. The mRNA of each one of this plurality of GAM51 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM51 RNA, herein designated GAM RNA, and which when bound by GAM51 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM51 target proteins.

[0557] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM51 gene, herein designated GAM GENE, on one or

more GAM51 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0558] It is yet further appreciated that specific functions, and accordingly utilities, of GAM51 correlate with, and may be deduced from, the identity of the target genes which GAM51 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0559] Nucleotide sequences of the GAM51 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM51 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM51 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM51 are further described

hereinbelow with reference to Table Table1.

[0560] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM51 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0561]

[0562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 52 (GAM52) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0563] GAM52 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM52 was detected is described hereinabove with reference to Figs. 2-8.

[0564] GAM52 gene, herein designated GAM GENE, and GAM52 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0565] GAM52 gene, herein designated GAM GENE, encodes a GAM52 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM52 precursor RNA is designated SEQ ID:480, and is provided hereinbelow with reference to the sequence listing part.

[0566] GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM52 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0567] An enzyme complex designated DICER COMPLEX, dices the GAM52 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM52 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of GAM52 RNA is designated SEQ ID:481, and is provided hereinbelow with reference to the sequence listing part.

[0568] GAM52 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM52 target RNA, herein designated GAM TARGET RNA. GAM52 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0569] GAM52 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM52 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM52 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM52 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM52 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0570] The complementary binding of GAM52 RNA, herein designated GAM RNA, to target binding sites on GAM52 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM52 target RNA, herein designated GAM TARGET RNA, into GAM52 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0571] It is appreciated that GAM52 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM52 target genes. The mRNA of each one of this plurality of GAM52 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM52 RNA, herein designated GAM RNA, and which when bound by GAM52 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM52 target proteins.

[0572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM52 gene, herein designated GAM GENE, on one or more GAM52 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM52 correlate with, and may be

deduced from, the identity of the target genes which GAM52 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0574] Nucleotide sequences of the GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM52 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM52 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM52 are further described hereinbelow with reference to Table Table1.

[0575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM52 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0576]

[0577] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 53 (GAM53) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0578] GAM53 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM53 was detected is described hereinabove with reference to Figs. 2-8.

[0579] GAM53 gene, herein designated GAM GENE, and GAM53 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0580] GAM53 gene, herein designated GAM GENE, encodes a GAM53 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM53 precursor RNA is designated SEQ ID:522, and is provided hereinbelow with reference to the sequence listing part.

[0581] GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM53 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0582] An enzyme complex designated DICER COMPLEX, dices the GAM53 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM53 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM53 RNA is designated SEQ ID:523, and is provided hereinbelow with reference to the sequence listing part.

[0583] GAM53 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM53 target RNA, herein designated GAM TARGET RNA. GAM53 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0584] GAM53 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM53 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM53 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM53 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM53 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0585] The complementary binding of GAM53 RNA, herein designated GAM RNA, to target binding sites on GAM53 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM53 target RNA, herein designated GAM TARGET RNA, into GAM53 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0586] It is appreciated that GAM53 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM53 target genes. The mRNA of each one of this plurality of GAM53 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM53 RNA, herein designated GAM RNA, and which when bound by GAM53 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM53 target proteins.

[0587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM53 gene, herein designated GAM GENE, on one or more GAM53 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0588] It is yet further appreciated that specific functions, and accordingly utilities, of GAM53 correlate with, and may be deduced from, the identity of the target genes which GAM53 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0589] Nucleotide sequences of the GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM53 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM53 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM53 are further described hereinbelow with reference to Table Table1.

[0590] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM53 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0591]

[0592] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 54 (GAM54) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0593] GAM54 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM54 was detected is described hereinabove with reference to Figs. 2-8.

[0594] GAM54 gene, herein designated GAM GENE, and GAM54 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0595] GAM54 gene, herein designated GAM GENE, encodes a GAM54 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM54 precursor RNA is designated

SEQ ID:531, and is provided hereinbelow with reference to the sequence listing part.

[0596] GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0597] An enzyme complex designated DICER COMPLEX, dices the GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM54 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM54 RNA is designated SEQ ID:532, and is provided hereinbelow with reference to the sequence listing part.

[0598] GAM54 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM54 target RNA, herein designated GAM TARGET RNA. GAM54 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0599] GAM54 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM54 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM54 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM54 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM54 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0600] The complementary binding of GAM54 RNA, herein designated GAM RNA, to target binding sites on GAM54 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM54 target RNA, herein designated GAM TARGET RNA, into GAM54 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0601] It is appreciated that GAM54 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM54 target genes. The mRNA of each one of this plurality of GAM54 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM54 RNA, herein designated GAM RNA, and which when bound by GAM54 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM54 target proteins.

[0602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM54 gene, herein designated GAM GENE, on one or more GAM54 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0603] It is yet further appreciated that specific functions, and accordingly utilities, of GAM54 correlate with, and may be deduced from, the identity of the target genes which GAM54 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0604] Nucleotide sequences of the GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM54 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM54 are further described hereinbelow with reference to Table Table1.

[0605] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM54 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0606]

[0607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 55 (GAM55) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0608] GAM55 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM55 was detected is described hereinabove with reference to Figs. 2-8.

[0609] GAM55 gene, herein designated GAM GENE, and GAM55

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0610] GAM55 gene, herein designated GAM GENE, encodes a GAM55 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM55 precursor RNA is designated SEQ ID:545, and is provided hereinbelow with reference to the sequence listing part.

[0611] GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0612] An enzyme complex designated DICER COMPLEX, dices the GAM55 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM55 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM55 RNA is designated SEQ ID:546, and is provided hereinbelow with reference to the sequence listing part.

[0613] GAM55 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM55 target RNA, herein designated GAM TARGET RNA. GAM55 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0614] GAM55 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM55 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM55 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM55 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM55 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0615] The complementary binding of GAM55 RNA, herein designated GAM RNA, to target binding sites on GAM55 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM55 target RNA, herein designated GAM TARGET RNA, into GAM55 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0616] It is appreciated that GAM55 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM55 target genes. The mRNA of each one of this plurality of GAM55 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM55 RNA, herein designated GAM RNA, and which when bound by GAM55 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM55 target proteins.

[0617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM55 gene, herein designated GAM GENE, on one or more GAM55 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM55 correlate with, and may be deduced from, the identity of the target genes which GAM55 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0619] Nucleotide sequences of the GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM55 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM55 are further described hereinbelow with reference to Table Table1.

[0620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM55 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0621]

[0622] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 56 (GAM56) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0623] GAM56 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM56 was detected is described hereinabove with reference to Figs. 2-8.

[0624] GAM56 gene, herein designated GAM GENE, and GAM56 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0625] GAM56 gene, herein designated GAM GENE, encodes a GAM56 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM56 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM56 precursor RNA is designated SEQ ID:556, and is provided hereinbelow with reference to the sequence listing part.

[0626] GAM56 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0627] An enzyme complex designated DICER COMPLEX, dices the GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM56 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM56 RNA is designated SEQ ID:557, and is provided hereinbelow with reference to the sequence listing part.

[0628] GAM56 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM56 target RNA, herein designated GAM TARGET RNA. GAM56 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein

coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0629] GAM56 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM56 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM56 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM56 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM56 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0630] The complementary binding of GAM56 RNA, herein designated GAM RNA, to target binding sites on GAM56 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM56 target RNA, herein designated GAM TARGET RNA, into GAM56 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0631] It is appreciated that GAM56 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM56 target genes. The mRNA of each one of this plurality of GAM56 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM56 RNA, herein designated GAM RNA, and which when bound by GAM56 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM56 target proteins.

[0632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM56 gene, herein designated GAM GENE, on one or more GAM56 target gene, herein designated GAM TARGET

GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM56 correlate with, and may be deduced from, the identity of the target genes which GAM56 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0634] Nucleotide sequences of the GAM56 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM56 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM56 are further described hereinbelow with reference to Table Table1.

[0635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM56 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0636]

[0637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 57 (GAM57) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0638] GAM57 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM57 was detected is described hereinabove with reference to Figs. 2-8.

[0639] GAM57 gene, herein designated GAM GENE, and GAM57 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0640] GAM57 gene, herein designated GAM GENE, encodes a GAM57 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM57 precursor RNA is designated SEQ ID:561, and is provided hereinbelow with reference to the sequence listing part.

[0641] GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0642] An enzyme complex designated DICER COMPLEX, dices the GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM57 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM57 RNA is designated SEQ ID:562, and is provided hereinbelow with reference to the sequence listing part.

[0643] GAM57 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM57 target RNA, herein designated GAM TARGET RNA. GAM57 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0644] GAM57 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM57 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM57 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM57 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM57 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0645] The complementary binding of GAM57 RNA, herein designated GAM RNA, to target binding sites on GAM57 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM57 target RNA, herein designated GAM TARGET RNA, into GAM57 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0646] It is appreciated that GAM57 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM57 target genes. The mRNA of each one of this plurality of GAM57 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM57 RNA,

herein designated GAM RNA, and which when bound by GAM57 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM57 target proteins.

[0647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM57 gene, herein designated GAM GENE, on one or more GAM57 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM57 correlate with, and may be deduced from, the identity of the target genes which

GAM57 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0649] Nucleotide sequences of the GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM57 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM57 are further described hereinbelow with reference to Table Table1.

[0650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM57 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0651]

[0652] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 58 (GAM58) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0653] GAM58 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM58 was detected is described hereinabove with reference to Figs. 2-8.

[0654] GAM58 gene, herein designated GAM GENE, and GAM58 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0655] GAM58 gene, herein designated GAM GENE, encodes a GAM58 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM58 precursor RNA is designated SEQ ID:573, and is provided hereinbelow with reference to the sequence listing part.

[0656] GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM58 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[0657] An enzyme complex designated DICER COMPLEX, dices the GAM58 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM58 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM58 RNA is designated SEQ ID:574, and is provided hereinbelow with reference to the sequence listing part.

[0658] GAM58 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM58 target RNA, herein designated GAM TARGET RNA. GAM58 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0659] GAM58 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM58 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM58 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM58 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM58 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0660] The complementary binding of GAM58 RNA, herein designated GAM RNA, to target binding sites on GAM58 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM58 target RNA, herein designated GAM

TARGET RNA, into GAM58 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0661] It is appreciated that GAM58 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM58 target genes. The mRNA of each one of this plurality of GAM58 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM58 RNA, herein designated GAM RNA, and which when bound by GAM58 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM58 target proteins.

[0662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM58 gene, herein designated GAM GENE, on one or more GAM58 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0663] It is yet further appreciated that specific functions, and accordingly utilities, of GAM58 correlate with, and may be deduced from, the identity of the target genes which GAM58 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0664] Nucleotide sequences of the GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM58 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM58 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM58 are further described hereinbelow with reference to Table Table1.

[0665] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM58 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[0666]

[0667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 59 (GAM59) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0668] GAM59 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM59 was detected is described hereinabove with reference to Figs. 2-8.

[0669] GAM59 gene, herein designated GAM GENE, and GAM59 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0670] GAM59 gene, herein designated GAM GENE, encodes a GAM59 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM59 precursor RNA is designated SEQ ID:588, and is provided hereinbelow with reference to

the sequence listing part.

[0671] GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0672] An enzyme complex designated DICER COMPLEX, dices the GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM59 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM59 RNA is designated SEQ ID:589, and is provided hereinbelow with reference to the sequence listing part.

[0673] GAM59 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM59 target RNA, herein designated GAM TARGET RNA. GAM59 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0674] GAM59 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM59 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM59 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM59 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM59 target RNA, herein designated GAM TARGET RNA. It is further

appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0675] The complementary binding of GAM59 RNA, herein designated GAM RNA, to target binding sites on GAM59 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM59 target RNA, herein designated GAM TARGET RNA, into GAM59 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0676] It is appreciated that GAM59 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM59 target genes. The mRNA of each one of this plurality of GAM59 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM59 RNA, herein designated GAM RNA, and which when bound by GAM59 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM59 target proteins.

[0677] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM59 gene, herein designated GAM GENE, on one or more GAM59 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM59 correlate with, and may be deduced from, the identity of the target genes which GAM59 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0679] Nucleotide sequences of the GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM59 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM59 are further described hereinbelow with reference to Table Table1.

[0680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM59 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0681]

[0682] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 60 (GAM60) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0683] GAM60 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM60 was detected is described hereinabove with reference to Figs. 2-8.

[0684] GAM60 gene, herein designated GAM GENE, and GAM60 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[0685] GAM60 gene, herein designated GAM GENE, encodes a GAM60 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM60 precursor RNA is designated SEQ ID:604, and is provided hereinbelow with reference to the sequence listing part.

[0686] GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0687] An enzyme complex designated DICER COMPLEX, dices the GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM60 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM60 RNA is designated SEQ ID:605, and is provided hereinbelow with reference to the sequence listing part.

[0688] GAM60 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM60 target RNA, herein designated GAM TARGET RNA. GAM60 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0689] GAM60 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM60 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM60 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM60 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM60 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0690] The complementary binding of GAM60 RNA, herein designated GAM RNA, to target binding sites on GAM60 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM60 target RNA, herein designated GAM TARGET RNA, into GAM60 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0691] It is appreciated that GAM60 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM60 target genes. The mRNA of each one of this plurality of GAM60 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM60 RNA, herein designated GAM RNA, and which when bound by GAM60 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM60 target proteins.

[0692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM60 gene, herein designated GAM GENE, on one or more GAM60 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[0693] It is yet further appreciated that specific functions, and accordingly utilities, of GAM60 correlate with, and may be deduced from, the identity of the target genes which GAM60 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0694] Nucleotide sequences of the GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM60 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM60 are further described hereinbelow with reference to Table Table1.

[0695] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM60 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0696]

[0697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

61 (GAM61) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0698] GAM61 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM61 was detected is described hereinabove with reference to Figs. 2-8.

[0699] GAM61 gene, herein designated GAM GENE, and GAM61 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0700] GAM61 gene, herein designated GAM GENE, encodes a GAM61 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM61 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM61 precursor RNA is designated SEQ ID:617, and is provided hereinbelow with reference to the sequence listing part.

[0701] GAM61 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM61 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0702] An enzyme complex designated DICER COMPLEX, dices the GAM61 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM61 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM61 RNA is designated SEQ ID:618, and is provided hereinbelow with reference to the sequence listing part.

[0703] GAM61 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM61 target RNA, herein designated GAM TARGET RNA. GAM61 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0704] GAM61 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM61 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM61 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM61 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM61 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0705] The complementary binding of GAM61 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM61 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM61 target RNA, herein designated GAM TARGET RNA, into GAM61 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0706] It is appreciated that GAM61 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM61 target genes. The mRNA of each one of this plurality of GAM61 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM61 RNA, herein designated GAM RNA, and which when bound by GAM61 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM61 target proteins.

[0707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM61 gene, herein designated GAM GENE, on one or more GAM61 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM61 correlate with, and may be deduced from, the identity of the target genes which GAM61 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0709] Nucleotide sequences of the GAM61 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM61 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM61 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM61 are further described hereinbelow with reference to Table Table1.

[0710] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM61 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0711]

[0712] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 62 (GAM62) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0713] GAM62 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM62 was detected is described hereinabove with reference to Figs. 2-8.

[0714] GAM62 gene, herein designated GAM GENE, and GAM62 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0715] GAM62 gene, herein designated GAM GENE, encodes a GAM62 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM62 precursor RNA, herein designated

GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM62 precursor RNA is designated SEQ ID:630, and is provided hereinbelow with reference to the sequence listing part.

[0716] GAM62 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0717] An enzyme complex designated DICER COMPLEX, dices the GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM62 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A

probable (over 53%) nucleotide sequence of GAM62 RNA is designated SEQ ID:631, and is provided hereinbelow with reference to the sequence listing part.

[0718] GAM62 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM62 target RNA, herein designated GAM TARGET RNA. GAM62 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0719] GAM62 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM62 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM62 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM62 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM62 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0720] The complementary binding of GAM62 RNA, herein designated GAM RNA, to target binding sites on GAM62 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM62 target RNA, herein designated GAM TARGET RNA, into GAM62 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0721] It is appreciated that GAM62 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM62 target genes. The mRNA of each one of this plurality of GAM62 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM62 RNA, herein designated GAM RNA, and which when bound by

GAM62 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM62 target proteins.

[0722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM62 gene, herein designated GAM GENE, on one or more GAM62 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0723] It is yet further appreciated that specific functions, and accordingly utilities, of GAM62 correlate with, and may be deduced from, the identity of the target genes which GAM62 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[0724] Nucleotide sequences of the GAM62 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM62 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM62 are further described hereinbelow with reference to Table Table1.

[0725] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM62 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0726]

[0727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 63 (GAM63) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0728] GAM63 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM63 was detected is described hereinabove with reference to Figs. 2-8.

[0729] GAM63 gene, herein designated GAM GENE, and GAM63 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0730] GAM63 gene, herein designated GAM GENE, encodes a GAM63 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM63 precursor RNA is designated SEQ ID:652, and is provided hereinbelow with reference to the sequence listing part.

[0731] GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[0732] An enzyme complex designated DICER COMPLEX, dices the GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM63 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM63 RNA is designated SEQ ID:653, and is provided hereinbelow with reference to the sequence listing part.

[0733] GAM63 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM63 target RNA, herein designated GAM TARGET RNA. GAM63 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0734] GAM63 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM63 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM63 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM63 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM63 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0735] The complementary binding of GAM63 RNA, herein designated GAM RNA, to target binding sites on GAM63 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM63 target RNA, herein designated GAM TARGET RNA, into GAM63 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0736] It is appreciated that GAM63 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM63 target genes. The mRNA of each one of this plurality of GAM63 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM63 RNA, herein designated GAM RNA, and which when bound by GAM63 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM63 target proteins.

[0737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM63 gene, herein designated GAM GENE, on one or more GAM63 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM63 correlate with, and may be deduced from, the identity of the target genes which GAM63 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0739] Nucleotide sequences of the GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM63 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM63 are further described hereinbelow with reference to Table Table1.

[0740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM63 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0741]

[0742] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 64 (GAM64) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0743] GAM64 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM64 was detected is described hereinabove with reference to Figs. 2-8.

[0744] GAM64 gene, herein designated GAM GENE, and GAM64 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0745] GAM64 gene, herein designated GAM GENE, encodes a GAM64 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM64 precursor RNA is designated SEQ ID:673, and is provided hereinbelow with reference to the sequence listing part.

[0746] GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0747] An enzyme complex designated DICER COMPLEX, dices the GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM64 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 38%) nucleotide sequence of GAM64 RNA is designated SEQ ID:674, and is provided hereinbelow with reference to the sequence listing part.

[0748] GAM64 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM64

target RNA, herein designated GAM TARGET RNA. GAM64 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0749] GAM64 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM64 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM64 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM64 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM64 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites

in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0750] The complementary binding of GAM64 RNA, herein designated GAM RNA, to target binding sites on GAM64 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM64 target RNA, herein designated GAM TARGET RNA, into GAM64 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0751] It is appreciated that GAM64 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM64 target genes. The mRNA of each one of this plurality of GAM64 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM64 RNA, herein designated GAM RNA, and which when bound by GAM64 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM64 target proteins.

[0752] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM64 gene, herein designated GAM GENE, on one or more GAM64 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0753] It is yet further appreciated that specific functions, and accordingly utilities, of GAM64 correlate with, and may be deduced from, the identity of the target genes which GAM64 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0754] Nucleotide sequences of the GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM64 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM64 are further described hereinbelow with reference to Table Table1.

[0755] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM64 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0756]

[0757] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 65 (GAM65) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0758] GAM65 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM65 was detected is described hereinabove with reference to Figs. 2-8.

[0759] GAM65 gene, herein designated GAM GENE, and GAM65 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0760] GAM65 gene, herein designated GAM GENE, encodes a GAM65 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM65 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM65 precursor RNA is designated SEQ ID:697, and is provided hereinbelow with reference to the sequence listing part.

[0761] GAM65 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0762] An enzyme complex designated DICER COMPLEX, dices the GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM65 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM65 RNA is designated SEQ ID:698, and is provided hereinbelow with reference to the sequence listing part.

[0763] GAM65 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM65 target RNA, herein designated GAM TARGET RNA. GAM65 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0764] GAM65 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM65 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM65 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM65 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM65 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0765] The complementary binding of GAM65 RNA, herein designated GAM RNA, to target binding sites on GAM65 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM65 target RNA, herein designated GAM TARGET RNA, into GAM65 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0766] It is appreciated that GAM65 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM65 target genes. The mRNA of each one of this plu-

rality of GAM65 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM65 RNA, herein designated GAM RNA, and which when bound by GAM65 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM65 target proteins.

[0767] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM65 gene, herein designated GAM GENE, on one or more GAM65 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0768] It is yet further appreciated that specific functions, and accordingly utilities, of GAM65 correlate with, and may be deduced from, the identity of the target genes which GAM65 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0769] Nucleotide sequences of the GAM65 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM65 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM65 are further described hereinbelow with reference to Table Table1.

[0770] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM65 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0771]

[0772] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 66 (GAM66) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[0773] GAM66 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM66 was detected is described hereinabove with reference to Figs. 2-8.

[0774] GAM66 gene, herein designated GAM GENE, and GAM66 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0775] GAM66 gene, herein designated GAM GENE, encodes a GAM66 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM66 precursor RNA is designated SEQ ID:721, and is provided hereinbelow with reference to the sequence listing part.

[0776] GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0777] An enzyme complex designated DICER COMPLEX, dices the GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM66 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM66 RNA is designated SEQ ID:722, and is provided hereinbelow with reference to the sequence listing part.

[0778] GAM66 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM66 target RNA, herein designated GAM TARGET RNA. GAM66 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[0779] GAM66 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM66 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM66 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM66 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM66 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0780] The complementary binding of GAM66 RNA, herein designated GAM RNA, to target binding sites on GAM66 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM66 target RNA, herein designated GAM TARGET RNA, into GAM66 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0781] It is appreciated that GAM66 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM66 target genes. The mRNA of each one of this plurality of GAM66 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM66 RNA, herein designated GAM RNA, and which when bound by GAM66 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM66 target proteins.

[0782] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM66 gene, herein designated GAM GENE, on one or more GAM66 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0783] It is yet further appreciated that specific functions, and accordingly utilities, of GAM66 correlate with, and may be deduced from, the identity of the target genes which GAM66 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0784] Nucleotide sequences of the GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM66 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM66 are further described hereinbelow with reference to Table Table1.

[0785] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM66 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0786]

[0787] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 67 (GAM67) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0788] GAM67 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM67 was detected is described hereinabove with reference to Figs. 2-8.

[0789] GAM67 gene, herein designated GAM GENE, and GAM67 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0790] GAM67 gene, herein designated GAM GENE, encodes a GAM67 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM67 precursor RNA is designated SEQ ID:737, and is provided hereinbelow with reference to the sequence listing part.

[0791] GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0792] An enzyme complex designated DICER COMPLEX, dices the GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM67 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 37%) nucleotide sequence of GAM67 RNA is

designated SEQ ID:738, and is provided hereinbelow with reference to the sequence listing part.

[0793] GAM67 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM67 target RNA, herein designated GAM TARGET RNA. GAM67 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0794] GAM67 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM67 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM67 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM67 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM67 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0795] The complementary binding of GAM67 RNA, herein designated GAM RNA, to target binding sites on GAM67 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM67 target RNA, herein designated GAM TARGET RNA, into GAM67 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0796] It is appreciated that GAM67 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM67 target genes. The mRNA of each one of this plurality of GAM67 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM67 RNA, herein designated GAM RNA, and which when bound by GAM67 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM67 target proteins.

[0797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM67 gene, herein designated GAM GENE, on one or more GAM67 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0798] It is yet further appreciated that specific functions, and accordingly utilities, of GAM67 correlate with, and may be deduced from, the identity of the target genes which GAM67 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0799] Nucleotide sequences of the GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM67 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM67 are further described hereinbelow with reference to Table Table1.

[0800] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM67 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0801]

[0802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 68 (GAM68) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0803] GAM68 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM68 was detected is described hereinabove

with reference to Figs. 2-8.

[0804] GAM68 gene, herein designated GAM GENE, and GAM68 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0805] GAM68 gene, herein designated GAM GENE, encodes a GAM68 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM68 precursor RNA is designated SEQ ID:748, and is provided hereinbelow with reference to the sequence listing part.

[0806] GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0807] An enzyme complex designated DICER COMPLEX, dices the GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM68 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of GAM68 RNA is designated SEQ ID:749, and is provided hereinbelow with reference to the sequence listing part.

[0808] GAM68 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM68 target RNA, herein designated GAM TARGET RNA. GAM68 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0809] GAM68 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM68 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM68 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM68 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM68 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0810] The complementary binding of GAM68 RNA, herein designated GAM RNA, to target binding sites on GAM68 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM68 target RNA, herein designated GAM TARGET RNA, into GAM68 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[0811] It is appreciated that GAM68 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM68 target genes. The mRNA of each one of this plurality of GAM68 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM68 RNA, herein designated GAM RNA, and which when bound by GAM68 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM68 target proteins.

[0812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM68 gene, herein designated GAM GENE, on one or more GAM68 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0813] It is yet further appreciated that specific functions, and accordingly utilities, of GAM68 correlate with, and may be deduced from, the identity of the target genes which GAM68 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0814] Nucleotide sequences of the GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM68 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM68 are further described hereinbelow with reference to Table Table1.

[0815] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM68 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0816]

[0817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 69 (GAM69) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0818] GAM69 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM69 was detected is described hereinabove with reference to Figs. 2-8.

[0819] GAM69 gene, herein designated GAM GENE, and GAM69 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0820] GAM69 gene, herein designated GAM GENE, encodes a GAM69 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM69 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM69 precursor RNA is designated SEQ ID:782, and is provided hereinbelow with reference to the sequence listing part.

[0821] GAM69 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM69 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0822] An enzyme complex designated DICER COMPLEX, dices the GAM69 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM69 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM69 RNA is designated SEQ ID:783, and is provided hereinbelow with reference to the sequence listing part.

[0823] GAM69 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM69 target RNA, herein designated GAM TARGET RNA. GAM69

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0824] GAM69 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM69 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM69 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM69 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM69 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0825] The complementary binding of GAM69 RNA, herein designated GAM RNA, to target binding sites on GAM69 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM69 target RNA, herein designated GAM TARGET RNA, into GAM69 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0826] It is appreciated that GAM69 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM69 target genes. The mRNA of each one of this plurality of GAM69 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM69 RNA, herein designated GAM RNA, and which when bound by GAM69 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM69 target proteins.

[0827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM69 gene, herein designated GAM GENE, on one or more GAM69 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM69 correlate with, and may be deduced from, the identity of the target genes which GAM69 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0829] Nucleotide sequences of the GAM69 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM69 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM69 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM69 are further described hereinbelow with reference to Table Table1.

[0830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM69 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0831]

[0832] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 70 (GAM70) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0833] GAM70 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM70 was detected is described hereinabove with reference to Figs. 2-8.

[0834] GAM70 gene, herein designated GAM GENE, and GAM70 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0835] GAM70 gene, herein designated GAM GENE, encodes a

GAM70 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM70 precursor RNA is designated SEQ ID:792, and is provided hereinbelow with reference to the sequence listing part.

[0836] GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0837] An enzyme complex designated DICER COMPLEX, dices the GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM70 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM70 RNA is designated SEQ ID:793, and is provided hereinbelow with reference to the sequence listing part.

[0838] GAM70 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM70 target RNA, herein designated GAM TARGET RNA. GAM70 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0839] GAM70 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM70 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM70 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM70 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM70 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0840] The complementary binding of GAM70 RNA, herein designated GAM RNA, to target binding sites on GAM70 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM70 target RNA, herein designated GAM TARGET RNA, into GAM70 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0841] It is appreciated that GAM70 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM70 target genes. The mRNA of each one of this plurality of GAM70 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM70 RNA, herein designated GAM RNA, and which when bound by GAM70 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM70 target proteins.

[0842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM70 gene, herein designated GAM GENE, on one or more GAM70 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0843] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM70 correlate with, and may be deduced from, the identity of the target genes which GAM70 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0844] Nucleotide sequences of the GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM70 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM70 are further described hereinbelow with reference to Table Table1.

[0845] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM70 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0846]

[0847] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 71 (GAM71) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[0848] GAM71 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM71 was detected is described hereinabove with reference to Figs. 2-8.

[0849] GAM71 gene, herein designated GAM GENE, and GAM71 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0850] GAM71 gene, herein designated GAM GENE, encodes a GAM71 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM71 precursor RNA is designated SEQ ID:818, and is provided hereinbelow with reference to the sequence listing part.

[0851] GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0852] An enzyme complex designated DICER COMPLEX, dices the GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM71 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM71 RNA is designated SEQ ID:819, and is provided hereinbelow with reference to the sequence listing part.

[0853] GAM71 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM71 target RNA, herein designated GAM TARGET RNA. GAM71 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0854] GAM71 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM71 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM71 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM71 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM71 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0855] The complementary binding of GAM71 RNA, herein designated GAM RNA, to target binding sites on GAM71 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM71 target RNA, herein designated GAM TARGET RNA, into GAM71 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0856] It is appreciated that GAM71 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM71 target genes. The mRNA of each one of this plurality of GAM71 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM71 RNA, herein designated GAM RNA, and which when bound by GAM71 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM71 target proteins.

[0857] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM71 gene, herein designated GAM GENE, on one or more GAM71 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0858] It is yet further appreciated that specific functions, and accordingly utilities, of GAM71 correlate with, and may be deduced from, the identity of the target genes which GAM71 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0859] Nucleotide sequences of the GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM71 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM71 are further described hereinbelow with reference to Table Table1.

[0860] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM71 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0861]

[0862] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 72 (GAM72) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0863] GAM72 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM72 was detected is described hereinabove with reference to Figs. 2-8.

[0864] GAM72 gene, herein designated GAM GENE, and GAM72 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0865] GAM72 gene, herein designated GAM GENE, encodes a GAM72 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM72 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM72 precursor RNA is designated SEQ ID:835, and is provided hereinbelow with reference to the sequence listing part.

[0866] GAM72 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0867] An enzyme complex designated DICER COMPLEX, dices the GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM72 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM72 RNA is designated SEQ ID:836, and is provided hereinbelow with

reference to the sequence listing part.

[0868] GAM72 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM72 target RNA, herein designated GAM TARGET RNA. GAM72 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0869] GAM72 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM72 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM72 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM72 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM72 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0870] The complementary binding of GAM72 RNA, herein designated GAM RNA, to target binding sites on GAM72 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM72 target RNA, herein designated GAM TARGET RNA, into GAM72 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0871] It is appreciated that GAM72 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM72 target genes. The mRNA of each one of this plurality of GAM72 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM72 RNA, herein designated GAM RNA, and which when bound by GAM72 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM72 tar-

get proteins.

[0872] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM72 gene, herein designated GAM GENE, on one or more GAM72 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0873] It is yet further appreciated that specific functions, and accordingly utilities, of GAM72 correlate with, and may be deduced from, the identity of the target genes which GAM72 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0874] Nucleotide sequences of the GAM72 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM72 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM72 are further described hereinbelow with reference to Table Table1.

[0875] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM72 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0876]

[0877] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 73 (GAM73) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0878] GAM73 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM73 was detected is described hereinabove with reference to Figs. 2-8.

[0879] GAM73 gene, herein designated GAM GENE, and GAM73 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0880] GAM73 gene, herein designated GAM GENE, encodes a GAM73 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM73 precursor RNA is designated SEQ ID:845, and is provided hereinbelow with reference to the sequence listing part.

[0881] GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0882] An enzyme complex designated DICER COMPLEX, dices

the GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM73 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM73 RNA is designated SEQ ID:846, and is provided hereinbelow with reference to the sequence listing part.

[0883] GAM73 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM73 target RNA, herein designated GAM TARGET RNA. GAM73 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0884] GAM73 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM73 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM73

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM73 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM73 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0885] The complementary binding of GAM73 RNA, herein designated GAM RNA, to target binding sites on GAM73 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM73 target RNA, herein designated GAM TARGET RNA, into GAM73 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0886] It is appreciated that GAM73 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM73 target genes. The mRNA of each one of this plurality of GAM73 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM73 RNA, herein designated GAM RNA, and which when bound by GAM73 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM73 target proteins.

[0887] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM73 gene, herein designated GAM GENE, on one or more GAM73 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complemen-

tary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0888] It is yet further appreciated that specific functions, and accordingly utilities, of GAM73 correlate with, and may be deduced from, the identity of the target genes which GAM73 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0889] Nucleotide sequences of the GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM73 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM73 are further described hereinbelow with reference to Table Table1.

[0890] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM73 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0891]

[0892] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 74 (GAM74) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0893] GAM74 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM74 was detected is described hereinabove with reference to Figs. 2-8.

[0894] GAM74 gene, herein designated GAM GENE, and GAM74 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0895] GAM74 gene, herein designated GAM GENE, encodes a GAM74 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM74 precursor RNA is designated SEQ ID:862, and is provided hereinbelow with reference to the sequence listing part.

[0896] GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM74 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0897] An enzyme complex designated DICER COMPLEX, dices the GAM74 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM74 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM74 RNA is designated SEQ ID:863, and is provided hereinbelow with reference to the sequence listing part.

[0898] GAM74 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM74 target RNA, herein designated GAM TARGET RNA. GAM74 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0899] GAM74 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM74 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM74 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM74 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM74 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[0900] The complementary binding of GAM74 RNA, herein designated GAM RNA, to target binding sites on GAM74 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM74 target RNA, herein designated GAM TARGET RNA, into GAM74 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0901] It is appreciated that GAM74 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM74 target genes. The mRNA of each one of this plurality of GAM74 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM74 RNA, herein designated GAM RNA, and which when bound by GAM74 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM74 target proteins.

[0902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM74 gene, herein designated GAM GENE, on one or

more GAM74 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0903] It is yet further appreciated that specific functions, and accordingly utilities, of GAM74 correlate with, and may be deduced from, the identity of the target genes which GAM74 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0904] Nucleotide sequences of the GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM74 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM74 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM74 are further described

hereinbelow with reference to Table Table1.

[0905] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM74 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0906]

[0907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 75 (GAM75) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0908] GAM75 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM75 was detected is described hereinabove with reference to Figs. 2-8.

[0909] GAM75 gene, herein designated GAM GENE, and GAM75 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0910] GAM75 gene, herein designated GAM GENE, encodes a GAM75 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM75 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM75 precursor RNA is designated SEQ ID:876, and is provided hereinbelow with reference to the sequence listing part.

[0911] GAM75 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM75 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0912] An enzyme complex designated DICER COMPLEX, dices the GAM75 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM75 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM75 RNA is designated SEQ ID:877, and is provided hereinbelow with reference to the sequence listing part.

[0913] GAM75 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM75 target RNA, herein designated GAM TARGET RNA. GAM75 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0914] GAM75 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM75 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM75 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM75 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM75 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0915] The complementary binding of GAM75 RNA, herein designated GAM RNA, to target binding sites on GAM75 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM75 target RNA, herein designated GAM TARGET RNA, into GAM75 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0916] It is appreciated that GAM75 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM75 target genes. The mRNA of each one of this plurality of GAM75 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM75 RNA, herein designated GAM RNA, and which when bound by GAM75 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM75 target proteins.

[0917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM75 gene, herein designated GAM GENE, on one or more GAM75 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM75 correlate with, and may be

deduced from, the identity of the target genes which GAM75 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0919] Nucleotide sequences of the GAM75 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM75 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM75 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM75 are further described hereinbelow with reference to Table Table1.

[0920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM75 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0921]

[0922] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 76 (GAM76) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0923] GAM76 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM76 was detected is described hereinabove with reference to Figs. 2-8.

[0924] GAM76 gene, herein designated GAM GENE, and GAM76 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0925] GAM76 gene, herein designated GAM GENE, encodes a GAM76 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM76 precursor RNA is designated SEQ ID:905, and is provided hereinbelow with reference to the sequence listing part.

[0926] GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0927] An enzyme complex designated DICER COMPLEX, dices the GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM76 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM76 RNA is designated SEQ ID:906, and is provided hereinbelow with reference to the sequence listing part.

[0928] GAM76 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM76 target RNA, herein designated GAM TARGET RNA. GAM76 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0929] GAM76 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM76 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM76 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM76 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM76 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0930] The complementary binding of GAM76 RNA, herein designated GAM RNA, to target binding sites on GAM76 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM76 target RNA, herein designated GAM TARGET RNA, into GAM76 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0931] It is appreciated that GAM76 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM76 target genes. The mRNA of each one of this plurality of GAM76 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM76 RNA, herein designated GAM RNA, and which when bound by GAM76 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM76 target proteins.

[0932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM76 gene, herein designated GAM GENE, on one or more GAM76 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0933] It is yet further appreciated that specific functions, and accordingly utilities, of GAM76 correlate with, and may be deduced from, the identity of the target genes which GAM76 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0934] Nucleotide sequences of the GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM76 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM76 are further described hereinbelow with reference to Table Table1.

[0935] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM76 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0936]

[0937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 77 (GAM77) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0938] GAM77 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM77 was detected is described hereinabove with reference to Figs. 2-8.

[0939] GAM77 gene, herein designated GAM GENE, and GAM77 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0940] GAM77 gene, herein designated GAM GENE, encodes a GAM77 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM77 precursor RNA is designated

SEQ ID:919, and is provided hereinbelow with reference to the sequence listing part.

[0941] GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0942] An enzyme complex designated DICER COMPLEX, dices the GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM77 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM77 RNA is designated SEQ ID:920, and is provided hereinbelow with reference to the sequence listing part.

[0943] GAM77 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM77 target RNA, herein designated GAM TARGET RNA. GAM77 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0944] GAM77 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM77 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM77 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM77 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM77 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0945] The complementary binding of GAM77 RNA, herein designated GAM RNA, to target binding sites on GAM77 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM77 target RNA, herein designated GAM TARGET RNA, into GAM77 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0946] It is appreciated that GAM77 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM77 target genes. The mRNA of each one of this plurality of GAM77 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM77 RNA, herein designated GAM RNA, and which when bound by GAM77 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM77 target proteins.

[0947] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM77 gene, herein designated GAM GENE, on one or more GAM77 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0948] It is yet further appreciated that specific functions, and accordingly utilities, of GAM77 correlate with, and may be deduced from, the identity of the target genes which GAM77 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0949] Nucleotide sequences of the GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM77 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM77 are further described hereinbelow with reference to Table Table1.

[0950] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM77 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0951]

[0952] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 78 (GAM78) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0953] GAM78 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM78 was detected is described hereinabove with reference to Figs. 2-8.

[0954] GAM78 gene, herein designated GAM GENE, and GAM78

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0955] GAM78 gene, herein designated GAM GENE, encodes a GAM78 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM78 precursor RNA is designated SEQ ID:938, and is provided hereinbelow with reference to the sequence listing part.

[0956] GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM78 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0957] An enzyme complex designated DICER COMPLEX, dices the GAM78 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM78 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 37%) nucleotide sequence of GAM78 RNA is designated SEQ ID:939, and is provided hereinbelow with reference to the sequence listing part.

[0958] GAM78 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM78 target RNA, herein designated GAM TARGET RNA. GAM78 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0959] GAM78 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM78 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM78 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM78 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM78 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0960] The complementary binding of GAM78 RNA, herein designated GAM RNA, to target binding sites on GAM78 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM78 target RNA, herein designated GAM TARGET RNA, into GAM78 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0961] It is appreciated that GAM78 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM78 target genes. The mRNA of each one of this plurality of GAM78 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM78 RNA, herein designated GAM RNA, and which when bound by GAM78 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM78 target proteins.

[0962] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM78 gene, herein designated GAM GENE, on one or more GAM78 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0963] It is yet further appreciated that specific functions, and accordingly utilities, of GAM78 correlate with, and may be deduced from, the identity of the target genes which GAM78 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0964] Nucleotide sequences of the GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM78 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM78 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM78 are further described hereinbelow with reference to Table Table1.

[0965] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM78 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0966]

[0967] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 79 (GAM79) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0968] GAM79 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM79 was detected is described hereinabove with reference to Figs. 2-8.

[0969] GAM79 gene, herein designated GAM GENE, and GAM79 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0970] GAM79 gene, herein designated GAM GENE, encodes a GAM79 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM79 precursor RNA is designated SEQ ID:952, and is provided hereinbelow with reference to the sequence listing part.

[0971] GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0972] An enzyme complex designated DICER COMPLEX, dices the GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM79 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM79 RNA is designated SEQ ID:953, and is provided hereinbelow with reference to the sequence listing part.

[0973] GAM79 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM79 target RNA, herein designated GAM TARGET RNA. GAM79 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein

coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0974] GAM79 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM79 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM79 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM79 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM79 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0975] The complementary binding of GAM79 RNA, herein designated GAM RNA, to target binding sites on GAM79 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM79 target RNA, herein designated GAM TARGET RNA, into GAM79 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0976] It is appreciated that GAM79 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM79 target genes. The mRNA of each one of this plurality of GAM79 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM79 RNA, herein designated GAM RNA, and which when bound by GAM79 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM79 target proteins.

[0977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM79 gene, herein designated GAM GENE, on one or more GAM79 target gene, herein designated GAM TARGET

GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0978] It is yet further appreciated that specific functions, and accordingly utilities, of GAM79 correlate with, and may be deduced from, the identity of the target genes which GAM79 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0979] Nucleotide sequences of the GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM79 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM79 are further described hereinbelow with reference to Table Table1.

[0980] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM79 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0981]

[0982] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 80 (GAM80) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0983] GAM80 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM80 was detected is described hereinabove with reference to Figs. 2-8.

[0984] GAM80 gene, herein designated GAM GENE, and GAM80 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0985] GAM80 gene, herein designated GAM GENE, encodes a GAM80 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM80 precursor RNA is designated SEQ ID:971, and is provided hereinbelow with reference to the sequence listing part.

[0986] GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0987] An enzyme complex designated DICER COMPLEX, dices the GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM80 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM80 RNA is designated SEQ ID:972, and is provided hereinbelow with reference to the sequence listing part.

[0988] GAM80 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM80 target RNA, herein designated GAM TARGET RNA. GAM80 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0989] GAM80 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM80 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM80 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM80 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM80 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0990] The complementary binding of GAM80 RNA, herein designated GAM RNA, to target binding sites on GAM80 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM80 target RNA, herein designated GAM TARGET RNA, into GAM80 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0991] It is appreciated that GAM80 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM80 target genes. The mRNA of each one of this plurality of GAM80 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM80 RNA,

herein designated GAM RNA, and which when bound by GAM80 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM80 target proteins.

[0992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM80 gene, herein designated GAM GENE, on one or more GAM80 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0993] It is yet further appreciated that specific functions, and accordingly utilities, of GAM80 correlate with, and may be deduced from, the identity of the target genes which

GAM80 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0994] Nucleotide sequences of the GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM80 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM80 are further described hereinbelow with reference to Table Table1.

[0995] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM80 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0996]

[0997] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 81 (GAM81) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0998] GAM81 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM81 was detected is described hereinabove with reference to Figs. 2-8.

[0999] GAM81 gene, herein designated GAM GENE, and GAM81 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1000] GAM81 gene, herein designated GAM GENE, encodes a GAM81 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM81 precursor RNA is designated SEQ ID:997, and is provided hereinbelow with reference to the sequence listing part.

[1001] GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1002] An enzyme complex designated DICER COMPLEX, dices the GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM81 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 35%) nucleotide sequence of GAM81 RNA is designated SEQ ID:998, and is provided hereinbelow with reference to the sequence listing part.

[1003] GAM81 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM81 target RNA, herein designated GAM TARGET RNA. GAM81 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1004] GAM81 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM81 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM81 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM81 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM81 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1005] The complementary binding of GAM81 RNA, herein designated GAM RNA, to target binding sites on GAM81 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM81 target RNA, herein designated GAM

TARGET RNA, into GAM81 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1006] It is appreciated that GAM81 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM81 target genes. The mRNA of each one of this plurality of GAM81 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM81 RNA, herein designated GAM RNA, and which when bound by GAM81 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM81 target proteins.

[1007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM81 gene, herein designated GAM GENE, on one or more GAM81 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1008] It is yet further appreciated that specific functions, and accordingly utilities, of GAM81 correlate with, and may be deduced from, the identity of the target genes which GAM81 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1009] Nucleotide sequences of the GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM81 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM81 are further described hereinbelow with reference to Table Table1.

[1010] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM81 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1011]

[1012] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 82 (GAM82) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1013] GAM82 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM82 was detected is described hereinabove with reference to Figs. 2-8.

[1014] GAM82 gene, herein designated GAM GENE, and GAM82 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1015] GAM82 gene, herein designated GAM GENE, encodes a GAM82 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM82 precursor RNA is designated SEQ ID:1017, and is provided hereinbelow with reference

to the sequence listing part.

[1016] GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1017] An enzyme complex designated DICER COMPLEX, dices the GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM82 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM82 RNA is designated SEQ ID:1018, and is provided hereinbelow with reference to the sequence listing part.

[1018] GAM82 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM82 target RNA, herein designated GAM TARGET RNA. GAM82 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1019] GAM82 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM82 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM82 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM82 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM82 target RNA, herein designated GAM TARGET RNA. It is further

appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1020] The complementary binding of GAM82 RNA, herein designated GAM RNA, to target binding sites on GAM82 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM82 target RNA, herein designated GAM TARGET RNA, into GAM82 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1021] It is appreciated that GAM82 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM82 target genes. The mRNA of each one of this plurality of GAM82 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM82 RNA, herein designated GAM RNA, and which when bound by GAM82 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM82 target proteins.

[1022] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM82 gene, herein designated GAM GENE, on one or more GAM82 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1023] It is yet further appreciated that specific functions, and accordingly utilities, of GAM82 correlate with, and may be deduced from, the identity of the target genes which GAM82 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1024] Nucleotide sequences of the GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM82 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM82 are further described hereinbelow with reference to Table Table1.

[1025] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM82 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1026]

[1027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 83 (GAM83) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1028] GAM83 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM83 was detected is described hereinabove with reference to Figs. 2-8.

[1029] GAM83 gene, herein designated GAM GENE, and GAM83 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[1030] GAM83 gene, herein designated GAM GENE, encodes a GAM83 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM83 precursor RNA is designated SEQ ID:1037, and is provided hereinbelow with reference to the sequence listing part.

[1031] GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1032] An enzyme complex designated DICER COMPLEX, dices the GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM83 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM83 RNA is designated SEQ ID:1038, and is provided hereinbelow with reference to the sequence listing part.

[1033] GAM83 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM83 target RNA, herein designated GAM TARGET RNA. GAM83 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1034] GAM83 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM83 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM83 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM83 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM83 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1035] The complementary binding of GAM83 RNA, herein designated GAM RNA, to target binding sites on GAM83 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM83 target RNA, herein designated GAM TARGET RNA, into GAM83 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1036] It is appreciated that GAM83 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM83 target genes. The mRNA of each one of this plurality of GAM83 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM83 RNA, herein designated GAM RNA, and which when bound by GAM83 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM83 target proteins.

[1037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM83 gene, herein designated GAM GENE, on one or more GAM83 target gene, herein designated GAM TARGET

GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM83 correlate with, and may be deduced from, the identity of the target genes which GAM83 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1039] Nucleotide sequences of the GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM83 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM83 are further described hereinbelow with reference to Table Table1.

[1040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM83 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1041]

[1042] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 84 (GAM84) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1043] GAM84 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM84 was detected is described hereinabove with reference to Figs. 2-8.

[1044] GAM84 gene, herein designated GAM GENE, and GAM84 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1045] GAM84 gene, herein designated GAM GENE, encodes a GAM84 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM84 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM84 precursor RNA is designated SEQ ID:1061, and is provided hereinbelow with reference to the sequence listing part.

[1046] GAM84 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1047] An enzyme complex designated DICER COMPLEX, dices the GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM84 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM84 RNA is designated SEQ ID:1062, and is provided hereinbelow with reference to the sequence listing part.

[1048] GAM84 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM84 target RNA, herein designated GAM TARGET RNA. GAM84 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1049] GAM84 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM84 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM84 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM84 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM84 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1050] The complementary binding of GAM84 RNA, herein designated GAM RNA, to target binding sites on GAM84 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM84 target RNA, herein designated GAM TARGET RNA, into GAM84 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1051] It is appreciated that GAM84 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM84 target genes. The mRNA of each one of this plurality of GAM84 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM84 RNA,

herein designated GAM RNA, and which when bound by GAM84 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM84 target proteins.

[1052] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM84 gene, herein designated GAM GENE, on one or more GAM84 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1053] It is yet further appreciated that specific functions, and accordingly utilities, of GAM84 correlate with, and may be deduced from, the identity of the target genes which

GAM84 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1054] Nucleotide sequences of the GAM84 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM84 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM84 are further described hereinbelow with reference to Table Table1.

[1055] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM84 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1056]

[1057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 85 (GAM85) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1058] GAM85 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM85 was detected is described hereinabove with reference to Figs. 2-8.

[1059] GAM85 gene, herein designated GAM GENE, and GAM85 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1060] GAM85 gene, herein designated GAM GENE, encodes a GAM85 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM85 precursor RNA is designated SEQ ID:1078, and is provided hereinbelow with reference to the sequence listing part.

[1061] GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM85 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1062] An enzyme complex designated DICER COMPLEX, dices the GAM85 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM85 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 18%) nucleotide sequence of GAM85 RNA is designated SEQ ID:1079, and is provided hereinbelow with reference to the sequence listing part.

[1063] GAM85 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM85 target RNA, herein designated GAM TARGET RNA. GAM85 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1064] GAM85 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM85 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM85 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM85 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM85 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1065] The complementary binding of GAM85 RNA, herein designated GAM RNA, to target binding sites on GAM85 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM85 target RNA, herein designated GAM

TARGET RNA, into GAM85 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1066] It is appreciated that GAM85 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM85 target genes. The mRNA of each one of this plurality of GAM85 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM85 RNA, herein designated GAM RNA, and which when bound by GAM85 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM85 target proteins.

[1067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM85 gene, herein designated GAM GENE, on one or more GAM85 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM85 correlate with, and may be deduced from, the identity of the target genes which GAM85 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1069] Nucleotide sequences of the GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM85 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM85 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM85 are further described hereinbelow with reference to Table Table1.

[1070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM85 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1071]

[1072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 86 (GAM86) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1073] GAM86 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM86 was detected is described hereinabove with reference to Figs. 2-8.

[1074] GAM86 gene, herein designated GAM GENE, and GAM86 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1075] GAM86 gene, herein designated GAM GENE, encodes a GAM86 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM86 precursor RNA is designated SEQ ID:1095, and is provided hereinbelow with reference

to the sequence listing part.

[1076] GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM86 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1077] An enzyme complex designated DICER COMPLEX, dices the GAM86 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM86 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM86 RNA is designated SEQ ID:1096, and is provided hereinbelow with reference to the sequence listing part.

[1078] GAM86 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM86 target RNA, herein designated GAM TARGET RNA. GAM86 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1079] GAM86 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM86 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM86 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM86 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM86 target RNA, herein designated GAM TARGET RNA. It is further

appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1080] The complementary binding of GAM86 RNA, herein designated GAM RNA, to target binding sites on GAM86 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM86 target RNA, herein designated GAM TARGET RNA, into GAM86 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1081] It is appreciated that GAM86 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM86 target genes. The mRNA of each one of this plurality of GAM86 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM86 RNA, herein designated GAM RNA, and which when bound by GAM86 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM86 target proteins.

[1082] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM86 gene, herein designated GAM GENE, on one or more GAM86 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM86 correlate with, and may be deduced from, the identity of the target genes which GAM86 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1084] Nucleotide sequences of the GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM86 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM86 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM86 are further described hereinbelow with reference to Table Table1.

[1085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM86 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1086]

[1087] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 87 (GAM87) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1088] GAM87 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM87 was detected is described hereinabove with reference to Figs. 2-8.

[1089] GAM87 gene, herein designated GAM GENE, and GAM87 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[1090] GAM87 gene, herein designated GAM GENE, encodes a GAM87 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM87 precursor RNA is designated SEQ ID:1111, and is provided hereinbelow with reference to the sequence listing part.

[1091] GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1092] An enzyme complex designated DICER COMPLEX, dices the GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM87 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM87 RNA is designated SEQ ID:1112, and is provided hereinbelow with reference to the sequence listing part.

[1093] GAM87 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM87 target RNA, herein designated GAM TARGET RNA. GAM87 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1094] GAM87 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM87 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM87 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM87 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM87 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1095] The complementary binding of GAM87 RNA, herein designated GAM RNA, to target binding sites on GAM87 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM87 target RNA, herein designated GAM TARGET RNA, into GAM87 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1096] It is appreciated that GAM87 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM87 target genes. The mRNA of each one of this plurality of GAM87 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM87 RNA, herein designated GAM RNA, and which when bound by GAM87 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM87 target proteins.

[1097] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM87 gene, herein designated GAM GENE, on one or more GAM87 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[1098] It is yet further appreciated that specific functions, and accordingly utilities, of GAM87 correlate with, and may be deduced from, the identity of the target genes which GAM87 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1099] Nucleotide sequences of the GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM87 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM87 are further described hereinbelow with reference to Table Table1.

[1100] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM87 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1101]

[1102] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

88 (GAM88) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1103] GAM88 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM88 was detected is described hereinabove with reference to Figs. 2-8.

[1104] GAM88 gene, herein designated GAM GENE, and GAM88 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1105] GAM88 gene, herein designated GAM GENE, encodes a GAM88 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM88 precursor RNA is designated SEQ ID:1124, and is provided hereinbelow with reference to the sequence listing part.

[1106] GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1107] An enzyme complex designated DICER COMPLEX, dices the GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM88 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM88 RNA is designated SEQ ID:1125, and is provided hereinbelow with reference to the sequence listing part.

[1108] GAM88 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM88 target RNA, herein designated GAM TARGET RNA. GAM88 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1109] GAM88 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM88 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM88 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM88 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM88 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1110] The complementary binding of GAM88 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM88 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM88 target RNA, herein designated GAM TARGET RNA, into GAM88 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1111] It is appreciated that GAM88 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM88 target genes. The mRNA of each one of this plurality of GAM88 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM88 RNA, herein designated GAM RNA, and which when bound by GAM88 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM88 target proteins.

[1112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM88 gene, herein designated GAM GENE, on one or more GAM88 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1113] It is yet further appreciated that specific functions, and accordingly utilities, of GAM88 correlate with, and may be deduced from, the identity of the target genes which GAM88 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1114] Nucleotide sequences of the GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM88 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM88 are further described hereinbelow with reference to Table Table1.

[1115] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM88 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1116]

[1117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 89 (GAM89) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1118] GAM89 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM89 was detected is described hereinabove with reference to Figs. 2-8.

[1119] GAM89 gene, herein designated GAM GENE, and GAM89 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1120] GAM89 gene, herein designated GAM GENE, encodes a GAM89 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM89 precursor RNA, herein designated

GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM89 precursor RNA is designated SEQ ID:1140, and is provided hereinbelow with reference to the sequence listing part.

[1121] GAM89 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM89 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1122] An enzyme complex designated DICER COMPLEX, dices the GAM89 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM89 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A

probable (over 56%) nucleotide sequence of GAM89 RNA is designated SEQ ID:1141, and is provided hereinbelow with reference to the sequence listing part.

[1123] GAM89 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM89 target RNA, herein designated GAM TARGET RNA. GAM89 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1124] GAM89 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM89 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM89 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM89 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM89 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1125] The complementary binding of GAM89 RNA, herein designated GAM RNA, to target binding sites on GAM89 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM89 target RNA, herein designated GAM TARGET RNA, into GAM89 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1126] It is appreciated that GAM89 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM89 target genes. The mRNA of each one of this plurality of GAM89 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM89 RNA, herein designated GAM RNA, and which when bound by

GAM89 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM89 target proteins.

[1127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM89 gene, herein designated GAM GENE, on one or more GAM89 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1128] It is yet further appreciated that specific functions, and accordingly utilities, of GAM89 correlate with, and may be deduced from, the identity of the target genes which GAM89 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[1129] Nucleotide sequences of the GAM89 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM89 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM89 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM89 are further described hereinbelow with reference to Table Table1.

[1130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM89 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1131]

[1132] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 90 (GAM90) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1133] GAM90 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM90 was detected is described hereinabove with reference to Figs. 2-8.

[1134] GAM90 gene, herein designated GAM GENE, and GAM90 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1135] GAM90 gene, herein designated GAM GENE, encodes a GAM90 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM90 precursor RNA is designated SEQ ID:1159, and is provided hereinbelow with reference to the sequence listing part.

[1136] GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1137] An enzyme complex designated DICER COMPLEX, dices the GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM90 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM90 RNA is designated SEQ ID:1160, and is provided hereinbelow with reference to the sequence listing part.

[1138] GAM90 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM90 target RNA, herein designated GAM TARGET RNA. GAM90 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1139] GAM90 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM90 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM90 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM90 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM90 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1140] The complementary binding of GAM90 RNA, herein designated GAM RNA, to target binding sites on GAM90 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM90 target RNA, herein designated GAM TARGET RNA, into GAM90 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1141] It is appreciated that GAM90 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM90 target genes. The mRNA of each one of this plurality of GAM90 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM90 RNA, herein designated GAM RNA, and which when bound by GAM90 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM90 target proteins.

[1142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM90 gene, herein designated GAM GENE, on one or more GAM90 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1143] It is yet further appreciated that specific functions, and accordingly utilities, of GAM90 correlate with, and may be deduced from, the identity of the target genes which GAM90 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1144] Nucleotide sequences of the GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM90 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM90 are further described hereinbelow with reference to Table Table1.

[1145] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM90 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1146]

[1147] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 91 (GAM91) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1148] GAM91 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM91 was detected is described hereinabove with reference to Figs. 2-8.

[1149] GAM91 gene, herein designated GAM GENE, and GAM91 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1150] GAM91 gene, herein designated GAM GENE, encodes a GAM91 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM91 precursor RNA is designated SEQ ID:1168, and is provided hereinbelow with reference to the sequence listing part.

[1151] GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1152] An enzyme complex designated DICER COMPLEX, dices the GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM91 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM91 RNA is designated SEQ ID:1169, and is provided hereinbelow with reference to the sequence listing part.

[1153] GAM91 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM91

target RNA, herein designated GAM TARGET RNA. GAM91 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1154] GAM91 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM91 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM91 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM91 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM91 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites

in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1155] The complementary binding of GAM91 RNA, herein designated GAM RNA, to target binding sites on GAM91 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM91 target RNA, herein designated GAM TARGET RNA, into GAM91 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1156] It is appreciated that GAM91 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM91 target genes. The mRNA of each one of this plurality of GAM91 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM91 RNA, herein designated GAM RNA, and which when bound by GAM91 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM91 target proteins.

[1157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM91 gene, herein designated GAM GENE, on one or more GAM91 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1158] It is yet further appreciated that specific functions, and accordingly utilities, of GAM91 correlate with, and may be deduced from, the identity of the target genes which GAM91 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1159] Nucleotide sequences of the GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM91 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM91 are further described hereinbelow with reference to Table Table1.

[1160] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM91 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1161]

[1162] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 92 (GAM92) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1163] GAM92 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM92 was detected is described hereinabove with reference to Figs. 2-8.

[1164] GAM92 gene, herein designated GAM GENE, and GAM92 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1165] GAM92 gene, herein designated GAM GENE, encodes a GAM92 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM92 precursor RNA is designated SEQ ID:1171, and is provided hereinbelow with reference to the sequence listing part.

[1166] GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1167] An enzyme complex designated DICER COMPLEX, dices the GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM92 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM92 RNA is designated SEQ ID:1172, and is provided hereinbelow with reference to the sequence listing part.

[1168] GAM92 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM92 target RNA, herein designated GAM TARGET RNA. GAM92 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1169] GAM92 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM92 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM92 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM92 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM92 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1170] The complementary binding of GAM92 RNA, herein designated GAM RNA, to target binding sites on GAM92 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM92 target RNA, herein designated GAM TARGET RNA, into GAM92 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1171] It is appreciated that GAM92 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM92 target genes. The mRNA of each one of this plu-

rality of GAM92 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM92 RNA, herein designated GAM RNA, and which when bound by GAM92 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM92 target proteins.

[1172] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM92 gene, herein designated GAM GENE, on one or more GAM92 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1173] It is yet further appreciated that specific functions, and accordingly utilities, of GAM92 correlate with, and may be deduced from, the identity of the target genes which GAM92 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1174] Nucleotide sequences of the GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM92 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM92 are further described hereinbelow with reference to Table Table1.

[1175] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM92 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1176]

[1177] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 93 (GAM93) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[1178] GAM93 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM93 was detected is described hereinabove with reference to Figs. 2-8.

[1179] GAM93 gene, herein designated GAM GENE, and GAM93 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1180] GAM93 gene, herein designated GAM GENE, encodes a GAM93 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM93 precursor RNA is designated SEQ ID:1196, and is provided hereinbelow with reference to the sequence listing part.

[1181] GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1182] An enzyme complex designated DICER COMPLEX, dices the GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM93 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM93 RNA is designated SEQ ID:1197, and is provided hereinbelow with reference to the sequence listing part.

[1183] GAM93 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM93 target RNA, herein designated GAM TARGET RNA. GAM93 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[1184] GAM93 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM93 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM93 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM93 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM93 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1185] The complementary binding of GAM93 RNA, herein designated GAM RNA, to target binding sites on GAM93 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM93 target RNA, herein designated GAM TARGET RNA, into GAM93 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1186] It is appreciated that GAM93 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM93 target genes. The mRNA of each one of this plurality of GAM93 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM93 RNA, herein designated GAM RNA, and which when bound by GAM93 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM93 target proteins.

[1187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM93 gene, herein designated GAM GENE, on one or more GAM93 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1188] It is yet further appreciated that specific functions, and accordingly utilities, of GAM93 correlate with, and may be deduced from, the identity of the target genes which GAM93 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1189] Nucleotide sequences of the GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM93 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM93 are further described hereinbelow with reference to Table Table1.

[1190] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM93 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1191]

[1192] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 94 (GAM94) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1193] GAM94 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM94 was detected is described hereinabove with reference to Figs. 2-8.

[1194] GAM94 gene, herein designated GAM GENE, and GAM94 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1195] GAM94 gene, herein designated GAM GENE, encodes a GAM94 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM94 precursor RNA is designated SEQ ID:1206, and is provided hereinbelow with reference to the sequence listing part.

[1196] GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1197] An enzyme complex designated DICER COMPLEX, dices the GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM94 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM94 RNA is

designated SEQ ID:1207, and is provided hereinbelow with reference to the sequence listing part.

[1198] GAM94 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM94 target RNA, herein designated GAM TARGET RNA. GAM94 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1199] GAM94 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM94 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM94 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM94 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM94 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1200] The complementary binding of GAM94 RNA, herein designated GAM RNA, to target binding sites on GAM94 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM94 target RNA, herein designated GAM TARGET RNA, into GAM94 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1201] It is appreciated that GAM94 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM94 target genes. The mRNA of each one of this plurality of GAM94 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM94 RNA, herein designated GAM RNA, and which when bound by GAM94 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM94 target proteins.

[1202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM94 gene, herein designated GAM GENE, on one or more GAM94 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1203] It is yet further appreciated that specific functions, and accordingly utilities, of GAM94 correlate with, and may be deduced from, the identity of the target genes which GAM94 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1204] Nucleotide sequences of the GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM94 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM94 are further described hereinbelow with reference to Table Table1.

[1205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM94 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1206]

[1207] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 95 (GAM95) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1208] GAM95 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM95 was detected is described hereinabove

with reference to Figs. 2-8.

[1209] GAM95 gene, herein designated GAM GENE, and GAM95 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1210] GAM95 gene, herein designated GAM GENE, encodes a GAM95 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM95 precursor RNA is designated SEQ ID:1220, and is provided hereinbelow with reference to the sequence listing part.

[1211] GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1212] An enzyme complex designated DICER COMPLEX, dices the GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM95 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 37%) nucleotide sequence of GAM95 RNA is designated SEQ ID:1221, and is provided hereinbelow with reference to the sequence listing part.

[1213] GAM95 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM95 target RNA, herein designated GAM TARGET RNA. GAM95 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1214] GAM95 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM95 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM95 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM95 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM95 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1215] The complementary binding of GAM95 RNA, herein designated GAM RNA, to target binding sites on GAM95 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM95 target RNA, herein designated GAM TARGET RNA, into GAM95 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[1216] It is appreciated that GAM95 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM95 target genes. The mRNA of each one of this plurality of GAM95 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM95 RNA, herein designated GAM RNA, and which when bound by GAM95 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM95 target proteins.

[1217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM95 gene, herein designated GAM GENE, on one or more GAM95 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1218] It is yet further appreciated that specific functions, and accordingly utilities, of GAM95 correlate with, and may be deduced from, the identity of the target genes which GAM95 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1219] Nucleotide sequences of the GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM95 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM95 are further described hereinbelow with reference to Table Table1.

[1220] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM95 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1221]

[1222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 96 (GAM96) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1223] GAM96 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM96 was detected is described hereinabove with reference to Figs. 2-8.

[1224] GAM96 gene, herein designated GAM GENE, and GAM96 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1225] GAM96 gene, herein designated GAM GENE, encodes a GAM96 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM96 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM96 precursor RNA is designated SEQ ID:1227, and is provided hereinbelow with reference to the sequence listing part.

[1226] GAM96 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM96 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1227] An enzyme complex designated DICER COMPLEX, dices the GAM96 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM96 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 34%) nucleotide sequence of GAM96 RNA is designated SEQ ID:1228, and is provided hereinbelow with reference to the sequence listing part.

[1228] GAM96 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM96 target RNA, herein designated GAM TARGET RNA. GAM96

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1229] GAM96 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM96 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM96 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM96 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM96 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1230] The complementary binding of GAM96 RNA, herein designated GAM RNA, to target binding sites on GAM96 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM96 target RNA, herein designated GAM TARGET RNA, into GAM96 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1231] It is appreciated that GAM96 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM96 target genes. The mRNA of each one of this plurality of GAM96 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM96 RNA, herein designated GAM RNA, and which when bound by GAM96 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM96 target proteins.

[1232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM96 gene, herein designated GAM GENE, on one or more GAM96 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM96 correlate with, and may be deduced from, the identity of the target genes which GAM96 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1234] Nucleotide sequences of the GAM96 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM96 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM96 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM96 are further described hereinbelow with reference to Table Table1.

[1235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM96 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1236]

[1237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 97 (GAM97) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1238] GAM97 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM97 was detected is described hereinabove with reference to Figs. 2-8.

[1239] GAM97 gene, herein designated GAM GENE, and GAM97 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1240] GAM97 gene, herein designated GAM GENE, encodes a

GAM97 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM97 precursor RNA is designated SEQ ID:1259, and is provided hereinbelow with reference to the sequence listing part.

[1241] GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1242] An enzyme complex designated DICER COMPLEX, dices the GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM97 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 18%) nucleotide sequence of GAM97 RNA is designated SEQ ID:1260, and is provided hereinbelow with reference to the sequence listing part.

[1243] GAM97 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM97 target RNA, herein designated GAM TARGET RNA. GAM97 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1244] GAM97 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM97 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM97 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM97 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM97 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1245] The complementary binding of GAM97 RNA, herein designated GAM RNA, to target binding sites on GAM97 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM97 target RNA, herein designated GAM TARGET RNA, into GAM97 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1246] It is appreciated that GAM97 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM97 target genes. The mRNA of each one of this plurality of GAM97 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM97 RNA, herein designated GAM RNA, and which when bound by GAM97 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM97 target proteins.

[1247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM97 gene, herein designated GAM GENE, on one or more GAM97 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1248] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM97 correlate with, and may be deduced from, the identity of the target genes which GAM97 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1249] Nucleotide sequences of the GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM97 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM97 are further described hereinbelow with reference to Table Table1.

[1250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM97 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1251]

[1252] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 98 (GAM98) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[1253] GAM98 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM98 was detected is described hereinabove with reference to Figs. 2-8.

[1254] GAM98 gene, herein designated GAM GENE, and GAM98 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1255] GAM98 gene, herein designated GAM GENE, encodes a GAM98 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM98 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM98 precursor RNA is designated SEQ ID:1276, and is provided hereinbelow with reference to the sequence listing part.

[1256] GAM98 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM98 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1257] An enzyme complex designated DICER COMPLEX, dices the GAM98 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM98 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM98 RNA is designated SEQ ID:1277, and is provided hereinbelow with reference to the sequence listing part.

[1258] GAM98 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM98 target RNA, herein designated GAM TARGET RNA. GAM98 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1259] GAM98 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM98 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM98 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM98 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM98 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1260] The complementary binding of GAM98 RNA, herein designated GAM RNA, to target binding sites on GAM98 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM98 target RNA, herein designated GAM TARGET RNA, into GAM98 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1261] It is appreciated that GAM98 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM98 target genes. The mRNA of each one of this plurality of GAM98 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM98 RNA, herein designated GAM RNA, and which when bound by GAM98 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM98 target proteins.

[1262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM98 gene, herein designated GAM GENE, on one or more GAM98 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM98 correlate with, and may be deduced from, the identity of the target genes which GAM98 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1264] Nucleotide sequences of the GAM98 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM98 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM98 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM98 are further described hereinbelow with reference to Table Table1.

[1265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM98 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1266]

[1267] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 99 (GAM99) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1268] GAM99 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM99 was detected is described hereinabove with reference to Figs. 2-8.

[1269] GAM99 gene, herein designated GAM GENE, and GAM99 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1270] GAM99 gene, herein designated GAM GENE, encodes a GAM99 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM99 precursor RNA is designated SEQ ID:1293, and is provided hereinbelow with reference to the sequence listing part.

[1271] GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1272] An enzyme complex designated DICER COMPLEX, dices the GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM99 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 35%) nucleotide sequence of GAM99 RNA is designated SEQ ID:1294, and is provided hereinbelow with

reference to the sequence listing part.

[1273] GAM99 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM99 target RNA, herein designated GAM TARGET RNA. GAM99 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1274] GAM99 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM99 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM99 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM99 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM99 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1275] The complementary binding of GAM99 RNA, herein designated GAM RNA, to target binding sites on GAM99 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM99 target RNA, herein designated GAM TARGET RNA, into GAM99 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1276] It is appreciated that GAM99 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM99 target genes. The mRNA of each one of this plurality of GAM99 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM99 RNA, herein designated GAM RNA, and which when bound by GAM99 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM99 tar-

get proteins.

[1277] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM99 gene, herein designated GAM GENE, on one or more GAM99 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1278] It is yet further appreciated that specific functions, and accordingly utilities, of GAM99 correlate with, and may be deduced from, the identity of the target genes which GAM99 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1279] Nucleotide sequences of the GAM99 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM99 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM99 are further described hereinbelow with reference to Table Table1.

[1280] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM99 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1281]

[1282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 100 (GAM100) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1283] GAM100 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM100 was detected is described hereinabove with reference to Figs. 2-8.

[1284] GAM100 gene, herein designated GAM GENE, and GAM100 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1285] GAM100 gene, herein designated GAM GENE, encodes a GAM100 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM100 precursor RNA is designated SEQ ID:1303, and is provided hereinbelow with reference to the sequence listing part.

[1286] GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1287] An enzyme complex designated DICER COMPLEX, dices

the GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM100 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM100 RNA is designated SEQ ID:1304, and is provided hereinbelow with reference to the sequence listing part.

[1288] GAM100 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM100 target RNA, herein designated GAM TARGET RNA.

GAM100 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1289] GAM100 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM100 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM100

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM100 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM100 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1290] The complementary binding of GAM100 RNA, herein designated GAM RNA, to target binding sites on GAM100 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM100 target RNA, herein designated GAM TARGET RNA, into GAM100 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1291] It is appreciated that GAM100 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM100 target genes. The mRNA of each one of this plurality of GAM100 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM100 RNA, herein designated GAM RNA, and which when bound by GAM100 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM100 target proteins.

[1292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM100 gene, herein designated GAM GENE, on one or more GAM100 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM100 correlate with, and may be deduced from, the identity of the target genes which GAM100 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1294] Nucleotide sequences of the GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM100 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM100 are further described hereinbelow with reference to Table Table1.

[1295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM100 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1296]

[1297] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 101 (GAM101) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1298] GAM101 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM101 was detected is described hereinabove with reference to Figs. 2-8.

[1299] GAM101 gene, herein designated GAM GENE, and GAM101 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1300] GAM101 gene, herein designated GAM GENE, encodes a GAM101 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM101 precursor RNA is designated SEQ ID:1315, and is provided hereinbelow with reference to the sequence listing part.

[1301] GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM101 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1302] An enzyme complex designated DICER COMPLEX, dices the GAM101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM101 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM101 RNA is designated SEQ ID:1316, and is provided hereinbelow with reference to the sequence listing part.

[1303] GAM101 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM101 target RNA, herein designated GAM TARGET RNA. GAM101 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1304] GAM101 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM101 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM101 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM101 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM101 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1305] The complementary binding of GAM101 RNA, herein designated GAM RNA, to target binding sites on GAM101 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM101 target RNA, herein designated GAM TARGET RNA, into GAM101 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1306] It is appreciated that GAM101 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM101 target genes. The mRNA of each one of this plurality of GAM101 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM101 RNA, herein designated GAM RNA, and which when bound by GAM101 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM101 target proteins.

[1307] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM101 gene, herein designated GAM GENE, on one or

more GAM101 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1308] It is yet further appreciated that specific functions, and accordingly utilities, of GAM101 correlate with, and may be deduced from, the identity of the target genes which GAM101 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1309] Nucleotide sequences of the GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM101 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM101 are further de-

scribed hereinbelow with reference to Table Table1.

[1310] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM101 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1311]

[1312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 102 (GAM102) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1313] GAM102 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM102 was detected is described hereinabove with reference to Figs. 2-8.

[1314] GAM102 gene, herein designated GAM GENE, and GAM102 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1315] GAM102 gene, herein designated GAM GENE, encodes a GAM102 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM102 precursor RNA is designated SEQ ID:1330, and is provided hereinbelow with reference to the sequence listing part.

[1316] GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1317] An enzyme complex designated DICER COMPLEX, dices the GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM102 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM102 RNA is designated SEQ ID:1316, and is provided hereinbelow with reference to the sequence listing part.

[1318] GAM102 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM102 target RNA, herein designated GAM TARGET RNA. GAM102 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1319] GAM102 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM102 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM102 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM102 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM102 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1320] The complementary binding of GAM102 RNA, herein designated GAM RNA, to target binding sites on GAM102 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM102 target RNA, herein designated GAM TARGET RNA, into GAM102 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1321] It is appreciated that GAM102 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM102 target genes. The mRNA of each one of this plurality of GAM102 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM102 RNA, herein designated GAM RNA, and which when bound by GAM102 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM102 target proteins.

[1322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM102 gene, herein designated GAM GENE, on one or more GAM102 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM102 correlate with, and may

be deduced from, the identity of the target genes which GAM102 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1324] Nucleotide sequences of the GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM102 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM102 are further described hereinbelow with reference to Table Table1.

[1325] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM102 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1326]

[1327] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 103 (GAM103) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1328] GAM103 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM103 was detected is described hereinabove with reference to Figs. 2-8.

[1329] GAM103 gene, herein designated GAM GENE, and GAM103 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1330] GAM103 gene, herein designated GAM GENE, encodes a GAM103 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM103 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM103 precursor RNA is designated SEQ ID:1336, and is provided hereinbelow with reference to the sequence listing part.

[1331] GAM103 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1332] An enzyme complex designated DICER COMPLEX, dices the GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM103 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM103 RNA is designated SEQ ID:1337, and is provided hereinbelow with reference to the sequence listing part.

[1333] GAM103 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM103 target RNA, herein designated GAM TARGET RNA. GAM103 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1334] GAM103 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM103 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM103 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM103 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM103 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1335] The complementary binding of GAM103 RNA, herein designated GAM RNA, to target binding sites on GAM103 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM103 target RNA, herein designated GAM TARGET RNA, into GAM103 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1336] It is appreciated that GAM103 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM103 target genes. The mRNA of each one of this plurality of GAM103 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM103 RNA, herein designated GAM RNA, and which when bound by GAM103 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM103 target proteins.

[1337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM103 gene, herein designated GAM GENE, on one or more GAM103 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1338] It is yet further appreciated that specific functions, and accordingly utilities, of GAM103 correlate with, and may be deduced from, the identity of the target genes which GAM103 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1339] Nucleotide sequences of the GAM103 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM103 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM103 are further described hereinbelow with reference to Table Table1.

[1340] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM103 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1341]

[1342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 104 (GAM104) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1343] GAM104 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM104 was detected is described hereinabove with reference to Figs. 2-8.

[1344] GAM104 gene, herein designated GAM GENE, and GAM104 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1345] GAM104 gene, herein designated GAM GENE, encodes a GAM104 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM104 precursor RNA is desig-

nated SEQ ID:1347, and is provided hereinbelow with reference to the sequence listing part.

[1346] GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1347] An enzyme complex designated DICER COMPLEX, dices the GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM104 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 31%) nucleotide sequence of GAM104 RNA is designated SEQ ID:1348, and is provided hereinbelow with reference to the sequence listing part.

[1348] GAM104 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM104 target RNA, herein designated GAM TARGET RNA. GAM104 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1349] GAM104 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM104 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM104 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM104 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM104

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1350] The complementary binding of GAM104 RNA, herein designated GAM RNA, to target binding sites on GAM104 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM104 target RNA, herein designated GAM TARGET RNA, into GAM104 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1351] It is appreciated that GAM104 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM104 target genes. The mRNA of each one of this plurality of GAM104 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM104 RNA, herein designated GAM RNA, and which when bound by GAM104 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM104 target proteins.

[1352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM104 gene, herein designated GAM GENE, on one or more GAM104 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM104 correlate with, and may be deduced from, the identity of the target genes which GAM104 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1354] Nucleotide sequences of the GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM104 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM104 are further described hereinbelow with reference to Table Table1.

[1355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM104 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1356]

[1357] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 105 (GAM105) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1358] GAM105 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM105 was detected is described hereinabove with reference to Figs. 2-8.

[1359] GAM105 gene, herein designated GAM GENE, and

GAM105 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1360] GAM105 gene, herein designated GAM GENE, encodes a GAM105 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM105 precursor RNA is designated SEQ ID:1391, and is provided hereinbelow with reference to the sequence listing part.

[1361] GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1362] An enzyme complex designated DICER COMPLEX, dices the GAM105 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM105 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM105 RNA is designated SEQ ID:1392, and is provided hereinbelow with reference to the sequence listing part.

[1363] GAM105 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM105 target RNA, herein designated GAM TARGET RNA. GAM105 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1364] GAM105 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM105 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM105 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM105 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM105 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1365] The complementary binding of GAM105 RNA, herein designated GAM RNA, to target binding sites on GAM105 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM105 target RNA, herein designated GAM TARGET RNA, into GAM105 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1366] It is appreciated that GAM105 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM105 target genes. The mRNA of each one of this plurality of GAM105 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM105 RNA, herein designated GAM RNA, and which when bound by GAM105 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM105 target proteins.

[1367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM105 gene, herein designated GAM GENE, on one or more GAM105 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1368] It is yet further appreciated that specific functions, and accordingly utilities, of GAM105 correlate with, and may be deduced from, the identity of the target genes which GAM105 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1369] Nucleotide sequences of the GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM105 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM105 are further described hereinbelow with reference to Table Table1.

[1370] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM105 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1371]

[1372] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 106 (GAM106) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1373] GAM106 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM106 was detected is described hereinabove with reference to Figs. 2-8.

[1374] GAM106 gene, herein designated GAM GENE, and GAM106 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1375] GAM106 gene, herein designated GAM GENE, encodes a GAM106 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM106 precursor RNA is designated SEQ ID:1403, and is provided hereinbelow with reference to the sequence listing part.

[1376] GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1377] An enzyme complex designated DICER COMPLEX, dices the GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM106 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM106 RNA is designated SEQ ID:1404, and is provided hereinbelow with reference to the sequence listing part.

[1378] GAM106 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM106 target RNA, herein designated GAM TARGET RNA. GAM106 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1379] GAM106 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM106 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM106 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM106 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM106 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1380] The complementary binding of GAM106 RNA, herein designated GAM RNA, to target binding sites on GAM106 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM106 target RNA, herein designated GAM TARGET RNA, into GAM106 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1381] It is appreciated that GAM106 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM106 target genes. The mRNA of each one of this plurality of GAM106 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM106 RNA, herein designated GAM RNA, and which when bound by GAM106 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM106 target proteins.

[1382] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM106 gene, herein designated GAM GENE, on one or more GAM106 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1383] It is yet further appreciated that specific functions, and accordingly utilities, of GAM106 correlate with, and may be deduced from, the identity of the target genes which GAM106 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1384] Nucleotide sequences of the GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM106 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM106 are further described hereinbelow with reference to Table Table1.

[1385] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM106 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1386]

[1387] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 107 (GAM107) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1388] GAM107 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM107 was detected is described hereinabove with reference to Figs. 2-8.

[1389] GAM107 gene, herein designated GAM GENE, and GAM107 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1390] GAM107 gene, herein designated GAM GENE, encodes a GAM107 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM107 precursor RNA is designated SEQ ID:1411, and is provided hereinbelow with reference to the sequence listing part.

[1391] GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1392] An enzyme complex designated DICER COMPLEX, dices the GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM107 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 34%) nucleotide sequence of GAM107 RNA is designated SEQ ID:1412, and is provided hereinbelow with reference to the sequence listing part.

[1393] GAM107 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM107 target RNA, herein designated GAM TARGET RNA. GAM107 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1394] GAM107 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM107 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM107 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM107 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM107 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1395] The complementary binding of GAM107 RNA, herein designated GAM RNA, to target binding sites on GAM107 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM107 target RNA, herein designated GAM TARGET RNA, into GAM107 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1396] It is appreciated that GAM107 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM107 target genes. The mRNA of each one of this plurality of GAM107 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM107 RNA,

herein designated GAM RNA, and which when bound by GAM107 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM107 target proteins.

[1397] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM107 gene, herein designated GAM GENE, on one or more GAM107 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1398] It is yet further appreciated that specific functions, and accordingly utilities, of GAM107 correlate with, and may be deduced from, the identity of the target genes which

GAM107 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1399] Nucleotide sequences of the GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM107 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM107 are further described hereinbelow with reference to Table Table1.

[1400] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM107 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1401]

[1402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 108 (GAM108) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1403] GAM108 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM108 was detected is described hereinabove with reference to Figs. 2-8.

[1404] GAM108 gene, herein designated GAM GENE, and GAM108 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1405] GAM108 gene, herein designated GAM GENE, encodes a GAM108 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM108 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM108 precursor RNA is designated SEQ ID:1428, and is provided hereinbelow with reference to the sequence listing part.

[1406] GAM108 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1407] An enzyme complex designated DICER COMPLEX, dices the GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM108 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM108 RNA is designated SEQ ID:1429, and is provided hereinbelow with reference to the sequence listing part.

[1408] GAM108 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM108 target RNA, herein designated GAM TARGET RNA.
GAM108 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1409] GAM108 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM108 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM108 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM108 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM108 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1410] The complementary binding of GAM108 RNA, herein designated GAM RNA, to target binding sites on GAM108 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM108 target RNA, herein desig-

nated GAM TARGET RNA, into GAM108 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1411] It is appreciated that GAM108 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM108 target genes. The mRNA of each one of this plurality of GAM108 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM108 RNA, herein designated GAM RNA, and which when bound by GAM108 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM108 target proteins.

[1412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM108 gene, herein designated GAM GENE, on one or more GAM108 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM108 correlate with, and may be deduced from, the identity of the target genes which GAM108 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1414] Nucleotide sequences of the GAM108 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM108 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM108 are further described hereinbelow with reference to Table Table1.

[1415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM108 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1416]

[1417] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 109 (GAM109) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1418] GAM109 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM109 was detected is described hereinabove with reference to Figs. 2-8.

[1419] GAM109 gene, herein designated GAM GENE, and GAM109 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1420] GAM109 gene, herein designated GAM GENE, encodes a GAM109 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM109 precursor RNA is designated SEQ ID:1443, and is provided hereinbelow with ref-

erence to the sequence listing part.

[1421] GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1422] An enzyme complex designated DICER COMPLEX, dices the GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM109 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM109 RNA is designated SEQ ID:1444, and is provided hereinbelow with reference to the sequence listing part.

[1423] GAM109 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM109 target RNA, herein designated GAM TARGET RNA.

GAM109 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1424] GAM109 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM109 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM109 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM109 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM109 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1425] The complementary binding of GAM109 RNA, herein designated GAM RNA, to target binding sites on GAM109 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM109 target RNA, herein designated GAM TARGET RNA, into GAM109 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1426] It is appreciated that GAM109 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM109 target genes. The mRNA of each one of this plurality of GAM109 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM109 RNA, herein designated GAM RNA, and which when bound by GAM109 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM109 target proteins.

[1427] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM109 gene, herein designated GAM GENE, on one or more GAM109 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1428] It is yet further appreciated that specific functions, and accordingly utilities, of GAM109 correlate with, and may be deduced from, the identity of the target genes which GAM109 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1429] Nucleotide sequences of the GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM109 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM109 are further described hereinbelow with reference to Table Table1.

[1430] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM109 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1431]

[1432] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 110 (GAM110) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1433] GAM110 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM110 was detected is described hereinabove with reference to Figs. 2-8.

[1434] GAM110 gene, herein designated GAM GENE, and GAM110 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[1435] GAM110 gene, herein designated GAM GENE, encodes a GAM110 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM110 precursor RNA is designated SEQ ID:1462, and is provided hereinbelow with reference to the sequence listing part.

[1436] GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1437] An enzyme complex designated DICER COMPLEX, dices the GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM110 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM110 RNA is designated SEQ ID:1463, and is provided hereinbelow with reference to the sequence listing part.

[1438] GAM110 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM110 target RNA, herein designated GAM TARGET RNA. GAM110 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1439] GAM110 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM110 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM110 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM110 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM110 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1440] The complementary binding of GAM110 RNA, herein designated GAM RNA, to target binding sites on GAM110 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM110 target RNA, herein designated GAM TARGET RNA, into GAM110 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1441] It is appreciated that GAM110 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM110 target genes. The mRNA of each one of this plurality of GAM110 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM110 RNA, herein designated GAM RNA, and which when bound by GAM110 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM110 target proteins.

[1442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM110 gene, herein designated GAM GENE, on one or more GAM110 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[1443] It is yet further appreciated that specific functions, and accordingly utilities, of GAM110 correlate with, and may be deduced from, the identity of the target genes which GAM110 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1444] Nucleotide sequences of the GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM110 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM110 are further described hereinbelow with reference to Table Table1.

[1445] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM110 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1446]

[1447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

111 (GAM111) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1448] GAM111 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM111 was detected is described hereinabove with reference to Figs. 2-8.

[1449] GAM111 gene, herein designated GAM GENE, and GAM111 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1450] GAM111 gene, herein designated GAM GENE, encodes a GAM111 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM111 precursor RNA is designated SEQ ID:1487, and is provided hereinbelow with reference to the sequence listing part.

[1451] GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1452] An enzyme complex designated DICER COMPLEX, dices the GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM111 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM111 RNA is designated SEQ ID:1488, and is provided hereinbelow with reference to the sequence listing part.

[1453] GAM111 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM111 target RNA, herein designated GAM TARGET RNA. GAM111 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1454] GAM111 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM111 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM111 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM111 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM111 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1455] The complementary binding of GAM111 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM111 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM111 target RNA, herein designated GAM TARGET RNA, into GAM111 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1456] It is appreciated that GAM111 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM111 target genes. The mRNA of each one of this plurality of GAM111 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM111 RNA, herein designated GAM RNA, and which when bound by GAM111 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM111 target proteins.

[1457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM111 gene, herein designated GAM GENE, on one or more GAM111 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1458] It is yet further appreciated that specific functions, and accordingly utilities, of GAM111 correlate with, and may be deduced from, the identity of the target genes which GAM111 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1459] Nucleotide sequences of the GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM111 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM111 are further described hereinbelow with reference to Table Table1.

[1460] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM111 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1461]

[1462] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 112 (GAM112) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1463] GAM112 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM112 was detected is described hereinabove with reference to Figs. 2-8.

[1464] GAM112 gene, herein designated GAM GENE, and GAM112 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1465] GAM112 gene, herein designated GAM GENE, encodes a GAM112 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM112 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM112 precursor RNA is designated SEQ ID:1494, and is provided hereinbelow with reference to the sequence listing part.

[1466] GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1467] An enzyme complex designated DICER COMPLEX, dices the GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM112 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 59%) nucleotide sequence of GAM112 RNA is designated SEQ ID:1495, and is provided hereinbelow with reference to the sequence listing part.

[1468] GAM112 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM112 target RNA, herein designated GAM TARGET RNA. GAM112 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1469] GAM112 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM112 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM112 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM112 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM112 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1470] The complementary binding of GAM112 RNA, herein designated GAM RNA, to target binding sites on GAM112 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM112 target RNA, herein designated GAM TARGET RNA, into GAM112 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1471] It is appreciated that GAM112 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM112 target genes. The mRNA of each one of this plurality of GAM112 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM112 RNA, herein designated GAM RNA, and which when bound by

GAM112 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM112 target proteins.

[1472] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM112 gene, herein designated GAM GENE, on one or more GAM112 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1473] It is yet further appreciated that specific functions, and accordingly utilities, of GAM112 correlate with, and may be deduced from, the identity of the target genes which GAM112 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[1474] Nucleotide sequences of the GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM112 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM112 are further described hereinbelow with reference to Table Table1.

[1475] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM112 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1476]

[1477] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 113 (GAM113) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1478] GAM113 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM113 was detected is described hereinabove with reference to Figs. 2-8.

[1479] GAM113 gene, herein designated GAM GENE, and GAM113 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1480] GAM113 gene, herein designated GAM GENE, encodes a GAM113 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM113 precursor RNA is designated SEQ ID:1515, and is provided hereinbelow with reference to the sequence listing part.

[1481] GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1482] An enzyme complex designated DICER COMPLEX, dices the GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM113 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM113 RNA is designated SEQ ID:1516, and is provided hereinbelow with reference to the sequence listing part.

[1483] GAM113 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM113 target RNA, herein designated GAM TARGET RNA. GAM113 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1484] GAM113 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM113 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM113 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM113 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM113 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1485] The complementary binding of GAM113 RNA, herein designated GAM RNA, to target binding sites on GAM113 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM113 target RNA, herein designated GAM TARGET RNA, into GAM113 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1486] It is appreciated that GAM113 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM113 target genes. The mRNA of each one of this plurality of GAM113 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM113 RNA, herein designated GAM RNA, and which when bound by GAM113 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM113 target proteins.

[1487] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM113 gene, herein designated GAM GENE, on one or more GAM113 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1488] It is yet further appreciated that specific functions, and accordingly utilities, of GAM113 correlate with, and may be deduced from, the identity of the target genes which GAM113 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1489] Nucleotide sequences of the GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM113 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM113 are further described hereinbelow with reference to Table Table1.

[1490] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM113 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1491]

[1492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 114 (GAM114) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1493] GAM114 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM114 was detected is described hereinabove with reference to Figs. 2-8.

[1494] GAM114 gene, herein designated GAM GENE, and GAM114 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1495] GAM114 gene, herein designated GAM GENE, encodes a GAM114 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM114 precursor RNA is designated SEQ ID:1525, and is provided hereinbelow with reference to the sequence listing part.

[1496] GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1497] An enzyme complex designated DICER COMPLEX, dices the GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM114 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM114 RNA is designated SEQ ID:1526, and is provided hereinbelow with reference to the sequence listing part.

[1498] GAM114 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM114

target RNA, herein designated GAM TARGET RNA.

GAM114 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1499] GAM114 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM114 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM114 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM114 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM114 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1500] The complementary binding of GAM114 RNA, herein designated GAM RNA, to target binding sites on GAM114 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM114 target RNA, herein designated GAM TARGET RNA, into GAM114 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1501] It is appreciated that GAM114 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM114 target genes. The mRNA of each one of this plurality of GAM114 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM114 RNA, herein designated GAM RNA, and which when bound by GAM114 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM114 target proteins.

[1502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM114 gene, herein designated GAM GENE, on one or more GAM114 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1503] It is yet further appreciated that specific functions, and accordingly utilities, of GAM114 correlate with, and may be deduced from, the identity of the target genes which GAM114 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1504] Nucleotide sequences of the GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM114 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM114 are further described hereinbelow with reference to Table Table1.

[1505] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM114 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1506]

[1507] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 115 (GAM115) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1508] GAM115 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM115 was detected is described hereinabove with reference to Figs. 2-8.

[1509] GAM115 gene, herein designated GAM GENE, and GAM115 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1510] GAM115 gene, herein designated GAM GENE, encodes a GAM115 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM115 precursor RNA is designated SEQ ID:1575, and is provided hereinbelow with reference to the sequence listing part.

[1511] GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1512] An enzyme complex designated DICER COMPLEX, dices the GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM115 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM115 RNA is designated SEQ ID:1576, and is provided hereinbelow with reference to the sequence listing part.

[1513] GAM115 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM115 target RNA, herein designated GAM TARGET RNA. GAM115 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1514] GAM115 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM115 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM115 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM115 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM115 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1515] The complementary binding of GAM115 RNA, herein designated GAM RNA, to target binding sites on GAM115 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM115 target RNA, herein designated GAM TARGET RNA, into GAM115 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1516] It is appreciated that GAM115 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM115 target genes. The mRNA of each one of this plu-

rality of GAM115 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM115 RNA, herein designated GAM RNA, and which when bound by GAM115 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM115 target proteins.

[1517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM115 gene, herein designated GAM GENE, on one or more GAM115 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1518] It is yet further appreciated that specific functions, and accordingly utilities, of GAM115 correlate with, and may be deduced from, the identity of the target genes which GAM115 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1519] Nucleotide sequences of the GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM115 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM115 are further described hereinbelow with reference to Table Table1.

[1520] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM115 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1521]

[1522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 116 (GAM116) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[1523] GAM116 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM116 was detected is described hereinabove with reference to Figs. 2-8.

[1524] GAM116 gene, herein designated GAM GENE, and GAM116 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1525] GAM116 gene, herein designated GAM GENE, encodes a GAM116 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM116 precursor RNA is designated SEQ ID:1589, and is provided hereinbelow with reference to the sequence listing part.

[1526] GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1527] An enzyme complex designated DICER COMPLEX, dices the GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM116 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM116 RNA is designated SEQ ID:1590, and is provided hereinbelow with reference to the sequence listing part.

[1528] GAM116 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM116 target RNA, herein designated GAM TARGET RNA.

GAM116 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[1529] GAM116 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM116 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM116 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM116 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM116 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1530] The complementary binding of GAM116 RNA, herein designated GAM RNA, to target binding sites on GAM116 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM116 target RNA, herein designated GAM TARGET RNA, into GAM116 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1531] It is appreciated that GAM116 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM116 target genes. The mRNA of each one of this plurality of GAM116 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM116 RNA, herein designated GAM RNA, and which when bound by GAM116 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM116 target proteins.

[1532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM116 gene, herein designated GAM GENE, on one or more GAM116 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM116 correlate with, and may be deduced from, the identity of the target genes which GAM116 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1534] Nucleotide sequences of the GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM116 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM116 are further described hereinbelow with reference to Table Table1.

[1535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM116 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1536]

[1537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 117 (GAM117) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1538] GAM117 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM117 was detected is described hereinabove with reference to Figs. 2-8.

[1539] GAM117 gene, herein designated GAM GENE, and GAM117 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1540] GAM117 gene, herein designated GAM GENE, encodes a GAM117 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM117 precursor RNA is designated SEQ ID:1616, and is provided hereinbelow with reference to the sequence listing part.

[1541] GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1542] An enzyme complex designated DICER COMPLEX, dices the GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM117 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of

GAM117 RNA is designated SEQ ID:1617, and is provided hereinbelow with reference to the sequence listing part.

[1543] GAM117 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM117 target RNA, herein designated GAM TARGET RNA. GAM117 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1544] GAM117 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM117 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM117 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM117 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM117 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1545] The complementary binding of GAM117 RNA, herein designated GAM RNA, to target binding sites on GAM117 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM117 target RNA, herein designated GAM TARGET RNA, into GAM117 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1546] It is appreciated that GAM117 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM117 target genes. The mRNA of each one of this plurality of GAM117 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM117 RNA, herein designated GAM RNA, and which when bound by GAM117 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM117 target proteins.

[1547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM117 gene, herein designated GAM GENE, on one or more GAM117 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM117 correlate with, and may be deduced from, the identity of the target genes which GAM117 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1549] Nucleotide sequences of the GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM117 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM117 are further described hereinbelow with reference to Table Table1.

[1550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM117 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1551]

[1552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 118 (GAM118) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1553] GAM118 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM118 was detected is described hereinabove

with reference to Figs. 2-8.

[1554] GAM118 gene, herein designated GAM GENE, and GAM118 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1555] GAM118 gene, herein designated GAM GENE, encodes a GAM118 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM118 precursor RNA is designated SEQ ID:1655, and is provided hereinbelow with reference to the sequence listing part.

[1556] GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1557] An enzyme complex designated DICER COMPLEX, dices the GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM118 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM118 RNA is designated SEQ ID:1617, and is provided hereinbelow with reference to the sequence listing part.

[1558] GAM118 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM118 target RNA, herein designated GAM TARGET RNA. GAM118 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1559] GAM118 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM118 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM118 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM118 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM118 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1560] The complementary binding of GAM118 RNA, herein designated GAM RNA, to target binding sites on GAM118 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM118 target RNA, herein designated GAM TARGET RNA, into GAM118 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[1561] It is appreciated that GAM118 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM118 target genes. The mRNA of each one of this plurality of GAM118 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM118 RNA, herein designated GAM RNA, and which when bound by GAM118 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM118 target proteins.

[1562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM118 gene, herein designated GAM GENE, on one or more GAM118 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1563] It is yet further appreciated that specific functions, and accordingly utilities, of GAM118 correlate with, and may be deduced from, the identity of the target genes which GAM118 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1564] Nucleotide sequences of the GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM118 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM118 are further described hereinbelow with reference to Table Table1.

[1565] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM118 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1566]

[1567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 119 (GAM119) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1568] GAM119 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM119 was detected is described hereinabove with reference to Figs. 2-8.

[1569] GAM119 gene, herein designated GAM GENE, and GAM119 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1570] GAM119 gene, herein designated GAM GENE, encodes a GAM119 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM119 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM119 precursor RNA is designated SEQ ID:1667, and is provided hereinbelow with reference to the sequence listing part.

[1571] GAM119 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1572] An enzyme complex designated DICER COMPLEX, dices the GAM119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM119 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 17%) nucleotide sequence of GAM119 RNA is designated SEQ ID:1668, and is provided hereinbelow with reference to the sequence listing part.

[1573] GAM119 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM119 target RNA, herein designated GAM TARGET RNA.

GAM119 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1574] GAM119 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM119 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM119 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM119 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM119 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1575] The complementary binding of GAM119 RNA, herein designated GAM RNA, to target binding sites on GAM119 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM119 target RNA, herein designated GAM TARGET RNA, into GAM119 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1576] It is appreciated that GAM119 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM119 target genes. The mRNA of each one of this plurality of GAM119 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM119 RNA, herein designated GAM RNA, and which when bound by GAM119 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM119 target proteins.

[1577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM119 gene, herein designated GAM GENE, on one or more GAM119 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM119 correlate with, and may be deduced from, the identity of the target genes which GAM119 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1579] Nucleotide sequences of the GAM119 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM119 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM119 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM119 are further described hereinbelow with reference to Table Table1.

[1580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM119 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1581]

[1582] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 120 (GAM120) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1583] GAM120 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM120 was detected is described hereinabove with reference to Figs. 2-8.

[1584] GAM120 gene, herein designated GAM GENE, and GAM120 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1585] GAM120 gene, herein designated GAM GENE, encodes a

GAM120 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM120 precursor RNA is designated SEQ ID:1684, and is provided hereinbelow with reference to the sequence listing part.

[1586] GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1587] An enzyme complex designated DICER COMPLEX, dices the GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM120 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM120 RNA is designated SEQ ID:1685, and is provided hereinbelow with reference to the sequence listing part.

[1588] GAM120 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM120 target RNA, herein designated GAM TARGET RNA. GAM120 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1589] GAM120 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM120 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM120 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM120 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM120 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1590] The complementary binding of GAM120 RNA, herein designated GAM RNA, to target binding sites on GAM120 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM120 target RNA, herein designated GAM TARGET RNA, into GAM120 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1591] It is appreciated that GAM120 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM120 target genes. The mRNA of each one of this plurality of GAM120 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM120 RNA, herein designated GAM RNA, and which when bound by GAM120 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM120 target proteins.

[1592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM120 gene, herein designated GAM GENE, on one or more GAM120 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1593] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM120 correlate with, and may be deduced from, the identity of the target genes which GAM120 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1594] Nucleotide sequences of the GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM120 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM120 are further described hereinbelow with reference to Table Table1.

[1595] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM120 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1596]

[1597] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 121 (GAM121) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[1598] GAM121 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM121 was detected is described hereinabove with reference to Figs. 2-8.

[1599] GAM121 gene, herein designated GAM GENE, and GAM121 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1600] GAM121 gene, herein designated GAM GENE, encodes a GAM121 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM121 precursor RNA is designated SEQ ID:1699, and is provided hereinbelow with reference to the sequence listing part.

[1601] GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1602] An enzyme complex designated DICER COMPLEX, dices the GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM121 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM121 RNA is designated SEQ ID:1700, and is provided hereinbelow with reference to the sequence listing part.

[1603] GAM121 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM121 target RNA, herein designated GAM TARGET RNA. GAM121 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1604] GAM121 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM121 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM121 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM121 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM121 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1605] The complementary binding of GAM121 RNA, herein designated GAM RNA, to target binding sites on GAM121 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM121 target RNA, herein designated GAM TARGET RNA, into GAM121 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1606] It is appreciated that GAM121 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM121 target genes. The mRNA of each one of this plurality of GAM121 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM121 RNA, herein designated GAM RNA, and which when bound by GAM121 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM121 target proteins.

[1607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM121 gene, herein designated GAM GENE, on one or more GAM121 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1608] It is yet further appreciated that specific functions, and accordingly utilities, of GAM121 correlate with, and may be deduced from, the identity of the target genes which GAM121 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1609] Nucleotide sequences of the GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM121 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM121 are further described hereinbelow with reference to Table Table1.

[1610] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM121 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1611]

[1612] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 122 (GAM122) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1613] GAM122 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM122 was detected is described hereinabove with reference to Figs. 2-8.

[1614] GAM122 gene, herein designated GAM GENE, and GAM122 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1615] GAM122 gene, herein designated GAM GENE, encodes a GAM122 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM122 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM122 precursor RNA is designated SEQ ID:1702, and is provided hereinbelow with reference to the sequence listing part.

[1616] GAM122 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1617] An enzyme complex designated DICER COMPLEX, dices the GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM122 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM122 RNA is designated SEQ ID:1703, and is provided

hereinbelow with reference to the sequence listing part.

[1618] GAM122 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM122 target RNA, herein designated GAM TARGET RNA.
GAM122 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1619] GAM122 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM122 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM122 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM122 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM122 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1620] The complementary binding of GAM122 RNA, herein designated GAM RNA, to target binding sites on GAM122 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM122 target RNA, herein designated GAM TARGET RNA, into GAM122 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1621] It is appreciated that GAM122 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM122 target genes. The mRNA of each one of this plurality of GAM122 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM122 RNA, herein designated GAM RNA, and which when bound by GAM122 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM122 tar-

get proteins.

[1622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM122 gene, herein designated GAM GENE, on one or more GAM122 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1623] It is yet further appreciated that specific functions, and accordingly utilities, of GAM122 correlate with, and may be deduced from, the identity of the target genes which GAM122 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1624] Nucleotide sequences of the GAM122 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM122 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM122 are further described hereinbelow with reference to Table Table1.

[1625] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM122 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1626]

[1627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 123 (GAM123) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1628] GAM123 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM123 was detected is described hereinabove with reference to Figs. 2-8.

[1629] GAM123 gene, herein designated GAM GENE, and GAM123 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1630] GAM123 gene, herein designated GAM GENE, encodes a GAM123 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM123 precursor RNA is designated SEQ ID:1722, and is provided hereinbelow with reference to the sequence listing part.

[1631] GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1632] An enzyme complex designated DICER COMPLEX, dices

the GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM123 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM123 RNA is designated SEQ ID:1723, and is provided hereinbelow with reference to the sequence listing part.

[1633] GAM123 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM123 target RNA, herein designated GAM TARGET RNA.
GAM123 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1634] GAM123 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM123 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM123

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM123 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM123 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1635] The complementary binding of GAM123 RNA, herein designated GAM RNA, to target binding sites on GAM123 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM123 target RNA, herein designated GAM TARGET RNA, into GAM123 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1636] It is appreciated that GAM123 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM123 target genes. The mRNA of each one of this plurality of GAM123 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM123 RNA, herein designated GAM RNA, and which when bound by GAM123 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM123 target proteins.

[1637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM123 gene, herein designated GAM GENE, on one or more GAM123 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM123 correlate with, and may be deduced from, the identity of the target genes which GAM123 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1639] Nucleotide sequences of the GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM123 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM123 are further described hereinbelow with reference to Table Table1.

[1640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM123 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1641]

[1642] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 124 (GAM124) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1643] GAM124 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM124 was detected is described hereinabove with reference to Figs. 2-8.

[1644] GAM124 gene, herein designated GAM GENE, and GAM124 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1645] GAM124 gene, herein designated GAM GENE, encodes a GAM124 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM124 precursor RNA is designated SEQ ID:1734, and is provided hereinbelow with reference to the sequence listing part.

[1646] GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM124 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1647] An enzyme complex designated DICER COMPLEX, dices the GAM124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM124 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM124 RNA is designated SEQ ID:1735, and is provided hereinbelow with reference to the sequence listing part.

[1648] GAM124 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM124 target RNA, herein designated GAM TARGET RNA. GAM124 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1649] GAM124 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM124 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM124 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM124 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM124 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1650] The complementary binding of GAM124 RNA, herein designated GAM RNA, to target binding sites on GAM124 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM124 target RNA, herein designated GAM TARGET RNA, into GAM124 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1651] It is appreciated that GAM124 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM124 target genes. The mRNA of each one of this plurality of GAM124 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM124 RNA, herein designated GAM RNA, and which when bound by GAM124 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM124 target proteins.

[1652] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM124 gene, herein designated GAM GENE, on one or

more GAM124 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1653] It is yet further appreciated that specific functions, and accordingly utilities, of GAM124 correlate with, and may be deduced from, the identity of the target genes which GAM124 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1654] Nucleotide sequences of the GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM124 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM124 are further de-

scribed hereinbelow with reference to Table Table1.

[1655] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM124 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1656]

[1657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 125 (GAM125) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1658] GAM125 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM125 was detected is described hereinabove with reference to Figs. 2-8.

[1659] GAM125 gene, herein designated GAM GENE, and GAM125 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1660] GAM125 gene, herein designated GAM GENE, encodes a GAM125 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM125 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM125 precursor RNA is designated SEQ ID:1741, and is provided hereinbelow with reference to the sequence listing part.

[1661] GAM125 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1662] An enzyme complex designated DICER COMPLEX, dices the GAM125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM125 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 21%) nucleotide sequence of GAM125 RNA is designated SEQ ID:1742, and is provided hereinbelow with reference to the sequence listing part.

[1663] GAM125 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM125 target RNA, herein designated GAM TARGET RNA. GAM125 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1664] GAM125 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM125 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM125 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM125 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM125 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1665] The complementary binding of GAM125 RNA, herein designated GAM RNA, to target binding sites on GAM125 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM125 target RNA, herein designated GAM TARGET RNA, into GAM125 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1666] It is appreciated that GAM125 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM125 target genes. The mRNA of each one of this plurality of GAM125 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM125 RNA, herein designated GAM RNA, and which when bound by GAM125 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM125 target proteins.

[1667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM125 gene, herein designated GAM GENE, on one or more GAM125 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM125 correlate with, and may

be deduced from, the identity of the target genes which GAM125 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1669] Nucleotide sequences of the GAM125 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM125 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM125 are further described hereinbelow with reference to Table Table1.

[1670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM125 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1671]

[1672] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 126 (GAM126) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1673] GAM126 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM126 was detected is described hereinabove with reference to Figs. 2-8.

[1674] GAM126 gene, herein designated GAM GENE, and GAM126 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1675] GAM126 gene, herein designated GAM GENE, encodes a GAM126 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM126 precursor RNA is designated SEQ ID:1770, and is provided hereinbelow with reference to the sequence listing part.

[1676] GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1677] An enzyme complex designated DICER COMPLEX, dices the GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM126 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM126 RNA is designated SEQ ID:1771, and is provided hereinbelow with reference to the sequence listing part.

[1678] GAM126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM126 target RNA, herein designated GAM TARGET RNA. GAM126 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1679] GAM126 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM126 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM126 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM126 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1680] The complementary binding of GAM126 RNA, herein designated GAM RNA, to target binding sites on GAM126 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM126 target RNA, herein designated GAM TARGET RNA, into GAM126 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1681] It is appreciated that GAM126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM126 target genes. The mRNA of each one of this plurality of GAM126 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM126 RNA, herein designated GAM RNA, and which when bound by GAM126 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM126 target proteins.

[1682] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM126 gene, herein designated GAM GENE, on one or more GAM126 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1683] It is yet further appreciated that specific functions, and accordingly utilities, of GAM126 correlate with, and may be deduced from, the identity of the target genes which GAM126 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1684] Nucleotide sequences of the GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM126 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM126 are further described hereinbelow with reference to Table Table1.

[1685] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM126 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1686]

[1687] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 127 (GAM127) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1688] GAM127 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM127 was detected is described hereinabove with reference to Figs. 2-8.

[1689] GAM127 gene, herein designated GAM GENE, and GAM127 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1690] GAM127 gene, herein designated GAM GENE, encodes a GAM127 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM127 precursor RNA is desig-

nated SEQ ID:1780, and is provided hereinbelow with reference to the sequence listing part.

[1691] GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1692] An enzyme complex designated DICER COMPLEX, dices the GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM127 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of GAM127 RNA is designated SEQ ID:1781, and is provided hereinbelow with reference to the sequence listing part.

[1693] GAM127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM127 target RNA, herein designated GAM TARGET RNA. GAM127 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1694] GAM127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM127 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM127 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM127 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM127

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1695] The complementary binding of GAM127 RNA, herein designated GAM RNA, to target binding sites on GAM127 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM127 target RNA, herein designated GAM TARGET RNA, into GAM127 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1696] It is appreciated that GAM127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM127 target genes. The mRNA of each one of this plurality of GAM127 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM127 RNA, herein designated GAM RNA, and which when bound by GAM127 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM127 target proteins.

[1697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM127 gene, herein designated GAM GENE, on one or more GAM127 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1698] It is yet further appreciated that specific functions, and accordingly utilities, of GAM127 correlate with, and may be deduced from, the identity of the target genes which GAM127 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1699] Nucleotide sequences of the GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM127 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM127 are further described hereinbelow with reference to Table Table1.

[1700] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM127 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1701]

[1702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 128 (GAM128) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1703] GAM128 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM128 was detected is described hereinabove with reference to Figs. 2-8.

[1704] GAM128 gene, herein designated GAM GENE, and

GAM128 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1705] GAM128 gene, herein designated GAM GENE, encodes a GAM128 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM128 precursor RNA is designated SEQ ID:1786, and is provided hereinbelow with reference to the sequence listing part.

[1706] GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1707] An enzyme complex designated DICER COMPLEX, dices the GAM128 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM128 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 19%) nucleotide sequence of GAM128 RNA is designated SEQ ID:1787, and is provided hereinbelow with reference to the sequence listing part.

[1708] GAM128 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM128 target RNA, herein designated GAM TARGET RNA. GAM128 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1709] GAM128 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM128 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM128 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM128 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM128 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1710] The complementary binding of GAM128 RNA, herein designated GAM RNA, to target binding sites on GAM128 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM128 target RNA, herein designated GAM TARGET RNA, into GAM128 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1711] It is appreciated that GAM128 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM128 target genes. The mRNA of each one of this plurality of GAM128 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM128 RNA, herein designated GAM RNA, and which when bound by GAM128 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM128 target proteins.

[1712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM128 gene, herein designated GAM GENE, on one or more GAM128 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM128 correlate with, and may be deduced from, the identity of the target genes which GAM128 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1714] Nucleotide sequences of the GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM128 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM128 are further described hereinbelow with reference to Table Table1.

[1715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM128 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1716]

[1717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 129 (GAM129) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1718] GAM129 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM129 was detected is described hereinabove with reference to Figs. 2-8.

[1719] GAM129 gene, herein designated GAM GENE, and GAM129 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1720] GAM129 gene, herein designated GAM GENE, encodes a GAM129 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM129 precursor RNA is designated SEQ ID:1803, and is provided hereinbelow with reference to the sequence listing part.

[1721] GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1722] An enzyme complex designated DICER COMPLEX, dices the GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM129 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 28%) nucleotide sequence of GAM129 RNA is designated SEQ ID:1804, and is provided hereinbelow with reference to the sequence listing part.

[1723] GAM129 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM129 target RNA, herein designated GAM TARGET RNA. GAM129 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1724] GAM129 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM129 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM129 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM129 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM129 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1725] The complementary binding of GAM129 RNA, herein designated GAM RNA, to target binding sites on GAM129 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM129 target RNA, herein designated GAM TARGET RNA, into GAM129 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1726] It is appreciated that GAM129 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM129 target genes. The mRNA of each one of this plurality of GAM129 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM129 RNA, herein designated GAM RNA, and which when bound by GAM129 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM129 target proteins.

[1727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM129 gene, herein designated GAM GENE, on one or more GAM129 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1728] It is yet further appreciated that specific functions, and accordingly utilities, of GAM129 correlate with, and may be deduced from, the identity of the target genes which GAM129 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1729] Nucleotide sequences of the GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM129 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM129 are further described hereinbelow with reference to Table Table1.

[1730] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM129 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1731]

[1732] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 130 (GAM130) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1733] GAM130 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM130 was detected is described hereinabove with reference to Figs. 2-8.

[1734] GAM130 gene, herein designated GAM GENE, and GAM130 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1735] GAM130 gene, herein designated GAM GENE, encodes a GAM130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM130 precursor RNA is designated SEQ ID:1812, and is provided hereinbelow with reference to the sequence listing part.

[1736] GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1737] An enzyme complex designated DICER COMPLEX, dices the GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM130 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM130 RNA is designated SEQ ID:1813, and is provided hereinbelow with reference to the sequence listing part.

[1738] GAM130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM130 target RNA, herein designated GAM TARGET RNA. GAM130 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1739] GAM130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM130 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM130 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM130 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1740] The complementary binding of GAM130 RNA, herein designated GAM RNA, to target binding sites on GAM130 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM130 target RNA, herein designated GAM TARGET RNA, into GAM130 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1741] It is appreciated that GAM130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM130 target genes. The mRNA of each one of this plurality of GAM130 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM130 RNA,

herein designated GAM RNA, and which when bound by GAM130 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM130 target proteins.

[1742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM130 gene, herein designated GAM GENE, on one or more GAM130 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1743] It is yet further appreciated that specific functions, and accordingly utilities, of GAM130 correlate with, and may be deduced from, the identity of the target genes which

GAM130 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1744] Nucleotide sequences of the GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM130 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM130 are further described hereinbelow with reference to Table Table1.

[1745] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM130 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1746]

[1747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 131 (GAM131) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1748] GAM131 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM131 was detected is described hereinabove with reference to Figs. 2-8.

[1749] GAM131 gene, herein designated GAM GENE, and GAM131 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1750] GAM131 gene, herein designated GAM GENE, encodes a GAM131 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM131 precursor RNA is designated SEQ ID:1825, and is provided hereinbelow with reference to the sequence listing part.

[1751] GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1752] An enzyme complex designated DICER COMPLEX, dices the GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM131 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM131 RNA is designated SEQ ID:1826, and is provided hereinbelow with reference to the sequence listing part.

[1753] GAM131 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM131 target RNA, herein designated GAM TARGET RNA.
GAM131 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1754] GAM131 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM131 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM131 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM131 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM131 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1755] The complementary binding of GAM131 RNA, herein designated GAM RNA, to target binding sites on GAM131 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM131 target RNA, herein desig-

nated GAM TARGET RNA, into GAM131 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1756] It is appreciated that GAM131 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM131 target genes. The mRNA of each one of this plurality of GAM131 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM131 RNA, herein designated GAM RNA, and which when bound by GAM131 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM131 target proteins.

[1757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM131 gene, herein designated GAM GENE, on one or more GAM131 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM131 correlate with, and may be deduced from, the identity of the target genes which GAM131 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1759] Nucleotide sequences of the GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM131 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM131 are further described hereinbelow with reference to Table Table1.

[1760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM131 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1761]

[1762] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 132 (GAM132) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1763] GAM132 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM132 was detected is described hereinabove with reference to Figs. 2-8.

[1764] GAM132 gene, herein designated GAM GENE, and GAM132 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1765] GAM132 gene, herein designated GAM GENE, encodes a GAM132 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM132 precursor RNA is designated SEQ ID:1842, and is provided hereinbelow with ref-

erence to the sequence listing part.

[1766] GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1767] An enzyme complex designated DICER COMPLEX, dices the GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM132 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 20%) nucleotide sequence of GAM132 RNA is designated SEQ ID:1843, and is provided hereinbelow with reference to the sequence listing part.

[1768] GAM132 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM132 target RNA, herein designated GAM TARGET RNA.

GAM132 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1769] GAM132 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM132 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM132 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM132 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM132 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1770] The complementary binding of GAM132 RNA, herein designated GAM RNA, to target binding sites on GAM132 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM132 target RNA, herein designated GAM TARGET RNA, into GAM132 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1771] It is appreciated that GAM132 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM132 target genes. The mRNA of each one of this plurality of GAM132 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM132 RNA, herein designated GAM RNA, and which when bound by GAM132 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM132 target proteins.

[1772] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM132 gene, herein designated GAM GENE, on one or more GAM132 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1773] It is yet further appreciated that specific functions, and accordingly utilities, of GAM132 correlate with, and may be deduced from, the identity of the target genes which GAM132 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1774] Nucleotide sequences of the GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM132 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM132 are further described hereinbelow with reference to Table Table1.

[1775] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM132 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1776]

[1777] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 133 (GAM133) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1778] GAM133 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM133 was detected is described hereinabove with reference to Figs. 2-8.

[1779] GAM133 gene, herein designated GAM GENE, and GAM133 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[1780] GAM133 gene, herein designated GAM GENE, encodes a GAM133 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM133 precursor RNA is designated SEQ ID:1857, and is provided hereinbelow with reference to the sequence listing part.

[1781] GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1782] An enzyme complex designated DICER COMPLEX, dices the GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM133 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM133 RNA is designated SEQ ID:1858, and is provided hereinbelow with reference to the sequence listing part.

[1783] GAM133 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM133 target RNA, herein designated GAM TARGET RNA. GAM133 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1784] GAM133 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM133 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM133 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM133 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM133 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1785] The complementary binding of GAM133 RNA, herein designated GAM RNA, to target binding sites on GAM133 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM133 target RNA, herein designated GAM TARGET RNA, into GAM133 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1786] It is appreciated that GAM133 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM133 target genes. The mRNA of each one of this plurality of GAM133 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM133 RNA, herein designated GAM RNA, and which when bound by GAM133 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM133 target proteins.

[1787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM133 gene, herein designated GAM GENE, on one or more GAM133 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[1788] It is yet further appreciated that specific functions, and accordingly utilities, of GAM133 correlate with, and may be deduced from, the identity of the target genes which GAM133 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1789] Nucleotide sequences of the GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM133 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM133 are further described hereinbelow with reference to Table Table1.

[1790] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM133 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1791]

[1792] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

134 (GAM134) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1793] GAM134 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM134 was detected is described hereinabove with reference to Figs. 2-8.

[1794] GAM134 gene, herein designated GAM GENE, and GAM134 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1795] GAM134 gene, herein designated GAM GENE, encodes a GAM134 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM134 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM134 precursor RNA is designated SEQ ID:1880, and is provided hereinbelow with reference to the sequence listing part.

[1796] GAM134 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1797] An enzyme complex designated DICER COMPLEX, dices the GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM134 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM134 RNA is designated SEQ ID:1881, and is provided hereinbelow with reference to the sequence listing part.

[1798] GAM134 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM134 target RNA, herein designated GAM TARGET RNA. GAM134 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1799] GAM134 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM134 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM134 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM134 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM134 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1800] The complementary binding of GAM134 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM134 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM134 target RNA, herein designated GAM TARGET RNA, into GAM134 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1801] It is appreciated that GAM134 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM134 target genes. The mRNA of each one of this plurality of GAM134 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM134 RNA, herein designated GAM RNA, and which when bound by GAM134 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM134 target proteins.

[1802] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM134 gene, herein designated GAM GENE, on one or more GAM134 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1803] It is yet further appreciated that specific functions, and accordingly utilities, of GAM134 correlate with, and may be deduced from, the identity of the target genes which GAM134 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1804] Nucleotide sequences of the GAM134 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM134 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM134 are further described hereinbelow with reference to Table Table1.

[1805] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM134 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1806]

[1807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 135 (GAM135) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1808] GAM135 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM135 was detected is described hereinabove with reference to Figs. 2-8.

[1809] GAM135 gene, herein designated GAM GENE, and GAM135 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1810] GAM135 gene, herein designated GAM GENE, encodes a GAM135 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM135 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM135 precursor RNA is designated SEQ ID:1887, and is provided hereinbelow with reference to the sequence listing part.

[1811] GAM135 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1812] An enzyme complex designated DICER COMPLEX, dices the GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM135 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 57%) nucleotide sequence of GAM135 RNA is designated SEQ ID:1888, and is provided hereinbelow with reference to the sequence listing part.

[1813] GAM135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM135 target RNA, herein designated GAM TARGET RNA. GAM135 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1814] GAM135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM135 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM135 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM135 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM135 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1815] The complementary binding of GAM135 RNA, herein designated GAM RNA, to target binding sites on GAM135 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM135 target RNA, herein designated GAM TARGET RNA, into GAM135 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1816] It is appreciated that GAM135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM135 target genes. The mRNA of each one of this plurality of GAM135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM135 RNA, herein designated GAM RNA, and which when bound by

GAM135 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM135 target proteins.

[1817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM135 gene, herein designated GAM GENE, on one or more GAM135 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1818] It is yet further appreciated that specific functions, and accordingly utilities, of GAM135 correlate with, and may be deduced from, the identity of the target genes which GAM135 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[1819] Nucleotide sequences of the GAM135 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM135 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM135 are further described hereinbelow with reference to Table Table1.

[1820] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM135 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1821]

[1822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 136 (GAM136) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1823] GAM136 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM136 was detected is described hereinabove with reference to Figs. 2-8.

[1824] GAM136 gene, herein designated GAM GENE, and GAM136 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1825] GAM136 gene, herein designated GAM GENE, encodes a GAM136 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM136 precursor RNA is designated SEQ ID:1898, and is provided hereinbelow with reference to the sequence listing part.

[1826] GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1827] An enzyme complex designated DICER COMPLEX, dices the GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM136 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM136 RNA is designated SEQ ID:1899, and is provided hereinbelow with reference to the sequence listing part.

[1828] GAM136 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM136 target RNA, herein designated GAM TARGET RNA. GAM136 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1829] GAM136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM136 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM136 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM136 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM136 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1830] The complementary binding of GAM136 RNA, herein designated GAM RNA, to target binding sites on GAM136 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM136 target RNA, herein designated GAM TARGET RNA, into GAM136 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1831] It is appreciated that GAM136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM136 target genes. The mRNA of each one of this plurality of GAM136 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM136 RNA, herein designated GAM RNA, and which when bound by GAM136 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM136 target proteins.

[1832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM136 gene, herein designated GAM GENE, on one or more GAM136 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM136 correlate with, and may be deduced from, the identity of the target genes which GAM136 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1834] Nucleotide sequences of the GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM136 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM136 are further described hereinbelow with reference to Table Table1.

[1835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM136 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1836]

[1837] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 137 (GAM137) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1838] GAM137 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM137 was detected is described hereinabove with reference to Figs. 2-8.

[1839] GAM137 gene, herein designated GAM GENE, and GAM137 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1840] GAM137 gene, herein designated GAM GENE, encodes a GAM137 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM137 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM137 precursor RNA is designated SEQ ID:1907, and is provided hereinbelow with reference to the sequence listing part.

[1841] GAM137 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1842] An enzyme complex designated DICER COMPLEX, dices the GAM137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM137 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM137 RNA is designated SEQ ID:1908, and is provided hereinbelow with reference to the sequence listing part.

[1843] GAM137 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM137

target RNA, herein designated GAM TARGET RNA.

GAM137 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1844] GAM137 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM137 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM137 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM137 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM137 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1845] The complementary binding of GAM137 RNA, herein designated GAM RNA, to target binding sites on GAM137 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM137 target RNA, herein designated GAM TARGET RNA, into GAM137 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1846] It is appreciated that GAM137 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM137 target genes. The mRNA of each one of this plurality of GAM137 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM137 RNA, herein designated GAM RNA, and which when bound by GAM137 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM137 target proteins.

[1847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM137 gene, herein designated GAM GENE, on one or more GAM137 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1848] It is yet further appreciated that specific functions, and accordingly utilities, of GAM137 correlate with, and may be deduced from, the identity of the target genes which GAM137 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1849] Nucleotide sequences of the GAM137 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM137 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM137 are further described hereinbelow with reference to Table Table1.

[1850] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM137 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1851]

[1852] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 138 (GAM138) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1853] GAM138 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM138 was detected is described hereinabove with reference to Figs. 2-8.

[1854] GAM138 gene, herein designated GAM GENE, and GAM138 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1855] GAM138 gene, herein designated GAM GENE, encodes a GAM138 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM138 precursor RNA is designated SEQ ID:1922, and is provided hereinbelow with reference to the sequence listing part.

[1856] GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1857] An enzyme complex designated DICER COMPLEX, dices the GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM138 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM138 RNA is designated SEQ ID:1923, and is provided hereinbelow with reference to the sequence listing part.

[1858] GAM138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM138 target RNA, herein designated GAM TARGET RNA. GAM138 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1859] GAM138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM138 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM138 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM138 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1860] The complementary binding of GAM138 RNA, herein designated GAM RNA, to target binding sites on GAM138 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM138 target RNA, herein designated GAM TARGET RNA, into GAM138 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1861] It is appreciated that GAM138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM138 target genes. The mRNA of each one of this plu-

rality of GAM138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM138 RNA, herein designated GAM RNA, and which when bound by GAM138 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM138 target proteins.

[1862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM138 gene, herein designated GAM GENE, on one or more GAM138 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1863] It is yet further appreciated that specific functions, and accordingly utilities, of GAM138 correlate with, and may be deduced from, the identity of the target genes which GAM138 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1864] Nucleotide sequences of the GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM138 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM138 are further described hereinbelow with reference to Table Table1.

[1865] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM138 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1866]

[1867] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 139 (GAM139) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[1868] GAM139 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM139 was detected is described hereinabove with reference to Figs. 2-8.

[1869] GAM139 gene, herein designated GAM GENE, and GAM139 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1870] GAM139 gene, herein designated GAM GENE, encodes a GAM139 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM139 precursor RNA is designated SEQ ID:1947, and is provided hereinbelow with reference to the sequence listing part.

[1871] GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1872] An enzyme complex designated DICER COMPLEX, dices the GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM139 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 38%) nucleotide sequence of GAM139 RNA is designated SEQ ID:1948, and is provided hereinbelow with reference to the sequence listing part.

[1873] GAM139 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM139 target RNA, herein designated GAM TARGET RNA.
GAM139 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[1874] GAM139 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM139 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM139 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM139 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM139 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1875] The complementary binding of GAM139 RNA, herein designated GAM RNA, to target binding sites on GAM139 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM139 target RNA, herein designated GAM TARGET RNA, into GAM139 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1876] It is appreciated that GAM139 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM139 target genes. The mRNA of each one of this plurality of GAM139 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM139 RNA, herein designated GAM RNA, and which when bound by GAM139 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM139 target proteins.

[1877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM139 gene, herein designated GAM GENE, on one or more GAM139 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM139 correlate with, and may be deduced from, the identity of the target genes which GAM139 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1879] Nucleotide sequences of the GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM139 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM139 are further described hereinbelow with reference to Table Table1.

[1880] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM139 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1881]

[1882] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 140 (GAM140) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1883] GAM140 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM140 was detected is described hereinabove with reference to Figs. 2-8.

[1884] GAM140 gene, herein designated GAM GENE, and GAM140 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1885] GAM140 gene, herein designated GAM GENE, encodes a GAM140 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM140 precursor RNA is designated SEQ ID:1954, and is provided hereinbelow with reference to the sequence listing part.

[1886] GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1887] An enzyme complex designated DICER COMPLEX, dices the GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM140 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of

GAM140 RNA is designated SEQ ID:1955, and is provided hereinbelow with reference to the sequence listing part.

[1888] GAM140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM140 target RNA, herein designated GAM TARGET RNA. GAM140 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1889] GAM140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM140 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM140 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM140 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1890] The complementary binding of GAM140 RNA, herein designated GAM RNA, to target binding sites on GAM140 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM140 target RNA, herein designated GAM TARGET RNA, into GAM140 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1891] It is appreciated that GAM140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM140 target genes. The mRNA of each one of this plurality of GAM140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM140 RNA, herein designated GAM RNA, and which when bound by GAM140 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM140 target proteins.

[1892] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM140 gene, herein designated GAM GENE, on one or more GAM140 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1893] It is yet further appreciated that specific functions, and accordingly utilities, of GAM140 correlate with, and may be deduced from, the identity of the target genes which GAM140 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1894] Nucleotide sequences of the GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM140 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM140 are further described hereinbelow with reference to Table Table1.

[1895] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM140 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1896]

[1897] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 141 (GAM141) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1898] GAM141 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM141 was detected is described hereinabove

with reference to Figs. 2-8.

[1899] GAM141 gene, herein designated GAM GENE, and GAM141 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1900] GAM141 gene, herein designated GAM GENE, encodes a GAM141 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM141 precursor RNA is designated SEQ ID:1967, and is provided hereinbelow with reference to the sequence listing part.

[1901] GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1902] An enzyme complex designated DICER COMPLEX, dices the GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM141 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM141 RNA is designated SEQ ID:1968, and is provided hereinbelow with reference to the sequence listing part.

[1903] GAM141 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM141 target RNA, herein designated GAM TARGET RNA. GAM141 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1904] GAM141 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM141 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM141 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM141 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM141 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1905] The complementary binding of GAM141 RNA, herein designated GAM RNA, to target binding sites on GAM141 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM141 target RNA, herein designated GAM TARGET RNA, into GAM141 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[1906] It is appreciated that GAM141 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM141 target genes. The mRNA of each one of this plurality of GAM141 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM141 RNA, herein designated GAM RNA, and which when bound by GAM141 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM141 target proteins.

[1907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM141 gene, herein designated GAM GENE, on one or more GAM141 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1908] It is yet further appreciated that specific functions, and accordingly utilities, of GAM141 correlate with, and may be deduced from, the identity of the target genes which GAM141 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1909] Nucleotide sequences of the GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM141 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM141 are further described hereinbelow with reference to Table Table1.

[1910] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM141 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1911]

[1912] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 142 (GAM142) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1913] GAM142 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM142 was detected is described hereinabove with reference to Figs. 2-8.

[1914] GAM142 gene, herein designated GAM GENE, and GAM142 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1915] GAM142 gene, herein designated GAM GENE, encodes a GAM142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM142 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM142 precursor RNA is designated SEQ ID:1983, and is provided hereinbelow with reference to the sequence listing part.

[1916] GAM142 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1917] An enzyme complex designated DICER COMPLEX, dices the GAM142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM142 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM142 RNA is designated SEQ ID:1984, and is provided hereinbelow with reference to the sequence listing part.

[1918] GAM142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM142 target RNA, herein designated GAM TARGET RNA.

GAM142 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1919] GAM142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM142 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM142 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM142 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM142 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1920] The complementary binding of GAM142 RNA, herein designated GAM RNA, to target binding sites on GAM142 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM142 target RNA, herein designated GAM TARGET RNA, into GAM142 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1921] It is appreciated that GAM142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM142 target genes. The mRNA of each one of this plurality of GAM142 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM142 RNA, herein designated GAM RNA, and which when bound by GAM142 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM142 target proteins.

[1922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM142 gene, herein designated GAM GENE, on one or more GAM142 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1923] It is yet further appreciated that specific functions, and accordingly utilities, of GAM142 correlate with, and may be deduced from, the identity of the target genes which GAM142 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1924] Nucleotide sequences of the GAM142 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM142 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM142 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM142 are further described hereinbelow with reference to Table Table1.

[1925] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM142 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1926]

[1927] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 143 (GAM143) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1928] GAM143 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM143 was detected is described hereinabove with reference to Figs. 2-8.

[1929] GAM143 gene, herein designated GAM GENE, and GAM143 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1930] GAM143 gene, herein designated GAM GENE, encodes a

GAM143 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM143 precursor RNA is designated SEQ ID:1992, and is provided hereinbelow with reference to the sequence listing part.

[1931] GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1932] An enzyme complex designated DICER COMPLEX, dices the GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM143 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM143 RNA is designated SEQ ID:1993, and is provided hereinbelow with reference to the sequence listing part.

[1933] GAM143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM143 target RNA, herein designated GAM TARGET RNA. GAM143 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1934] GAM143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM143 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM143 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM143 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1935] The complementary binding of GAM143 RNA, herein designated GAM RNA, to target binding sites on GAM143 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM143 target RNA, herein designated GAM TARGET RNA, into GAM143 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1936] It is appreciated that GAM143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM143 target genes. The mRNA of each one of this plurality of GAM143 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM143 RNA, herein designated GAM RNA, and which when bound by GAM143 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM143 target proteins.

[1937] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM143 gene, herein designated GAM GENE, on one or more GAM143 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1938] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM143 correlate with, and may be deduced from, the identity of the target genes which GAM143 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1939] Nucleotide sequences of the GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM143 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM143 are further described hereinbelow with reference to Table Table1.

[1940] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM143 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1941]

[1942] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 144 (GAM144) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[1943] GAM144 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM144 was detected is described hereinabove with reference to Figs. 2-8.

[1944] GAM144 gene, herein designated GAM GENE, and GAM144 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1945] GAM144 gene, herein designated GAM GENE, encodes a GAM144 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM144 precursor RNA is designated SEQ ID:2008, and is provided hereinbelow with reference to the sequence listing part.

[1946] GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1947] An enzyme complex designated DICER COMPLEX, dices the GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM144 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM144 RNA is designated SEQ ID:2009, and is provided hereinbelow with reference to the sequence listing part.

[1948] GAM144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM144 target RNA, herein designated GAM TARGET RNA. GAM144 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1949] GAM144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM144 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM144 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM144 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1950] The complementary binding of GAM144 RNA, herein designated GAM RNA, to target binding sites on GAM144 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM144 target RNA, herein designated GAM TARGET RNA, into GAM144 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1951] It is appreciated that GAM144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM144 target genes. The mRNA of each one of this plurality of GAM144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM144 RNA, herein designated GAM RNA, and which when bound by GAM144 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM144 target proteins.

[1952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM144 gene, herein designated GAM GENE, on one or more GAM144 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1953] It is yet further appreciated that specific functions, and accordingly utilities, of GAM144 correlate with, and may be deduced from, the identity of the target genes which GAM144 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1954] Nucleotide sequences of the GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM144 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM144 are further described hereinbelow with reference to Table Table1.

[1955] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM144 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1956]

[1957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 145 (GAM145) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1958] GAM145 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM145 was detected is described hereinabove with reference to Figs. 2-8.

[1959] GAM145 gene, herein designated GAM GENE, and GAM145 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1960] GAM145 gene, herein designated GAM GENE, encodes a GAM145 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM145 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM145 precursor RNA is designated SEQ ID:2020, and is provided hereinbelow with reference to the sequence listing part.

[1961] GAM145 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1962] An enzyme complex designated DICER COMPLEX, dices the GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM145 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM145 RNA is designated SEQ ID:2021, and is provided

hereinbelow with reference to the sequence listing part.

[1963] GAM145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM145 target RNA, herein designated GAM TARGET RNA.

GAM145 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1964] GAM145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM145 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM145 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM145 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM145 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1965] The complementary binding of GAM145 RNA, herein designated GAM RNA, to target binding sites on GAM145 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM145 target RNA, herein designated GAM TARGET RNA, into GAM145 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1966] It is appreciated that GAM145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM145 target genes. The mRNA of each one of this plurality of GAM145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM145 RNA, herein designated GAM RNA, and which when bound by GAM145 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM145 tar-

get proteins.

[1967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM145 gene, herein designated GAM GENE, on one or more GAM145 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1968] It is yet further appreciated that specific functions, and accordingly utilities, of GAM145 correlate with, and may be deduced from, the identity of the target genes which GAM145 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1969] Nucleotide sequences of the GAM145 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM145 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM145 are further described hereinbelow with reference to Table Table1.

[1970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM145 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1971]

[1972] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 146 (GAM146) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1973] GAM146 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM146 was detected is described hereinabove with reference to Figs. 2-8.

[1974] GAM146 gene, herein designated GAM GENE, and GAM146 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1975] GAM146 gene, herein designated GAM GENE, encodes a GAM146 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM146 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM146 precursor RNA is designated SEQ ID:2040, and is provided hereinbelow with reference to the sequence listing part.

[1976] GAM146 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1977] An enzyme complex designated DICER COMPLEX, dices

the GAM146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM146 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of GAM146 RNA is designated SEQ ID:2041, and is provided hereinbelow with reference to the sequence listing part.

[1978] GAM146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM146 target RNA, herein designated GAM TARGET RNA. GAM146 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1979] GAM146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM146

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM146 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM146 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1980] The complementary binding of GAM146 RNA, herein designated GAM RNA, to target binding sites on GAM146 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM146 target RNA, herein designated GAM TARGET RNA, into GAM146 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1981] It is appreciated that GAM146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM146 target genes. The mRNA of each one of this plurality of GAM146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM146 RNA, herein designated GAM RNA, and which when bound by GAM146 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM146 target proteins.

[1982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM146 gene, herein designated GAM GENE, on one or more GAM146 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1983] It is yet further appreciated that specific functions, and accordingly utilities, of GAM146 correlate with, and may be deduced from, the identity of the target genes which GAM146 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1984] Nucleotide sequences of the GAM146 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM146 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM146 are further described hereinbelow with reference to Table Table1.

[1985] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM146 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1986]

[1987] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 147 (GAM147) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1988] GAM147 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM147 was detected is described hereinabove with reference to Figs. 2-8.

[1989] GAM147 gene, herein designated GAM GENE, and GAM147 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1990] GAM147 gene, herein designated GAM GENE, encodes a GAM147 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM147 precursor RNA is designated SEQ ID:2112, and is provided hereinbelow with reference to the sequence listing part.

[1991] GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM147 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1992] An enzyme complex designated DICER COMPLEX, dices the GAM147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM147 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 22%) nucleotide sequence of GAM147 RNA is designated SEQ ID:2113, and is provided hereinbelow with reference to the sequence listing part.

[1993] GAM147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM147 target RNA, herein designated GAM TARGET RNA. GAM147 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1994] GAM147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM147 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM147 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM147 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1995] The complementary binding of GAM147 RNA, herein designated GAM RNA, to target binding sites on GAM147 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM147 target RNA, herein designated GAM TARGET RNA, into GAM147 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1996] It is appreciated that GAM147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM147 target genes. The mRNA of each one of this plurality of GAM147 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM147 RNA, herein designated GAM RNA, and which when bound by GAM147 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM147 target proteins.

[1997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM147 gene, herein designated GAM GENE, on one or

more GAM147 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM147 correlate with, and may be deduced from, the identity of the target genes which GAM147 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1999] Nucleotide sequences of the GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM147 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM147 are further de-

scribed hereinbelow with reference to Table Table1.

[2000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM147 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2001]

[2002] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 148 (GAM148) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2003] GAM148 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM148 was detected is described hereinabove with reference to Figs. 2-8.

[2004] GAM148 gene, herein designated GAM GENE, and GAM148 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2005] GAM148 gene, herein designated GAM GENE, encodes a GAM148 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM148 precursor RNA is designated SEQ ID:2125, and is provided hereinbelow with reference to the sequence listing part.

[2006] GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2007] An enzyme complex designated DICER COMPLEX, dices the GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM148 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM148 RNA is designated SEQ ID:2126, and is provided hereinbelow with reference to the sequence listing part.

[2008] GAM148 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM148 target RNA, herein designated GAM TARGET RNA. GAM148 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2009] GAM148 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM148 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM148 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM148 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2010] The complementary binding of GAM148 RNA, herein designated GAM RNA, to target binding sites on GAM148 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM148 target RNA, herein designated GAM TARGET RNA, into GAM148 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2011] It is appreciated that GAM148 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM148 target genes. The mRNA of each one of this plurality of GAM148 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM148 RNA, herein designated GAM RNA, and which when bound by GAM148 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM148 target proteins.

[2012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM148 gene, herein designated GAM GENE, on one or more GAM148 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2013] It is yet further appreciated that specific functions, and accordingly utilities, of GAM148 correlate with, and may

be deduced from, the identity of the target genes which GAM148 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2014] Nucleotide sequences of the GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM148 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM148 are further described hereinbelow with reference to Table Table1.

[2015] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM148 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2016]

[2017] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 149 (GAM149) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2018] GAM149 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM149 was detected is described hereinabove with reference to Figs. 2-8.

[2019] GAM149 gene, herein designated GAM GENE, and GAM149 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2020] GAM149 gene, herein designated GAM GENE, encodes a GAM149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM149 precursor RNA is designated SEQ ID:2132, and is provided hereinbelow with reference to the sequence listing part.

[2021] GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2022] An enzyme complex designated DICER COMPLEX, dices the GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM149 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM149 RNA is designated SEQ ID:2133, and is provided hereinbelow with reference to the sequence listing part.

[2023] GAM149 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM149 target RNA, herein designated GAM TARGET RNA. GAM149 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2024] GAM149 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM149 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM149 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2025] The complementary binding of GAM149 RNA, herein designated GAM RNA, to target binding sites on GAM149 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM149 target RNA, herein designated GAM TARGET RNA, into GAM149 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2026] It is appreciated that GAM149 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM149 target genes. The mRNA of each one of this plurality of GAM149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM149 RNA, herein designated GAM RNA, and which when bound by GAM149 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM149 target proteins.

[2027] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM149 gene, herein designated GAM GENE, on one or more GAM149 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2028] It is yet further appreciated that specific functions, and accordingly utilities, of GAM149 correlate with, and may be deduced from, the identity of the target genes which GAM149 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2029] Nucleotide sequences of the GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM149 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM149 are further described hereinbelow with reference to Table Table1.

[2030] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM149 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2031]

[2032] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 150 (GAM150) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2033] GAM150 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM150 was detected is described hereinabove with reference to Figs. 2-8.

[2034] GAM150 gene, herein designated GAM GENE, and GAM150 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2035] GAM150 gene, herein designated GAM GENE, encodes a GAM150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM150 precursor RNA is desig-

nated SEQ ID:2141, and is provided hereinbelow with reference to the sequence listing part.

[2036] GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2037] An enzyme complex designated DICER COMPLEX, dices the GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM150 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM150 RNA is designated SEQ ID:2142, and is provided hereinbelow with reference to the sequence listing part.

[2038] GAM150 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM150 target RNA, herein designated GAM TARGET RNA. GAM150 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2039] GAM150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM150 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM150 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM150

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2040] The complementary binding of GAM150 RNA, herein designated GAM RNA, to target binding sites on GAM150 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM150 target RNA, herein designated GAM TARGET RNA, into GAM150 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2041] It is appreciated that GAM150 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM150 target genes. The mRNA of each one of this plurality of GAM150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM150 RNA, herein designated GAM RNA, and which when bound by GAM150 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM150 target proteins.

[2042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM150 gene, herein designated GAM GENE, on one or more GAM150 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2043] It is yet further appreciated that specific functions, and accordingly utilities, of GAM150 correlate with, and may be deduced from, the identity of the target genes which GAM150 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2044] Nucleotide sequences of the GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM150 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM150 are further described hereinbelow with reference to Table Table1.

[2045] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM150 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2046]

[2047] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 151 (GAM151) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2048] GAM151 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM151 was detected is described hereinabove with reference to Figs. 2-8.

[2049] GAM151 gene, herein designated GAM GENE, and

GAM151 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2050] GAM151 gene, herein designated GAM GENE, encodes a GAM151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM151 precursor RNA is designated SEQ ID:2157, and is provided hereinbelow with reference to the sequence listing part.

[2051] GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2052] An enzyme complex designated DICER COMPLEX, dices the GAM151 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM151 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM151 RNA is designated SEQ ID:2158, and is provided hereinbelow with reference to the sequence listing part.

[2053] GAM151 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM151 target RNA, herein designated GAM TARGET RNA. GAM151 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2054] GAM151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM151 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM151 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM151 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2055] The complementary binding of GAM151 RNA, herein designated GAM RNA, to target binding sites on GAM151 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM151 target RNA, herein designated GAM TARGET RNA, into GAM151 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2056] It is appreciated that GAM151 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM151 target genes. The mRNA of each one of this plurality of GAM151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM151 RNA, herein designated GAM RNA, and which when bound by GAM151 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM151 target proteins.

[2057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM151 gene, herein designated GAM GENE, on one or more GAM151 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2058] It is yet further appreciated that specific functions, and accordingly utilities, of GAM151 correlate with, and may be deduced from, the identity of the target genes which GAM151 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2059] Nucleotide sequences of the GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM151 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM151 are further described hereinbelow with reference to Table Table1.

[2060] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM151 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2061]

[2062] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 152 (GAM152) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2063] GAM152 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM152 was detected is described hereinabove with reference to Figs. 2-8.

[2064] GAM152 gene, herein designated GAM GENE, and GAM152 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2065] GAM152 gene, herein designated GAM GENE, encodes a GAM152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM152 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM152 precursor RNA is designated SEQ ID:2170, and is provided hereinbelow with reference to the sequence listing part.

[2066] GAM152 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2067] An enzyme complex designated DICER COMPLEX, dices the GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM152 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM152 RNA is designated SEQ ID:2171, and is provided

hereinbelow with reference to the sequence listing part.

[2068] GAM152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM152 target RNA, herein designated GAM TARGET RNA.
GAM152 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2069] GAM152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM152 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM152 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM152 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2070] The complementary binding of GAM152 RNA, herein designated GAM RNA, to target binding sites on GAM152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM152 target RNA, herein designated GAM TARGET RNA, into GAM152 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2071] It is appreciated that GAM152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM152 target genes. The mRNA of each one of this plurality of GAM152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM152 RNA, herein designated GAM RNA, and which when bound by GAM152 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM152 tar-

get proteins.

[2072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM152 gene, herein designated GAM GENE, on one or more GAM152 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2073] It is yet further appreciated that specific functions, and accordingly utilities, of GAM152 correlate with, and may be deduced from, the identity of the target genes which GAM152 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2074] Nucleotide sequences of the GAM152 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM152 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM152 are further described hereinbelow with reference to Table Table1.

[2075] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM152 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2076]

[2077] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 153 (GAM153) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2078] GAM153 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM153 was detected is described hereinabove with reference to Figs. 2-8.

[2079] GAM153 gene, herein designated GAM GENE, and GAM153 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2080] GAM153 gene, herein designated GAM GENE, encodes a GAM153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM153 precursor RNA is designated SEQ ID:2182, and is provided hereinbelow with reference to the sequence listing part.

[2081] GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2082] An enzyme complex designated DICER COMPLEX, dices

the GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM153 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM153 RNA is designated SEQ ID:2183, and is provided hereinbelow with reference to the sequence listing part.

[2083] GAM153 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM153 target RNA, herein designated GAM TARGET RNA. GAM153 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2084] GAM153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM153

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM153 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM153 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2085] The complementary binding of GAM153 RNA, herein designated GAM RNA, to target binding sites on GAM153 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM153 target RNA, herein designated GAM TARGET RNA, into GAM153 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2086] It is appreciated that GAM153 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM153 target genes. The mRNA of each one of this plurality of GAM153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM153 RNA, herein designated GAM RNA, and which when bound by GAM153 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM153 target proteins.

[2087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM153 gene, herein designated GAM GENE, on one or more GAM153 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2088] It is yet further appreciated that specific functions, and accordingly utilities, of GAM153 correlate with, and may be deduced from, the identity of the target genes which GAM153 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2089] Nucleotide sequences of the GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM153 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM153 are further described hereinbelow with reference to Table Table1.

[2090] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM153 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2091]

[2092] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 154 (GAM154) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2093] GAM154 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM154 was detected is described hereinabove with reference to Figs. 2-8.

[2094] GAM154 gene, herein designated GAM GENE, and GAM154 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2095] GAM154 gene, herein designated GAM GENE, encodes a GAM154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM154 precursor RNA is designated SEQ ID:2194, and is provided hereinbelow with reference to the sequence listing part.

[2096] GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM154 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2097] An enzyme complex designated DICER COMPLEX, dices the GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM154 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM154 RNA is designated SEQ ID:2195, and is provided hereinbelow with reference to the sequence listing part.

[2098] GAM154 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM154 target RNA, herein designated GAM TARGET RNA. GAM154 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2099] GAM154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM154 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM154 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM154 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[2100] The complementary binding of GAM154 RNA, herein designated GAM RNA, to target binding sites on GAM154 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM154 target RNA, herein designated GAM TARGET RNA, into GAM154 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2101] It is appreciated that GAM154 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM154 target genes. The mRNA of each one of this plurality of GAM154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM154 RNA, herein designated GAM RNA, and which when bound by GAM154 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM154 target proteins.

[2102] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM154 gene, herein designated GAM GENE, on one or

more GAM154 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2103] It is yet further appreciated that specific functions, and accordingly utilities, of GAM154 correlate with, and may be deduced from, the identity of the target genes which GAM154 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2104] Nucleotide sequences of the GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM154 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM154 are further de-

scribed hereinbelow with reference to Table Table1.

[2105] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM154 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2106]

[2107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 155 (GAM155) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2108] GAM155 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM155 was detected is described hereinabove with reference to Figs. 2-8.

[2109] GAM155 gene, herein designated GAM GENE, and GAM155 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2110] GAM155 gene, herein designated GAM GENE, encodes a GAM155 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM155 precursor RNA is designated SEQ ID:2204, and is provided hereinbelow with reference to the sequence listing part.

[2111] GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2112] An enzyme complex designated DICER COMPLEX, dices the GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM155 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM155 RNA is designated SEQ ID:2205, and is provided hereinbelow with reference to the sequence listing part.

[2113] GAM155 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM155 target RNA, herein designated GAM TARGET RNA. GAM155 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2114] GAM155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM155 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM155 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM155 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2115] The complementary binding of GAM155 RNA, herein designated GAM RNA, to target binding sites on GAM155 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM155 target RNA, herein designated GAM TARGET RNA, into GAM155 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2116] It is appreciated that GAM155 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM155 target genes. The mRNA of each one of this plurality of GAM155 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM155 RNA, herein designated GAM RNA, and which when bound by GAM155 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM155 target proteins.

[2117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM155 gene, herein designated GAM GENE, on one or more GAM155 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2118] It is yet further appreciated that specific functions, and accordingly utilities, of GAM155 correlate with, and may

be deduced from, the identity of the target genes which GAM155 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2119] Nucleotide sequences of the GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM155 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM155 are further described hereinbelow with reference to Table Table1.

[2120] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM155 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2121]

[2122] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 156 (GAM156) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2123] GAM156 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM156 was detected is described hereinabove with reference to Figs. 2-8.

[2124] GAM156 gene, herein designated GAM GENE, and GAM156 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2125] GAM156 gene, herein designated GAM GENE, encodes a GAM156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM156 precursor RNA is designated SEQ ID:2227, and is provided hereinbelow with reference to the sequence listing part.

[2126] GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2127] An enzyme complex designated DICER COMPLEX, dices the GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM156 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of GAM156 RNA is designated SEQ ID:2228, and is provided hereinbelow with reference to the sequence listing part.

[2128] GAM156 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM156 target RNA, herein designated GAM TARGET RNA. GAM156 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2129] GAM156 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM156 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM156 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2130] The complementary binding of GAM156 RNA, herein designated GAM RNA, to target binding sites on GAM156 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM156 target RNA, herein designated GAM TARGET RNA, into GAM156 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2131] It is appreciated that GAM156 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM156 target genes. The mRNA of each one of this plurality of GAM156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM156 RNA, herein designated GAM RNA, and which when bound by GAM156 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM156 target proteins.

[2132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM156 gene, herein designated GAM GENE, on one or more GAM156 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM156 correlate with, and may be deduced from, the identity of the target genes which GAM156 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2134] Nucleotide sequences of the GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM156 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM156 are further described hereinbelow with reference to Table Table1.

[2135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM156 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2136]

[2137] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 157 (GAM157) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2138] GAM157 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM157 was detected is described hereinabove with reference to Figs. 2-8.

[2139] GAM157 gene, herein designated GAM GENE, and GAM157 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2140] GAM157 gene, herein designated GAM GENE, encodes a GAM157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM157 precursor RNA is desig-

nated SEQ ID:2240, and is provided hereinbelow with reference to the sequence listing part.

[2141] GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2142] An enzyme complex designated DICER COMPLEX, dices the GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM157 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM157 RNA is designated SEQ ID:2241, and is provided hereinbelow with reference to the sequence listing part.

[2143] GAM157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM157 target RNA, herein designated GAM TARGET RNA. GAM157 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2144] GAM157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM157 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM157

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2145] The complementary binding of GAM157 RNA, herein designated GAM RNA, to target binding sites on GAM157 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM157 target RNA, herein designated GAM TARGET RNA, into GAM157 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2146] It is appreciated that GAM157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM157 target genes. The mRNA of each one of this plurality of GAM157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM157 RNA, herein designated GAM RNA, and which when bound by GAM157 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM157 target proteins.

[2147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM157 gene, herein designated GAM GENE, on one or more GAM157 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2148] It is yet further appreciated that specific functions, and accordingly utilities, of GAM157 correlate with, and may be deduced from, the identity of the target genes which GAM157 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2149] Nucleotide sequences of the GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM157 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM157 are further described hereinbelow with reference to Table Table1.

[2150] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM157 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2151]

[2152] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 158 (GAM158) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2153] GAM158 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM158 was detected is described hereinabove with reference to Figs. 2-8.

[2154] GAM158 gene, herein designated GAM GENE, and

GAM158 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2155] GAM158 gene, herein designated GAM GENE, encodes a GAM158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM158 precursor RNA is designated SEQ ID:2266, and is provided hereinbelow with reference to the sequence listing part.

[2156] GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2157] An enzyme complex designated DICER COMPLEX, dices the GAM158 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM158 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM158 RNA is designated SEQ ID:2267, and is provided hereinbelow with reference to the sequence listing part.

[2158] GAM158 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM158 target RNA, herein designated GAM TARGET RNA. GAM158 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2159] GAM158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM158 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM158 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2160] The complementary binding of GAM158 RNA, herein designated GAM RNA, to target binding sites on GAM158 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM158 target RNA, herein designated GAM TARGET RNA, into GAM158 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2161] It is appreciated that GAM158 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM158 target genes. The mRNA of each one of this plurality of GAM158 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM158 RNA, herein designated GAM RNA, and which when bound by GAM158 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM158 target proteins.

[2162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM158 gene, herein designated GAM GENE, on one or more GAM158 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2163] It is yet further appreciated that specific functions, and accordingly utilities, of GAM158 correlate with, and may be deduced from, the identity of the target genes which GAM158 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2164] Nucleotide sequences of the GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM158 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM158 are further described hereinbelow with reference to Table Table1.

[2165] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM158 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2166]

[2167] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 159 (GAM159) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2168] GAM159 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM159 was detected is described hereinabove with reference to Figs. 2-8.

[2169] GAM159 gene, herein designated GAM GENE, and GAM159 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2170] GAM159 gene, herein designated GAM GENE, encodes a GAM159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM159 precursor RNA is designated SEQ ID:2277, and is provided hereinbelow with reference to the sequence listing part.

[2171] GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2172] An enzyme complex designated DICER COMPLEX, dices the GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM159 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM159 RNA is designated SEQ ID:2278, and is provided hereinbelow with reference to the sequence listing part.

[2173] GAM159 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM159 target RNA, herein designated GAM TARGET RNA. GAM159 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2174] GAM159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM159 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM159 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2175] The complementary binding of GAM159 RNA, herein designated GAM RNA, to target binding sites on GAM159 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM159 target RNA, herein designated GAM TARGET RNA, into GAM159 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2176] It is appreciated that GAM159 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM159 target genes. The mRNA of each one of this plurality of GAM159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM159 RNA, herein designated GAM RNA, and which when bound by GAM159 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM159 target proteins.

[2177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM159 gene, herein designated GAM GENE, on one or more GAM159 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM159 correlate with, and may be deduced from, the identity of the target genes which GAM159 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2179] Nucleotide sequences of the GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM159 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM159 are further described hereinbelow with reference to Table Table1.

[2180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM159 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2181]

[2182] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 160 (GAM160) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2183] GAM160 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM160 was detected is described hereinabove with reference to Figs. 2-8.

[2184] GAM160 gene, herein designated GAM GENE, and GAM160 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2185] GAM160 gene, herein designated GAM GENE, encodes a GAM160 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM160 precursor RNA is designated SEQ ID:2290, and is provided hereinbelow with reference to the sequence listing part.

[2186] GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2187] An enzyme complex designated DICER COMPLEX, dices the GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM160 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM160 RNA is designated SEQ ID:2291, and is provided hereinbelow with reference to the sequence listing part.

[2188] GAM160 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM160 target RNA, herein designated GAM TARGET RNA. GAM160 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2189] GAM160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM160 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM160 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM160 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2190] The complementary binding of GAM160 RNA, herein designated GAM RNA, to target binding sites on GAM160 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM160 target RNA, herein designated GAM TARGET RNA, into GAM160 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2191] It is appreciated that GAM160 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM160 target genes. The mRNA of each one of this plurality of GAM160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM160 RNA,

herein designated GAM RNA, and which when bound by GAM160 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM160 target proteins.

[2192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM160 gene, herein designated GAM GENE, on one or more GAM160 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2193] It is yet further appreciated that specific functions, and accordingly utilities, of GAM160 correlate with, and may be deduced from, the identity of the target genes which

GAM160 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2194] Nucleotide sequences of the GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM160 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM160 are further described hereinbelow with reference to Table Table1.

[2195] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM160 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2196]

[2197] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 161 (GAM161) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2198] GAM161 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM161 was detected is described hereinabove with reference to Figs. 2-8.

[2199] GAM161 gene, herein designated GAM GENE, and GAM161 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2200] GAM161 gene, herein designated GAM GENE, encodes a GAM161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM161 precursor RNA is designated SEQ ID:2295, and is provided hereinbelow with reference to the sequence listing part.

[2201] GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[2202] An enzyme complex designated DICER COMPLEX, dices the GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM161 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM161 RNA is designated SEQ ID:2296, and is provided hereinbelow with reference to the sequence listing part.

[2203] GAM161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM161 target RNA, herein designated GAM TARGET RNA.
GAM161 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2204] GAM161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM161 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM161 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2205] The complementary binding of GAM161 RNA, herein designated GAM RNA, to target binding sites on GAM161 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM161 target RNA, herein desig-

nated GAM TARGET RNA, into GAM161 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2206] It is appreciated that GAM161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM161 target genes. The mRNA of each one of this plurality of GAM161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM161 RNA, herein designated GAM RNA, and which when bound by GAM161 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM161 target proteins.

[2207] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM161 gene, herein designated GAM GENE, on one or more GAM161 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2208] It is yet further appreciated that specific functions, and accordingly utilities, of GAM161 correlate with, and may be deduced from, the identity of the target genes which GAM161 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2209] Nucleotide sequences of the GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM161 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM161 are further described hereinbelow with reference to Table Table1.

[2210] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM161 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[2211]

[2212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 162 (GAM162) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2213] GAM162 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM162 was detected is described hereinabove with reference to Figs. 2-8.

[2214] GAM162 gene, herein designated GAM GENE, and GAM162 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2215] GAM162 gene, herein designated GAM GENE, encodes a GAM162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM162 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM162 precursor RNA is designated SEQ ID:2312, and is provided hereinbelow with ref-

erence to the sequence listing part.

[2216] GAM162 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2217] An enzyme complex designated DICER COMPLEX, dices the GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM162 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 23%) nucleotide sequence of GAM162 RNA is designated SEQ ID:2313, and is provided hereinbelow with reference to the sequence listing part.

[2218] GAM162 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM162 target RNA, herein designated GAM TARGET RNA.

GAM162 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2219] GAM162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM162 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM162 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM162 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2220] The complementary binding of GAM162 RNA, herein designated GAM RNA, to target binding sites on GAM162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM162 target RNA, herein designated GAM TARGET RNA, into GAM162 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2221] It is appreciated that GAM162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM162 target genes. The mRNA of each one of this plurality of GAM162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM162 RNA, herein designated GAM RNA, and which when bound by GAM162 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM162 target proteins.

[2222] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM162 gene, herein designated GAM GENE, on one or more GAM162 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM162 correlate with, and may be deduced from, the identity of the target genes which GAM162 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2224] Nucleotide sequences of the GAM162 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM162 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM162 are further described hereinbelow with reference to Table Table1.

[2225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM162 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2226]

[2227] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 163 (GAM163) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2228] GAM163 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM163 was detected is described hereinabove with reference to Figs. 2-8.

[2229] GAM163 gene, herein designated GAM GENE, and GAM163 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2230] GAM163 gene, herein designated GAM GENE, encodes a GAM163 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM163 precursor RNA is designated SEQ ID:2328, and is provided hereinbelow with reference to the sequence listing part.

[2231] GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2232] An enzyme complex designated DICER COMPLEX, dices the GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM163 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of GAM163 RNA is designated SEQ ID:2329, and is provided hereinbelow with reference to the sequence listing part.

[2233] GAM163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM163 target RNA, herein designated GAM TARGET RNA. GAM163 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2234] GAM163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM163 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM163 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2235] The complementary binding of GAM163 RNA, herein designated GAM RNA, to target binding sites on GAM163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM163 target RNA, herein designated GAM TARGET RNA, into GAM163 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2236] It is appreciated that GAM163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM163 target genes. The mRNA of each one of this plurality of GAM163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM163 RNA, herein designated GAM RNA, and which when bound by GAM163 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM163 target proteins.

[2237] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM163 gene, herein designated GAM GENE, on one or more GAM163 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2238] It is yet further appreciated that specific functions, and accordingly utilities, of GAM163 correlate with, and may be deduced from, the identity of the target genes which GAM163 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2239] Nucleotide sequences of the GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM163 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM163 are further described hereinbelow with reference to Table Table1.

[2240] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM163 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2241]

[2242] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

164 (GAM164) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2243] GAM164 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM164 was detected is described hereinabove with reference to Figs. 2-8.

[2244] GAM164 gene, herein designated GAM GENE, and GAM164 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2245] GAM164 gene, herein designated GAM GENE, encodes a GAM164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM164 precursor RNA is designated SEQ ID:2345, and is provided hereinbelow with reference to the sequence listing part.

[2246] GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2247] An enzyme complex designated DICER COMPLEX, dices the GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM164 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM164 RNA is designated SEQ ID:2346, and is provided hereinbelow with reference to the sequence listing part.

[2248] GAM164 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM164 target RNA, herein designated GAM TARGET RNA. GAM164 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2249] GAM164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM164 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM164 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM164 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2250] The complementary binding of GAM164 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM164 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM164 target RNA, herein designated GAM TARGET RNA, into GAM164 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2251] It is appreciated that GAM164 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM164 target genes. The mRNA of each one of this plurality of GAM164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM164 RNA, herein designated GAM RNA, and which when bound by GAM164 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM164 target proteins.

[2252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM164 gene, herein designated GAM GENE, on one or more GAM164 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2253] It is yet further appreciated that specific functions, and accordingly utilities, of GAM164 correlate with, and may be deduced from, the identity of the target genes which GAM164 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2254] Nucleotide sequences of the GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM164 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM164 are further described hereinbelow with reference to Table Table1.

[2255] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM164 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2256]

[2257] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 165 (GAM165) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2258] GAM165 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM165 was detected is described hereinabove with reference to Figs. 2-8.

[2259] GAM165 gene, herein designated GAM GENE, and GAM165 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2260] GAM165 gene, herein designated GAM GENE, encodes a GAM165 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM165 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM165 precursor RNA is designated SEQ ID:2363, and is provided hereinbelow with reference to the sequence listing part.

[2261] GAM165 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2262] An enzyme complex designated DICER COMPLEX, dices the GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM165 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 64%) nucleotide sequence of GAM165 RNA is designated SEQ ID:2364, and is provided hereinbelow with reference to the sequence listing part.

[2263] GAM165 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM165 target RNA, herein designated GAM TARGET RNA. GAM165 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2264] GAM165 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM165 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM165 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM165 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2265] The complementary binding of GAM165 RNA, herein designated GAM RNA, to target binding sites on GAM165 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM165 target RNA, herein designated GAM TARGET RNA, into GAM165 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2266] It is appreciated that GAM165 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM165 target genes. The mRNA of each one of this plurality of GAM165 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM165 RNA, herein designated GAM RNA, and which when bound by

GAM165 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM165 target proteins.

[2267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM165 gene, herein designated GAM GENE, on one or more GAM165 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2268] It is yet further appreciated that specific functions, and accordingly utilities, of GAM165 correlate with, and may be deduced from, the identity of the target genes which GAM165 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2269] Nucleotide sequences of the GAM165 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM165 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM165 are further described hereinbelow with reference to Table Table1.

[2270] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM165 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2271]

[2272] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 166 (GAM166) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2273] GAM166 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM166 was detected is described hereinabove with reference to Figs. 2-8.

[2274] GAM166 gene, herein designated GAM GENE, and GAM166 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2275] GAM166 gene, herein designated GAM GENE, encodes a GAM166 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM166 precursor RNA is designated SEQ ID:2389, and is provided hereinbelow with reference to the sequence listing part.

[2276] GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[2277] An enzyme complex designated DICER COMPLEX, dices the GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM166 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 19%) nucleotide sequence of GAM166 RNA is designated SEQ ID:2390, and is provided hereinbelow with reference to the sequence listing part.

[2278] GAM166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM166 target RNA, herein designated GAM TARGET RNA. GAM166 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2279] GAM166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM166 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM166 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM166 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM166 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2280] The complementary binding of GAM166 RNA, herein designated GAM RNA, to target binding sites on GAM166 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM166 target RNA, herein designated GAM TARGET RNA, into GAM166 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2281] It is appreciated that GAM166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM166 target genes. The mRNA of each one of this plurality of GAM166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM166 RNA, herein designated GAM RNA, and which when bound by GAM166 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM166 target proteins.

[2282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM166 gene, herein designated GAM GENE, on one or more GAM166 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2283] It is yet further appreciated that specific functions, and accordingly utilities, of GAM166 correlate with, and may be deduced from, the identity of the target genes which GAM166 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2284] Nucleotide sequences of the GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM166 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM166 are further described hereinbelow with reference to Table Table1.

[2285] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM166 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2286]

[2287] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 167 (GAM167) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2288] GAM167 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM167 was detected is described hereinabove with reference to Figs. 2-8.

[2289] GAM167 gene, herein designated GAM GENE, and GAM167 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2290] GAM167 gene, herein designated GAM GENE, encodes a GAM167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM167 precursor RNA is designated SEQ ID:2400, and is provided hereinbelow with reference to the sequence listing part.

[2291] GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2292] An enzyme complex designated DICER COMPLEX, dices the GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM167 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of GAM167 RNA is designated SEQ ID:2401, and is provided hereinbelow with reference to the sequence listing part.

[2293] GAM167 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM167

target RNA, herein designated GAM TARGET RNA.

GAM167 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2294] GAM167 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM167 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM167 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM167 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2295] The complementary binding of GAM167 RNA, herein designated GAM RNA, to target binding sites on GAM167 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM167 target RNA, herein designated GAM TARGET RNA, into GAM167 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2296] It is appreciated that GAM167 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM167 target genes. The mRNA of each one of this plurality of GAM167 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM167 RNA, herein designated GAM RNA, and which when bound by GAM167 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM167 target proteins.

[2297] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM167 gene, herein designated GAM GENE, on one or more GAM167 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2298] It is yet further appreciated that specific functions, and accordingly utilities, of GAM167 correlate with, and may be deduced from, the identity of the target genes which GAM167 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2299] Nucleotide sequences of the GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM167 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM167 are further described hereinbelow with reference to Table Table1.

[2300] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM167 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2301]

[2302] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 168 (GAM168) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2303] GAM168 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM168 was detected is described hereinabove with reference to Figs. 2-8.

[2304] GAM168 gene, herein designated GAM GENE, and GAM168 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2305] GAM168 gene, herein designated GAM GENE, encodes a GAM168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM168 precursor RNA is designated SEQ ID:2422, and is provided hereinbelow with reference to the sequence listing part.

[2306] GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2307] An enzyme complex designated DICER COMPLEX, dices the GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM168 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM168 RNA is designated SEQ ID:2423, and is provided hereinbelow with reference to the sequence listing part.

[2308] GAM168 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM168 target RNA, herein designated GAM TARGET RNA. GAM168 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2309] GAM168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM168 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM168 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2310] The complementary binding of GAM168 RNA, herein designated GAM RNA, to target binding sites on GAM168 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM168 target RNA, herein designated GAM TARGET RNA, into GAM168 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2311] It is appreciated that GAM168 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM168 target genes. The mRNA of each one of this plu-

rality of GAM168 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM168 RNA, herein designated GAM RNA, and which when bound by GAM168 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM168 target proteins.

[2312] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM168 gene, herein designated GAM GENE, on one or more GAM168 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2313] It is yet further appreciated that specific functions, and accordingly utilities, of GAM168 correlate with, and may be deduced from, the identity of the target genes which GAM168 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2314] Nucleotide sequences of the GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM168 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM168 are further described hereinbelow with reference to Table Table1.

[2315] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM168 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2316]

[2317] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 169 (GAM169) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2318] GAM169 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM169 was detected is described hereinabove with reference to Figs. 2-8.

[2319] GAM169 gene, herein designated GAM GENE, and GAM169 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2320] GAM169 gene, herein designated GAM GENE, encodes a GAM169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM169 precursor RNA is designated SEQ ID:2434, and is provided hereinbelow with reference to the sequence listing part.

[2321] GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2322] An enzyme complex designated DICER COMPLEX, dices the GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM169 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM169 RNA is designated SEQ ID:2435, and is provided hereinbelow with reference to the sequence listing part.

[2323] GAM169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM169 target RNA, herein designated GAM TARGET RNA.

GAM169 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[2324] GAM169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM169 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM169 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2325] The complementary binding of GAM169 RNA, herein designated GAM RNA, to target binding sites on GAM169 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM169 target RNA, herein designated GAM TARGET RNA, into GAM169 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2326] It is appreciated that GAM169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM169 target genes. The mRNA of each one of this plurality of GAM169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM169 RNA, herein designated GAM RNA, and which when bound by GAM169 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM169 target proteins.

[2327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM169 gene, herein designated GAM GENE, on one or more GAM169 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2328] It is yet further appreciated that specific functions, and accordingly utilities, of GAM169 correlate with, and may be deduced from, the identity of the target genes which GAM169 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2329] Nucleotide sequences of the GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM169 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM169 are further described hereinbelow with reference to Table Table1.

[2330] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM169 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2331]

[2332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 170 (GAM170) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2333] GAM170 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM170 was detected is described hereinabove with reference to Figs. 2-8.

[2334] GAM170 gene, herein designated GAM GENE, and GAM170 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2335] GAM170 gene, herein designated GAM GENE, encodes a GAM170 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM170 precursor RNA is designated SEQ ID:2448, and is provided hereinbelow with reference to the sequence listing part.

[2336] GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2337] An enzyme complex designated DICER COMPLEX, dices the GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM170 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of

GAM170 RNA is designated SEQ ID:2449, and is provided hereinbelow with reference to the sequence listing part.

[2338] GAM170 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM170 target RNA, herein designated GAM TARGET RNA. GAM170 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2339] GAM170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM170 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM170 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2340] The complementary binding of GAM170 RNA, herein designated GAM RNA, to target binding sites on GAM170 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM170 target RNA, herein designated GAM TARGET RNA, into GAM170 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2341] It is appreciated that GAM170 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM170 target genes. The mRNA of each one of this plurality of GAM170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM170 RNA, herein designated GAM RNA, and which when bound by GAM170 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM170 target proteins.

[2342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM170 gene, herein designated GAM GENE, on one or more GAM170 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2343] It is yet further appreciated that specific functions, and accordingly utilities, of GAM170 correlate with, and may be deduced from, the identity of the target genes which GAM170 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2344] Nucleotide sequences of the GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM170 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM170 are further described hereinbelow with reference to Table Table1.

[2345] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM170 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2346]

[2347] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 171 (GAM171) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2348] GAM171 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM171 was detected is described hereinabove

with reference to Figs. 2-8.

[2349] GAM171 gene, herein designated GAM GENE, and GAM171 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2350] GAM171 gene, herein designated GAM GENE, encodes a GAM171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM171 precursor RNA is designated SEQ ID:2458, and is provided hereinbelow with reference to the sequence listing part.

[2351] GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2352] An enzyme complex designated DICER COMPLEX, dices the GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM171 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM171 RNA is designated SEQ ID:2459, and is provided hereinbelow with reference to the sequence listing part.

[2353] GAM171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM171 target RNA, herein designated GAM TARGET RNA. GAM171 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2354] GAM171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM171 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM171 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM171 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2355] The complementary binding of GAM171 RNA, herein designated GAM RNA, to target binding sites on GAM171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM171 target RNA, herein designated GAM TARGET RNA, into GAM171 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[2356] It is appreciated that GAM171 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM171 target genes. The mRNA of each one of this plurality of GAM171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM171 RNA, herein designated GAM RNA, and which when bound by GAM171 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM171 target proteins.

[2357] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM171 gene, herein designated GAM GENE, on one or more GAM171 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2358] It is yet further appreciated that specific functions, and accordingly utilities, of GAM171 correlate with, and may be deduced from, the identity of the target genes which GAM171 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2359] Nucleotide sequences of the GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM171 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM171 are further described hereinbelow with reference to Table Table1.

[2360] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM171 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2361]

[2362] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 172 (GAM172) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2363] GAM172 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM172 was detected is described hereinabove with reference to Figs. 2-8.

[2364] GAM172 gene, herein designated GAM GENE, and GAM172 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2365] GAM172 gene, herein designated GAM GENE, encodes a GAM172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM172 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM172 precursor RNA is designated SEQ ID:2477, and is provided hereinbelow with reference to the sequence listing part.

[2366] GAM172 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2367] An enzyme complex designated DICER COMPLEX, dices the GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM172 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM172 RNA is designated SEQ ID:2478, and is provided hereinbelow with reference to the sequence listing part.

[2368] GAM172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM172 target RNA, herein designated GAM TARGET RNA.

GAM172 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2369] GAM172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM172 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM172 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM172 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2370] The complementary binding of GAM172 RNA, herein designated GAM RNA, to target binding sites on GAM172 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM172 target RNA, herein designated GAM TARGET RNA, into GAM172 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2371] It is appreciated that GAM172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM172 target genes. The mRNA of each one of this plurality of GAM172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM172 RNA, herein designated GAM RNA, and which when bound by GAM172 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM172 target proteins.

[2372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM172 gene, herein designated GAM GENE, on one or more GAM172 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2373] It is yet further appreciated that specific functions, and accordingly utilities, of GAM172 correlate with, and may be deduced from, the identity of the target genes which GAM172 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2374] Nucleotide sequences of the GAM172 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM172 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM172 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM172 are further described hereinbelow with reference to Table Table1.

[2375] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM172 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2376]

[2377] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 173 (GAM173) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2378] GAM173 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM173 was detected is described hereinabove with reference to Figs. 2-8.

[2379] GAM173 gene, herein designated GAM GENE, and GAM173 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2380] GAM173 gene, herein designated GAM GENE, encodes a

GAM173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM173 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM173 precursor RNA is designated SEQ ID:2516, and is provided hereinbelow with reference to the sequence listing part.

[2381] GAM173 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2382] An enzyme complex designated DICER COMPLEX, dices the GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM173 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM173 RNA is designated SEQ ID:2517, and is provided hereinbelow with reference to the sequence listing part.

[2383] GAM173 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM173 target RNA, herein designated GAM TARGET RNA. GAM173 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2384] GAM173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM173 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM173 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM173 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM173 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2385] The complementary binding of GAM173 RNA, herein designated GAM RNA, to target binding sites on GAM173 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM173 target RNA, herein designated GAM TARGET RNA, into GAM173 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2386] It is appreciated that GAM173 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM173 target genes. The mRNA of each one of this plurality of GAM173 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM173 RNA, herein designated GAM RNA, and which when bound by GAM173 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM173 target proteins.

[2387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM173 gene, herein designated GAM GENE, on one or more GAM173 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2388] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM173 correlate with, and may be deduced from, the identity of the target genes which GAM173 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2389] Nucleotide sequences of the GAM173 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM173 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM173 are further described hereinbelow with reference to Table Table1.

[2390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM173 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2391]

[2392] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 174 (GAM174) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2393] GAM174 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM174 was detected is described hereinabove with reference to Figs. 2-8.

[2394] GAM174 gene, herein designated GAM GENE, and GAM174 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2395] GAM174 gene, herein designated GAM GENE, encodes a GAM174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM174 precursor RNA is designated SEQ ID:2524, and is provided hereinbelow with reference to the sequence listing part.

[2396] GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2397] An enzyme complex designated DICER COMPLEX, dices the GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM174 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM174 RNA is designated SEQ ID:2525, and is provided hereinbelow with reference to the sequence listing part.

[2398] GAM174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM174 target RNA, herein designated GAM TARGET RNA. GAM174 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2399] GAM174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM174 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM174 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2400] The complementary binding of GAM174 RNA, herein designated GAM RNA, to target binding sites on GAM174 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM174 target RNA, herein designated GAM TARGET RNA, into GAM174 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2401] It is appreciated that GAM174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM174 target genes. The mRNA of each one of this plurality of GAM174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM174 RNA, herein designated GAM RNA, and which when bound by GAM174 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM174 target proteins.

[2402] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM174 gene, herein designated GAM GENE, on one or more GAM174 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2403] It is yet further appreciated that specific functions, and accordingly utilities, of GAM174 correlate with, and may be deduced from, the identity of the target genes which GAM174 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2404] Nucleotide sequences of the GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM174 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM174 are further described hereinbelow with reference to Table Table1.

[2405] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM174 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2406]

[2407] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 175 (GAM175) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2408] GAM175 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM175 was detected is described hereinabove with reference to Figs. 2-8.

[2409] GAM175 gene, herein designated GAM GENE, and GAM175 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2410] GAM175 gene, herein designated GAM GENE, encodes a GAM175 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM175 precursor RNA is designated SEQ ID:2532, and is provided hereinbelow with reference to the sequence listing part.

[2411] GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2412] An enzyme complex designated DICER COMPLEX, dices the GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM175 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM175 RNA is designated SEQ ID:2533, and is provided

hereinbelow with reference to the sequence listing part.

[2413] GAM175 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM175 target RNA, herein designated GAM TARGET RNA.
GAM175 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2414] GAM175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM175 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM175 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2415] The complementary binding of GAM175 RNA, herein designated GAM RNA, to target binding sites on GAM175 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM175 target RNA, herein designated GAM TARGET RNA, into GAM175 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2416] It is appreciated that GAM175 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM175 target genes. The mRNA of each one of this plurality of GAM175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM175 RNA, herein designated GAM RNA, and which when bound by GAM175 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM175 tar-

get proteins.

[2417] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM175 gene, herein designated GAM GENE, on one or more GAM175 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2418] It is yet further appreciated that specific functions, and accordingly utilities, of GAM175 correlate with, and may be deduced from, the identity of the target genes which GAM175 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2419] Nucleotide sequences of the GAM175 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM175 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM175 are further described hereinbelow with reference to Table Table1.

[2420] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM175 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2421]

[2422] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 176 (GAM176) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2423] GAM176 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM176 was detected is described hereinabove with reference to Figs. 2-8.

[2424] GAM176 gene, herein designated GAM GENE, and GAM176 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2425] GAM176 gene, herein designated GAM GENE, encodes a GAM176 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM176 precursor RNA is designated SEQ ID:2540, and is provided hereinbelow with reference to the sequence listing part.

[2426] GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2427] An enzyme complex designated DICER COMPLEX, dices

the GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM176 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM176 RNA is designated SEQ ID:2541, and is provided hereinbelow with reference to the sequence listing part.

[2428] GAM176 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM176 target RNA, herein designated GAM TARGET RNA. GAM176 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2429] GAM176 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM176 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM176

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM176 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM176 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2430] The complementary binding of GAM176 RNA, herein designated GAM RNA, to target binding sites on GAM176 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM176 target RNA, herein designated GAM TARGET RNA, into GAM176 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2431] It is appreciated that GAM176 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM176 target genes. The mRNA of each one of this plurality of GAM176 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM176 RNA, herein designated GAM RNA, and which when bound by GAM176 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM176 target proteins.

[2432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM176 gene, herein designated GAM GENE, on one or more GAM176 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2433] It is yet further appreciated that specific functions, and accordingly utilities, of GAM176 correlate with, and may be deduced from, the identity of the target genes which GAM176 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2434] Nucleotide sequences of the GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM176 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM176 are further described hereinbelow with reference to Table Table1.

[2435] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM176 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2436]

[2437] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 177 (GAM177) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2438] GAM177 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM177 was detected is described hereinabove with reference to Figs. 2-8.

[2439] GAM177 gene, herein designated GAM GENE, and GAM177 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2440] GAM177 gene, herein designated GAM GENE, encodes a GAM177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM177 precursor RNA is designated SEQ ID:2564, and is provided hereinbelow with reference to the sequence listing part.

[2441] GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM177 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2442] An enzyme complex designated DICER COMPLEX, dices the GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM177 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 35%) nucleotide sequence of GAM177 RNA is designated SEQ ID:2565, and is provided hereinbelow with reference to the sequence listing part.

[2443] GAM177 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM177 target RNA, herein designated GAM TARGET RNA. GAM177 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2444] GAM177 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM177 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM177 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM177 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[2445] The complementary binding of GAM177 RNA, herein designated GAM RNA, to target binding sites on GAM177 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM177 target RNA, herein designated GAM TARGET RNA, into GAM177 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2446] It is appreciated that GAM177 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM177 target genes. The mRNA of each one of this plurality of GAM177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM177 RNA, herein designated GAM RNA, and which when bound by GAM177 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM177 target proteins.

[2447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM177 gene, herein designated GAM GENE, on one or

more GAM177 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2448] It is yet further appreciated that specific functions, and accordingly utilities, of GAM177 correlate with, and may be deduced from, the identity of the target genes which GAM177 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2449] Nucleotide sequences of the GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM177 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM177 are further de-

scribed hereinbelow with reference to Table Table1.

[2450] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM177 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2451]

[2452] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 178 (GAM178) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2453] GAM178 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM178 was detected is described hereinabove with reference to Figs. 2-8.

[2454] GAM178 gene, herein designated GAM GENE, and GAM178 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2455] GAM178 gene, herein designated GAM GENE, encodes a GAM178 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM178 precursor RNA is designated SEQ ID:2583, and is provided hereinbelow with reference to the sequence listing part.

[2456] GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2457] An enzyme complex designated DICER COMPLEX, dices the GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM178 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM178 RNA is designated SEQ ID:2584, and is provided hereinbelow with reference to the sequence listing part.

[2458] GAM178 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM178 target RNA, herein designated GAM TARGET RNA. GAM178 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2459] GAM178 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM178 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM178 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM178 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2460] The complementary binding of GAM178 RNA, herein designated GAM RNA, to target binding sites on GAM178 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM178 target RNA, herein designated GAM TARGET RNA, into GAM178 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2461] It is appreciated that GAM178 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM178 target genes. The mRNA of each one of this plurality of GAM178 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM178 RNA, herein designated GAM RNA, and which when bound by GAM178 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM178 target proteins.

[2462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM178 gene, herein designated GAM GENE, on one or more GAM178 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2463] It is yet further appreciated that specific functions, and accordingly utilities, of GAM178 correlate with, and may

be deduced from, the identity of the target genes which GAM178 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2464] Nucleotide sequences of the GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM178 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM178 are further described hereinbelow with reference to Table Table1.

[2465] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM178 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2466]

[2467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 179 (GAM179) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2468] GAM179 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM179 was detected is described hereinabove with reference to Figs. 2-8.

[2469] GAM179 gene, herein designated GAM GENE, and GAM179 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2470] GAM179 gene, herein designated GAM GENE, encodes a GAM179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM179 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM179 precursor RNA is designated SEQ ID:2595, and is provided hereinbelow with reference to the sequence listing part.

[2471] GAM179 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2472] An enzyme complex designated DICER COMPLEX, dices the GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM179 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM179 RNA is designated SEQ ID:2596, and is provided hereinbelow with reference to the sequence listing part.

[2473] GAM179 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM179 target RNA, herein designated GAM TARGET RNA. GAM179 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2474] GAM179 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM179 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM179 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2475] The complementary binding of GAM179 RNA, herein designated GAM RNA, to target binding sites on GAM179 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM179 target RNA, herein designated GAM TARGET RNA, into GAM179 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2476] It is appreciated that GAM179 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM179 target genes. The mRNA of each one of this plurality of GAM179 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM179 RNA, herein designated GAM RNA, and which when bound by GAM179 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM179 target proteins.

[2477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM179 gene, herein designated GAM GENE, on one or more GAM179 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM179 correlate with, and may be deduced from, the identity of the target genes which GAM179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2479] Nucleotide sequences of the GAM179 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM179 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM179 are further described hereinbelow with reference to Table Table1.

[2480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM179 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2481]

[2482] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 180 (GAM180) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2483] GAM180 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM180 was detected is described hereinabove with reference to Figs. 2-8.

[2484] GAM180 gene, herein designated GAM GENE, and GAM180 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2485] GAM180 gene, herein designated GAM GENE, encodes a GAM180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM180 precursor RNA is desig-

nated SEQ ID:2600, and is provided hereinbelow with reference to the sequence listing part.

[2486] GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2487] An enzyme complex designated DICER COMPLEX, dices the GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM180 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of GAM180 RNA is designated SEQ ID:2601, and is provided hereinbelow with reference to the sequence listing part.

[2488] GAM180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM180 target RNA, herein designated GAM TARGET RNA. GAM180 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2489] GAM180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM180 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM180

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2490] The complementary binding of GAM180 RNA, herein designated GAM RNA, to target binding sites on GAM180 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM180 target RNA, herein designated GAM TARGET RNA, into GAM180 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2491] It is appreciated that GAM180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM180 target genes. The mRNA of each one of this plurality of GAM180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM180 RNA, herein designated GAM RNA, and which when bound by GAM180 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM180 target proteins.

[2492] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM180 gene, herein designated GAM GENE, on one or more GAM180 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2493] It is yet further appreciated that specific functions, and accordingly utilities, of GAM180 correlate with, and may be deduced from, the identity of the target genes which GAM180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2494] Nucleotide sequences of the GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM180 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM180 are further described hereinbelow with reference to Table Table1.

[2495] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM180 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2496]

[2497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 181 (GAM181) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2498] GAM181 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM181 was detected is described hereinabove with reference to Figs. 2-8.

[2499] GAM181 gene, herein designated GAM GENE, and

GAM181 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2500] GAM181 gene, herein designated GAM GENE, encodes a GAM181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM181 precursor RNA is designated SEQ ID:2619, and is provided hereinbelow with reference to the sequence listing part.

[2501] GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2502] An enzyme complex designated DICER COMPLEX, dices the GAM181 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM181 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM181 RNA is designated SEQ ID:2620, and is provided hereinbelow with reference to the sequence listing part.

[2503] GAM181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM181 target RNA, herein designated GAM TARGET RNA. GAM181 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2504] GAM181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM181 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM181 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2505] The complementary binding of GAM181 RNA, herein designated GAM RNA, to target binding sites on GAM181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM181 target RNA, herein designated GAM TARGET RNA, into GAM181 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2506] It is appreciated that GAM181 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM181 target genes. The mRNA of each one of this plurality of GAM181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM181 RNA, herein designated GAM RNA, and which when bound by GAM181 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM181 target proteins.

[2507] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM181 gene, herein designated GAM GENE, on one or more GAM181 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM181 correlate with, and may be deduced from, the identity of the target genes which GAM181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2509] Nucleotide sequences of the GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM181 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM181 are further described hereinbelow with reference to Table Table1.

[2510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM181 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2511]

[2512] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 182 (GAM182) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2513] GAM182 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM182 was detected is described hereinabove with reference to Figs. 2-8.

[2514] GAM182 gene, herein designated GAM GENE, and GAM182 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2515] GAM182 gene, herein designated GAM GENE, encodes a GAM182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM182 precursor RNA is designated SEQ ID:2643, and is provided hereinbelow with reference to the sequence listing part.

[2516] GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2517] An enzyme complex designated DICER COMPLEX, dices the GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM182 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM182 RNA is designated SEQ ID:2644, and is provided hereinbelow with reference to the sequence listing part.

[2518] GAM182 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM182 target RNA, herein designated GAM TARGET RNA. GAM182 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2519] GAM182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM182 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM182 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2520] The complementary binding of GAM182 RNA, herein designated GAM RNA, to target binding sites on GAM182 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM182 target RNA, herein designated GAM TARGET RNA, into GAM182 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2521] It is appreciated that GAM182 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM182 target genes. The mRNA of each one of this plurality of GAM182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM182 RNA, herein designated GAM RNA, and which when bound by GAM182 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM182 target proteins.

[2522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM182 gene, herein designated GAM GENE, on one or more GAM182 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2523] It is yet further appreciated that specific functions, and accordingly utilities, of GAM182 correlate with, and may be deduced from, the identity of the target genes which GAM182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2524] Nucleotide sequences of the GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM182 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM182 are further described hereinbelow with reference to Table Table1.

[2525] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM182 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2526]

[2527] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 183 (GAM183) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2528] GAM183 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM183 was detected is described hereinabove with reference to Figs. 2-8.

[2529] GAM183 gene, herein designated GAM GENE, and GAM183 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2530] GAM183 gene, herein designated GAM GENE, encodes a GAM183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM183 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM183 precursor RNA is designated SEQ ID:2666, and is provided hereinbelow with reference to the sequence listing part.

[2531] GAM183 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2532] An enzyme complex designated DICER COMPLEX, dices the GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM183 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 32%) nucleotide sequence of GAM183 RNA is designated SEQ ID:2667, and is provided hereinbelow with reference to the sequence listing part.

[2533] GAM183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM183 target RNA, herein designated GAM TARGET RNA. GAM183 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2534] GAM183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM183 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM183 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2535] The complementary binding of GAM183 RNA, herein designated GAM RNA, to target binding sites on GAM183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM183 target RNA, herein designated GAM TARGET RNA, into GAM183 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2536] It is appreciated that GAM183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM183 target genes. The mRNA of each one of this plurality of GAM183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM183 RNA,

herein designated GAM RNA, and which when bound by GAM183 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM183 target proteins.

[2537] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM183 gene, herein designated GAM GENE, on one or more GAM183 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2538] It is yet further appreciated that specific functions, and accordingly utilities, of GAM183 correlate with, and may be deduced from, the identity of the target genes which

GAM183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2539] Nucleotide sequences of the GAM183 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM183 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM183 are further described hereinbelow with reference to Table Table1.

[2540] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM183 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2541]

[2542] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 184 (GAM184) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2543] GAM184 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM184 was detected is described hereinabove with reference to Figs. 2-8.

[2544] GAM184 gene, herein designated GAM GENE, and GAM184 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2545] GAM184 gene, herein designated GAM GENE, encodes a GAM184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM184 precursor RNA is designated SEQ ID:2682, and is provided hereinbelow with reference to the sequence listing part.

[2546] GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[2547] An enzyme complex designated DICER COMPLEX, dices the GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM184 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM184 RNA is designated SEQ ID:2683, and is provided hereinbelow with reference to the sequence listing part.

[2548] GAM184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM184 target RNA, herein designated GAM TARGET RNA.
GAM184 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2549] GAM184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM184 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM184 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM184 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2550] The complementary binding of GAM184 RNA, herein designated GAM RNA, to target binding sites on GAM184 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM184 target RNA, herein desig-

nated GAM TARGET RNA, into GAM184 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2551] It is appreciated that GAM184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM184 target genes. The mRNA of each one of this plurality of GAM184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM184 RNA, herein designated GAM RNA, and which when bound by GAM184 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM184 target proteins.

[2552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM184 gene, herein designated GAM GENE, on one or more GAM184 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2553] It is yet further appreciated that specific functions, and accordingly utilities, of GAM184 correlate with, and may be deduced from, the identity of the target genes which GAM184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2554] Nucleotide sequences of the GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM184 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM184 are further described hereinbelow with reference to Table Table1.

[2555] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM184 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[2556]

[2557] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 185 (GAM185) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2558] GAM185 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM185 was detected is described hereinabove with reference to Figs. 2-8.

[2559] GAM185 gene, herein designated GAM GENE, and GAM185 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2560] GAM185 gene, herein designated GAM GENE, encodes a GAM185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM185 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM185 precursor RNA is designated SEQ ID:2692, and is provided hereinbelow with ref-

erence to the sequence listing part.

[2561] GAM185 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2562] An enzyme complex designated DICER COMPLEX, dices the GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM185 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM185 RNA is designated SEQ ID:2693, and is provided hereinbelow with reference to the sequence listing part.

[2563] GAM185 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM185 target RNA, herein designated GAM TARGET RNA.

GAM185 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2564] GAM185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM185 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM185 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM185 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2565] The complementary binding of GAM185 RNA, herein designated GAM RNA, to target binding sites on GAM185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM185 target RNA, herein designated GAM TARGET RNA, into GAM185 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2566] It is appreciated that GAM185 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM185 target genes. The mRNA of each one of this plurality of GAM185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM185 RNA, herein designated GAM RNA, and which when bound by GAM185 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM185 target proteins.

[2567] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM185 gene, herein designated GAM GENE, on one or more GAM185 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM185 correlate with, and may be deduced from, the identity of the target genes which GAM185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2569] Nucleotide sequences of the GAM185 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM185 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM185 are further described hereinbelow with reference to Table Table1.

[2570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM185 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2571]

[2572] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 186 (GAM186) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2573] GAM186 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM186 was detected is described hereinabove with reference to Figs. 2-8.

[2574] GAM186 gene, herein designated GAM GENE, and GAM186 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2575] GAM186 gene, herein designated GAM GENE, encodes a GAM186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM186 precursor RNA is designated SEQ ID:2706, and is provided hereinbelow with reference to the sequence listing part.

[2576] GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2577] An enzyme complex designated DICER COMPLEX, dices the GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM186 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM186 RNA is designated SEQ ID:2707, and is provided hereinbelow with reference to the sequence listing part.

[2578] GAM186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM186 target RNA, herein designated GAM TARGET RNA. GAM186 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2579] GAM186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM186 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM186 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2580] The complementary binding of GAM186 RNA, herein designated GAM RNA, to target binding sites on GAM186 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM186 target RNA, herein designated GAM TARGET RNA, into GAM186 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2581] It is appreciated that GAM186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM186 target genes. The mRNA of each one of this plurality of GAM186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM186 RNA, herein designated GAM RNA, and which when bound by GAM186 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM186 target proteins.

[2582] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM186 gene, herein designated GAM GENE, on one or more GAM186 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2583] It is yet further appreciated that specific functions, and accordingly utilities, of GAM186 correlate with, and may be deduced from, the identity of the target genes which GAM186 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2584] Nucleotide sequences of the GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM186 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM186 are further described hereinbelow with reference to Table Table1.

[2585] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM186 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2586]

[2587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

187 (GAM187) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2588] GAM187 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM187 was detected is described hereinabove with reference to Figs. 2-8.

[2589] GAM187 gene, herein designated GAM GENE, and GAM187 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2590] GAM187 gene, herein designated GAM GENE, encodes a GAM187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM187 precursor RNA is designated SEQ ID:2715, and is provided hereinbelow with reference to the sequence listing part.

[2591] GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2592] An enzyme complex designated DICER COMPLEX, dices the GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM187 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM187 RNA is designated SEQ ID:2716, and is provided hereinbelow with reference to the sequence listing part.

[2593] GAM187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM187 target RNA, herein designated GAM TARGET RNA. GAM187 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2594] GAM187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM187 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM187 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM187 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2595] The complementary binding of GAM187 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM187 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM187 target RNA, herein designated GAM TARGET RNA, into GAM187 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2596] It is appreciated that GAM187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM187 target genes. The mRNA of each one of this plurality of GAM187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM187 RNA, herein designated GAM RNA, and which when bound by GAM187 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM187 target proteins.

[2597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM187 gene, herein designated GAM GENE, on one or more GAM187 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM187 correlate with, and may be deduced from, the identity of the target genes which GAM187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2599] Nucleotide sequences of the GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM187 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM187 are further described hereinbelow with reference to Table Table1.

[2600] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM187 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2601]

[2602] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 188 (GAM188) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2603] GAM188 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM188 was detected is described hereinabove with reference to Figs. 2-8.

[2604] GAM188 gene, herein designated GAM GENE, and GAM188 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2605] GAM188 gene, herein designated GAM GENE, encodes a GAM188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM188 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM188 precursor RNA is designated SEQ ID:2734, and is provided hereinbelow with reference to the sequence listing part.

[2606] GAM188 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2607] An enzyme complex designated DICER COMPLEX, dices the GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM188 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 61%) nucleotide sequence of GAM188 RNA is designated SEQ ID:2735, and is provided hereinbelow with reference to the sequence listing part.

[2608] GAM188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM188 target RNA, herein designated GAM TARGET RNA. GAM188 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2609] GAM188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM188 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM188 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM188 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2610] The complementary binding of GAM188 RNA, herein designated GAM RNA, to target binding sites on GAM188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM188 target RNA, herein designated GAM TARGET RNA, into GAM188 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2611] It is appreciated that GAM188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM188 target genes. The mRNA of each one of this plurality of GAM188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM188 RNA, herein designated GAM RNA, and which when bound by

GAM188 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM188 target proteins.

[2612] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM188 gene, herein designated GAM GENE, on one or more GAM188 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2613] It is yet further appreciated that specific functions, and accordingly utilities, of GAM188 correlate with, and may be deduced from, the identity of the target genes which GAM188 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2614] Nucleotide sequences of the GAM188 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM188 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM188 are further described hereinbelow with reference to Table Table1.

[2615] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM188 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2616]

[2617] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 189 (GAM189) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2618] GAM189 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM189 was detected is described hereinabove with reference to Figs. 2-8.

[2619] GAM189 gene, herein designated GAM GENE, and GAM189 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2620] GAM189 gene, herein designated GAM GENE, encodes a GAM189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM189 precursor RNA is designated SEQ ID:2737, and is provided hereinbelow with reference to the sequence listing part.

[2621] GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[2622] An enzyme complex designated DICER COMPLEX, dices the GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM189 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM189 RNA is designated SEQ ID:2738, and is provided hereinbelow with reference to the sequence listing part.

[2623] GAM189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM189 target RNA, herein designated GAM TARGET RNA. GAM189 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2624] GAM189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM189 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM189 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM189 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2625] The complementary binding of GAM189 RNA, herein designated GAM RNA, to target binding sites on GAM189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM189 target RNA, herein designated GAM TARGET RNA, into GAM189 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2626] It is appreciated that GAM189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM189 target genes. The mRNA of each one of this plurality of GAM189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM189 RNA, herein designated GAM RNA, and which when bound by GAM189 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM189 target proteins.

[2627] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM189 gene, herein designated GAM GENE, on one or more GAM189 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2628] It is yet further appreciated that specific functions, and accordingly utilities, of GAM189 correlate with, and may be deduced from, the identity of the target genes which GAM189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2629] Nucleotide sequences of the GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM189 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM189 are further described hereinbelow with reference to Table Table1.

[2630] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM189 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2631]

[2632] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 190 (GAM190) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2633] GAM190 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM190 was detected is described hereinabove with reference to Figs. 2-8.

[2634] GAM190 gene, herein designated GAM GENE, and GAM190 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2635] GAM190 gene, herein designated GAM GENE, encodes a GAM190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM190 precursor RNA is designated SEQ ID:2744, and is provided hereinbelow with reference to the sequence listing part.

[2636] GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2637] An enzyme complex designated DICER COMPLEX, dices the GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM190 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM190 RNA is designated SEQ ID:2745, and is provided hereinbelow with reference to the sequence listing part.

[2638] GAM190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM190

target RNA, herein designated GAM TARGET RNA.

GAM190 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2639] GAM190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM190 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM190 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2640] The complementary binding of GAM190 RNA, herein designated GAM RNA, to target binding sites on GAM190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM190 target RNA, herein designated GAM TARGET RNA, into GAM190 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2641] It is appreciated that GAM190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM190 target genes. The mRNA of each one of this plurality of GAM190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM190 RNA, herein designated GAM RNA, and which when bound by GAM190 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM190 target proteins.

[2642] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM190 gene, herein designated GAM GENE, on one or more GAM190 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2643] It is yet further appreciated that specific functions, and accordingly utilities, of GAM190 correlate with, and may be deduced from, the identity of the target genes which GAM190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2644] Nucleotide sequences of the GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM190 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM190 are further described hereinbelow with reference to Table Table1.

[2645] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM190 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2646]

[2647] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 191 (GAM191) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2648] GAM191 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM191 was detected is described hereinabove with reference to Figs. 2-8.

[2649] GAM191 gene, herein designated GAM GENE, and GAM191 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2650] GAM191 gene, herein designated GAM GENE, encodes a GAM191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM191 precursor RNA is designated SEQ ID:2753, and is provided hereinbelow with reference to the sequence listing part.

[2651] GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2652] An enzyme complex designated DICER COMPLEX, dices the GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM191 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM191 RNA is designated SEQ ID:2754, and is provided hereinbelow with reference to the sequence listing part.

[2653] GAM191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM191 target RNA, herein designated GAM TARGET RNA. GAM191 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2654] GAM191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM191 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM191 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM191 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2655] The complementary binding of GAM191 RNA, herein designated GAM RNA, to target binding sites on GAM191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM191 target RNA, herein designated GAM TARGET RNA, into GAM191 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2656] It is appreciated that GAM191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM191 target genes. The mRNA of each one of this plu-

rality of GAM191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM191 RNA, herein designated GAM RNA, and which when bound by GAM191 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM191 target proteins.

[2657] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM191 gene, herein designated GAM GENE, on one or more GAM191 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2658] It is yet further appreciated that specific functions, and accordingly utilities, of GAM191 correlate with, and may be deduced from, the identity of the target genes which GAM191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2659] Nucleotide sequences of the GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM191 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM191 are further described hereinbelow with reference to Table Table1.

[2660] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM191 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2661]

[2662] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 192 (GAM192) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2663] GAM192 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM192 was detected is described hereinabove with reference to Figs. 2-8.

[2664] GAM192 gene, herein designated GAM GENE, and GAM192 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2665] GAM192 gene, herein designated GAM GENE, encodes a GAM192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM192 precursor RNA is designated SEQ ID:2763, and is provided hereinbelow with reference to the sequence listing part.

[2666] GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2667] An enzyme complex designated DICER COMPLEX, dices the GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM192 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM192 RNA is designated SEQ ID:2764, and is provided hereinbelow with reference to the sequence listing part.

[2668] GAM192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM192 target RNA, herein designated GAM TARGET RNA.

GAM192 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[2669] GAM192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM192 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM192 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM192 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2670] The complementary binding of GAM192 RNA, herein designated GAM RNA, to target binding sites on GAM192 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM192 target RNA, herein designated GAM TARGET RNA, into GAM192 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2671] It is appreciated that GAM192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM192 target genes. The mRNA of each one of this plurality of GAM192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM192 RNA, herein designated GAM RNA, and which when bound by GAM192 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM192 target proteins.

[2672] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM192 gene, herein designated GAM GENE, on one or more GAM192 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2673] It is yet further appreciated that specific functions, and accordingly utilities, of GAM192 correlate with, and may be deduced from, the identity of the target genes which GAM192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2674] Nucleotide sequences of the GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM192 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM192 are further described hereinbelow with reference to Table Table1.

[2675] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM192 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2676]

[2677] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 193 (GAM193) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2678] GAM193 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM193 was detected is described hereinabove with reference to Figs. 2-8.

[2679] GAM193 gene, herein designated GAM GENE, and GAM193 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2680] GAM193 gene, herein designated GAM GENE, encodes a GAM193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM193 precursor RNA is designated SEQ ID:2783, and is provided hereinbelow with reference to the sequence listing part.

[2681] GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2682] An enzyme complex designated DICER COMPLEX, dices the GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM193 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of

GAM193 RNA is designated SEQ ID:2784, and is provided hereinbelow with reference to the sequence listing part.

[2683] GAM193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM193 target RNA, herein designated GAM TARGET RNA.

GAM193 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2684] GAM193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM193 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM193 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2685] The complementary binding of GAM193 RNA, herein designated GAM RNA, to target binding sites on GAM193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM193 target RNA, herein designated GAM TARGET RNA, into GAM193 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2686] It is appreciated that GAM193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM193 target genes. The mRNA of each one of this plurality of GAM193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM193 RNA, herein designated GAM RNA, and which when bound by GAM193 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM193 target proteins.

[2687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM193 gene, herein designated GAM GENE, on one or more GAM193 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2688] It is yet further appreciated that specific functions, and accordingly utilities, of GAM193 correlate with, and may be deduced from, the identity of the target genes which GAM193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2689] Nucleotide sequences of the GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM193 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM193 are further described hereinbelow with reference to Table Table1.

[2690] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM193 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2691]

[2692] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 194 (GAM194) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2693] GAM194 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM194 was detected is described hereinabove

with reference to Figs. 2-8.

[2694] GAM194 gene, herein designated GAM GENE, and GAM194 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2695] GAM194 gene, herein designated GAM GENE, encodes a GAM194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM194 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM194 precursor RNA is designated SEQ ID:2794, and is provided hereinbelow with reference to the sequence listing part.

[2696] GAM194 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2697] An enzyme complex designated DICER COMPLEX, dices the GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM194 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM194 RNA is designated SEQ ID:2795, and is provided hereinbelow with reference to the sequence listing part.

[2698] GAM194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM194 target RNA, herein designated GAM TARGET RNA. GAM194 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2699] GAM194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM194 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM194 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM194 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM194 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2700] The complementary binding of GAM194 RNA, herein designated GAM RNA, to target binding sites on GAM194 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM194 target RNA, herein designated GAM TARGET RNA, into GAM194 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[2701] It is appreciated that GAM194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM194 target genes. The mRNA of each one of this plurality of GAM194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM194 RNA, herein designated GAM RNA, and which when bound by GAM194 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM194 target proteins.

[2702] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM194 gene, herein designated GAM GENE, on one or more GAM194 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2703] It is yet further appreciated that specific functions, and accordingly utilities, of GAM194 correlate with, and may be deduced from, the identity of the target genes which GAM194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2704] Nucleotide sequences of the GAM194 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM194 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM194 are further described hereinbelow with reference to Table Table1.

[2705] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM194 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2706]

[2707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 195 (GAM195) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2708] GAM195 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM195 was detected is described hereinabove with reference to Figs. 2-8.

[2709] GAM195 gene, herein designated GAM GENE, and GAM195 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2710] GAM195 gene, herein designated GAM GENE, encodes a GAM195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM195 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM195 precursor RNA is designated SEQ ID:2807, and is provided hereinbelow with reference to the sequence listing part.

[2711] GAM195 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2712] An enzyme complex designated DICER COMPLEX, dices the GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM195 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM195 RNA is designated SEQ ID:2808, and is provided hereinbelow with reference to the sequence listing part.

[2713] GAM195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM195 target RNA, herein designated GAM TARGET RNA.

GAM195 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2714] GAM195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM195 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM195 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2715] The complementary binding of GAM195 RNA, herein designated GAM RNA, to target binding sites on GAM195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM195 target RNA, herein designated GAM TARGET RNA, into GAM195 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2716] It is appreciated that GAM195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM195 target genes. The mRNA of each one of this plurality of GAM195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM195 RNA, herein designated GAM RNA, and which when bound by GAM195 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM195 target proteins.

[2717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM195 gene, herein designated GAM GENE, on one or more GAM195 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM195 correlate with, and may be deduced from, the identity of the target genes which GAM195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2719] Nucleotide sequences of the GAM195 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM195 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM195 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM195 are further described hereinbelow with reference to Table Table1.

[2720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM195 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2721]

[2722] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 196 (GAM196) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2723] GAM196 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM196 was detected is described hereinabove with reference to Figs. 2-8.

[2724] GAM196 gene, herein designated GAM GENE, and GAM196 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2725] GAM196 gene, herein designated GAM GENE, encodes a

GAM196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM196 precursor RNA is designated SEQ ID:2826, and is provided hereinbelow with reference to the sequence listing part.

[2726] GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2727] An enzyme complex designated DICER COMPLEX, dices the GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM196 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM196 RNA is designated SEQ ID:2827, and is provided hereinbelow with reference to the sequence listing part.

[2728] GAM196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM196 target RNA, herein designated GAM TARGET RNA. GAM196 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2729] GAM196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM196 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM196 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2730] The complementary binding of GAM196 RNA, herein designated GAM RNA, to target binding sites on GAM196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM196 target RNA, herein designated GAM TARGET RNA, into GAM196 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2731] It is appreciated that GAM196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM196 target genes. The mRNA of each one of this plurality of GAM196 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM196 RNA, herein designated GAM RNA, and which when bound by GAM196 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM196 target proteins.

[2732] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM196 gene, herein designated GAM GENE, on one or more GAM196 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2733] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM196 correlate with, and may be deduced from, the identity of the target genes which GAM196 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2734] Nucleotide sequences of the GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM196 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM196 are further described hereinbelow with reference to Table Table1.

[2735] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM196 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2736]

[2737] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 197 (GAM197) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2738] GAM197 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM197 was detected is described hereinabove with reference to Figs. 2-8.

[2739] GAM197 gene, herein designated GAM GENE, and GAM197 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2740] GAM197 gene, herein designated GAM GENE, encodes a GAM197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM197 precursor RNA is designated SEQ ID:2846, and is provided hereinbelow with reference to the sequence listing part.

[2741] GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2742] An enzyme complex designated DICER COMPLEX, dices the GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM197 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM197 RNA is designated SEQ ID:2847, and is provided hereinbelow with reference to the sequence listing part.

[2743] GAM197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM197 target RNA, herein designated GAM TARGET RNA. GAM197 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2744] GAM197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM197 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM197 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM197 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2745] The complementary binding of GAM197 RNA, herein designated GAM RNA, to target binding sites on GAM197 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM197 target RNA, herein designated GAM TARGET RNA, into GAM197 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2746] It is appreciated that GAM197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM197 target genes. The mRNA of each one of this plurality of GAM197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM197 RNA, herein designated GAM RNA, and which when bound by GAM197 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM197 target proteins.

[2747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM197 gene, herein designated GAM GENE, on one or more GAM197 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2748] It is yet further appreciated that specific functions, and accordingly utilities, of GAM197 correlate with, and may be deduced from, the identity of the target genes which GAM197 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2749] Nucleotide sequences of the GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM197 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM197 are further described hereinbelow with reference to Table Table1.

[2750] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM197 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2751]

[2752] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 198 (GAM198) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2753] GAM198 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM198 was detected is described hereinabove with reference to Figs. 2-8.

[2754] GAM198 gene, herein designated GAM GENE, and GAM198 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2755] GAM198 gene, herein designated GAM GENE, encodes a GAM198 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM198 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM198 precursor RNA is designated SEQ ID:2858, and is provided hereinbelow with reference to the sequence listing part.

[2756] GAM198 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2757] An enzyme complex designated DICER COMPLEX, dices the GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM198 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM198 RNA is designated SEQ ID:2859, and is provided

hereinbelow with reference to the sequence listing part.

[2758] GAM198 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM198 target RNA, herein designated GAM TARGET RNA.

GAM198 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2759] GAM198 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM198 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM198 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM198 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM198 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2760] The complementary binding of GAM198 RNA, herein designated GAM RNA, to target binding sites on GAM198 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM198 target RNA, herein designated GAM TARGET RNA, into GAM198 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2761] It is appreciated that GAM198 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM198 target genes. The mRNA of each one of this plurality of GAM198 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM198 RNA, herein designated GAM RNA, and which when bound by GAM198 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM198 tar-

get proteins.

[2762] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM198 gene, herein designated GAM GENE, on one or more GAM198 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2763] It is yet further appreciated that specific functions, and accordingly utilities, of GAM198 correlate with, and may be deduced from, the identity of the target genes which GAM198 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2764] Nucleotide sequences of the GAM198 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM198 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM198 are further described hereinbelow with reference to Table Table1.

[2765] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM198 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2766]

[2767] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 199 (GAM199) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2768] GAM199 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM199 was detected is described hereinabove with reference to Figs. 2-8.

[2769] GAM199 gene, herein designated GAM GENE, and GAM199 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2770] GAM199 gene, herein designated GAM GENE, encodes a GAM199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM199 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM199 precursor RNA is designated SEQ ID:2874, and is provided hereinbelow with reference to the sequence listing part.

[2771] GAM199 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2772] An enzyme complex designated DICER COMPLEX, dices

the GAM199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM199 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of GAM199 RNA is designated SEQ ID:2875, and is provided hereinbelow with reference to the sequence listing part.

[2773] GAM199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM199 target RNA, herein designated GAM TARGET RNA. GAM199 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2774] GAM199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM199

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM199 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM199 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2775] The complementary binding of GAM199 RNA, herein designated GAM RNA, to target binding sites on GAM199 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM199 target RNA, herein designated GAM TARGET RNA, into GAM199 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2776] It is appreciated that GAM199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM199 target genes. The mRNA of each one of this plurality of GAM199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM199 RNA, herein designated GAM RNA, and which when bound by GAM199 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM199 target proteins.

[2777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM199 gene, herein designated GAM GENE, on one or more GAM199 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2778] It is yet further appreciated that specific functions, and accordingly utilities, of GAM199 correlate with, and may be deduced from, the identity of the target genes which GAM199 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2779] Nucleotide sequences of the GAM199 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM199 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM199 are further described hereinbelow with reference to Table Table1.

[2780] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM199 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2781]

[2782] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 200 (GAM200) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2783] GAM200 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM200 was detected is described hereinabove with reference to Figs. 2-8.

[2784] GAM200 gene, herein designated GAM GENE, and GAM200 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2785] GAM200 gene, herein designated GAM GENE, encodes a GAM200 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM200 precursor RNA is designated SEQ ID:2880, and is provided hereinbelow with reference to the sequence listing part.

[2786] GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM200 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2787] An enzyme complex designated DICER COMPLEX, dices the GAM200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM200 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 20%) nucleotide sequence of GAM200 RNA is designated SEQ ID:2881, and is provided hereinbelow with reference to the sequence listing part.

[2788] GAM200 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM200 target RNA, herein designated GAM TARGET RNA. GAM200 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2789] GAM200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM200 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM200 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM200 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[2790] The complementary binding of GAM200 RNA, herein designated GAM RNA, to target binding sites on GAM200 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM200 target RNA, herein designated GAM TARGET RNA, into GAM200 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2791] It is appreciated that GAM200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM200 target genes. The mRNA of each one of this plurality of GAM200 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM200 RNA, herein designated GAM RNA, and which when bound by GAM200 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM200 target proteins.

[2792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM200 gene, herein designated GAM GENE, on one or

more GAM200 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2793] It is yet further appreciated that specific functions, and accordingly utilities, of GAM200 correlate with, and may be deduced from, the identity of the target genes which GAM200 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2794] Nucleotide sequences of the GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM200 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM200 are further de-

scribed hereinbelow with reference to Table Table1.

[2795] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM200 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2796]

[2797] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 201 (GAM201) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2798] GAM201 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM201 was detected is described hereinabove with reference to Figs. 2-8.

[2799] GAM201 gene, herein designated GAM GENE, and GAM201 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2800] GAM201 gene, herein designated GAM GENE, encodes a GAM201 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM201 precursor RNA is designated SEQ ID:2898, and is provided hereinbelow with reference to the sequence listing part.

[2801] GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2802] An enzyme complex designated DICER COMPLEX, dices the GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM201 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM201 RNA is designated SEQ ID:2899, and is provided hereinbelow with reference to the sequence listing part.

[2803] GAM201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM201 target RNA, herein designated GAM TARGET RNA. GAM201 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2804] GAM201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM201 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM201 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM201 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2805] The complementary binding of GAM201 RNA, herein designated GAM RNA, to target binding sites on GAM201 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM201 target RNA, herein designated GAM TARGET RNA, into GAM201 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2806] It is appreciated that GAM201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM201 target genes. The mRNA of each one of this plurality of GAM201 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM201 RNA, herein designated GAM RNA, and which when bound by GAM201 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM201 target proteins.

[2807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM201 gene, herein designated GAM GENE, on one or more GAM201 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2808] It is yet further appreciated that specific functions, and accordingly utilities, of GAM201 correlate with, and may

be deduced from, the identity of the target genes which GAM201 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2809] Nucleotide sequences of the GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM201 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM201 are further described hereinbelow with reference to Table Table1.

[2810] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM201 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2811]

[2812] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 202 (GAM202) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2813] GAM202 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM202 was detected is described hereinabove with reference to Figs. 2-8.

[2814] GAM202 gene, herein designated GAM GENE, and GAM202 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2815] GAM202 gene, herein designated GAM GENE, encodes a GAM202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM202 precursor RNA is designated SEQ ID:2921, and is provided hereinbelow with reference to the sequence listing part.

[2816] GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2817] An enzyme complex designated DICER COMPLEX, dices the GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM202 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM202 RNA is designated SEQ ID:2922, and is provided hereinbelow with reference to the sequence listing part.

[2818] GAM202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM202 target RNA, herein designated GAM TARGET RNA. GAM202 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2819] GAM202 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM202 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM202 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM202 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM202 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2820] The complementary binding of GAM202 RNA, herein designated GAM RNA, to target binding sites on GAM202 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM202 target RNA, herein designated GAM TARGET RNA, into GAM202 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2821] It is appreciated that GAM202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM202 target genes. The mRNA of each one of this plurality of GAM202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM202 RNA, herein designated GAM RNA, and which when bound by GAM202 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM202 target proteins.

[2822] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM202 gene, herein designated GAM GENE, on one or more GAM202 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2823] It is yet further appreciated that specific functions, and accordingly utilities, of GAM202 correlate with, and may be deduced from, the identity of the target genes which GAM202 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2824] Nucleotide sequences of the GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM202 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM202 are further described hereinbelow with reference to Table Table1.

[2825] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM202 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2826]

[2827] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 203 (GAM203) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2828] GAM203 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM203 was detected is described hereinabove with reference to Figs. 2-8.

[2829] GAM203 gene, herein designated GAM GENE, and GAM203 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2830] GAM203 gene, herein designated GAM GENE, encodes a GAM203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM203 precursor RNA is desig-

nated SEQ ID:2946, and is provided hereinbelow with reference to the sequence listing part.

[2831] GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2832] An enzyme complex designated DICER COMPLEX, dices the GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM203 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM203 RNA is designated SEQ ID:2947, and is provided hereinbelow with reference to the sequence listing part.

[2833] GAM203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM203 target RNA, herein designated GAM TARGET RNA. GAM203 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2834] GAM203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM203 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM203 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM203

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2835] The complementary binding of GAM203 RNA, herein designated GAM RNA, to target binding sites on GAM203 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM203 target RNA, herein designated GAM TARGET RNA, into GAM203 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2836] It is appreciated that GAM203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM203 target genes. The mRNA of each one of this plurality of GAM203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM203 RNA, herein designated GAM RNA, and which when bound by GAM203 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM203 target proteins.

[2837] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM203 gene, herein designated GAM GENE, on one or more GAM203 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2838] It is yet further appreciated that specific functions, and accordingly utilities, of GAM203 correlate with, and may be deduced from, the identity of the target genes which GAM203 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2839] Nucleotide sequences of the GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM203 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM203 are further described hereinbelow with reference to Table Table1.

[2840] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM203 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2841]

[2842] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 204 (GAM204) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2843] GAM204 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM204 was detected is described hereinabove with reference to Figs. 2-8.

[2844] GAM204 gene, herein designated GAM GENE, and

GAM204 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2845] GAM204 gene, herein designated GAM GENE, encodes a GAM204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM204 precursor RNA is designated SEQ ID:2953, and is provided hereinbelow with reference to the sequence listing part.

[2846] GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2847] An enzyme complex designated DICER COMPLEX, dices the GAM204 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM204 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM204 RNA is designated SEQ ID:2954, and is provided hereinbelow with reference to the sequence listing part.

[2848] GAM204 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM204 target RNA, herein designated GAM TARGET RNA. GAM204 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2849] GAM204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM204 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM204 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM204 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2850] The complementary binding of GAM204 RNA, herein designated GAM RNA, to target binding sites on GAM204 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM204 target RNA, herein designated GAM TARGET RNA, into GAM204 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2851] It is appreciated that GAM204 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM204 target genes. The mRNA of each one of this plurality of GAM204 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM204 RNA, herein designated GAM RNA, and which when bound by GAM204 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM204 target proteins.

[2852] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM204 gene, herein designated GAM GENE, on one or more GAM204 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2853] It is yet further appreciated that specific functions, and accordingly utilities, of GAM204 correlate with, and may be deduced from, the identity of the target genes which GAM204 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2854] Nucleotide sequences of the GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM204 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM204 are further described hereinbelow with reference to Table Table1.

[2855] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM204 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2856]

[2857] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 205 (GAM205) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2858] GAM205 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM205 was detected is described hereinabove with reference to Figs. 2-8.

[2859] GAM205 gene, herein designated GAM GENE, and GAM205 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2860] GAM205 gene, herein designated GAM GENE, encodes a GAM205 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM205 precursor RNA is designated SEQ ID:2967, and is provided hereinbelow with reference to the sequence listing part.

[2861] GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2862] An enzyme complex designated DICER COMPLEX, dices the GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM205 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM205 RNA is designated SEQ ID:2968, and is provided hereinbelow with reference to the sequence listing part.

[2863] GAM205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM205 target RNA, herein designated GAM TARGET RNA. GAM205 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2864] GAM205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM205 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM205 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM205 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2865] The complementary binding of GAM205 RNA, herein designated GAM RNA, to target binding sites on GAM205 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM205 target RNA, herein designated GAM TARGET RNA, into GAM205 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2866] It is appreciated that GAM205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM205 target genes. The mRNA of each one of this plurality of GAM205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM205 RNA, herein designated GAM RNA, and which when bound by GAM205 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM205 target proteins.

[2867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM205 gene, herein designated GAM GENE, on one or more GAM205 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM205 correlate with, and may be deduced from, the identity of the target genes which GAM205 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2869] Nucleotide sequences of the GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM205 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM205 are further described hereinbelow with reference to Table Table1.

[2870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM205 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2871]

[2872] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 206 (GAM206) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2873] GAM206 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM206 was detected is described hereinabove with reference to Figs. 2-8.

[2874] GAM206 gene, herein designated GAM GENE, and GAM206 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2875] GAM206 gene, herein designated GAM GENE, encodes a GAM206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM206 precursor RNA is designated SEQ ID:2973, and is provided hereinbelow with reference to the sequence listing part.

[2876] GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2877] An enzyme complex designated DICER COMPLEX, dices the GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM206 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM206 RNA is designated SEQ ID:2974, and is provided hereinbelow with reference to the sequence listing part.

[2878] GAM206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM206 target RNA, herein designated GAM TARGET RNA. GAM206 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2879] GAM206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM206 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM206 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM206 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2880] The complementary binding of GAM206 RNA, herein designated GAM RNA, to target binding sites on GAM206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM206 target RNA, herein designated GAM TARGET RNA, into GAM206 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2881] It is appreciated that GAM206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM206 target genes. The mRNA of each one of this plurality of GAM206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM206 RNA,

herein designated GAM RNA, and which when bound by GAM206 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM206 target proteins.

[2882] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM206 gene, herein designated GAM GENE, on one or more GAM206 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2883] It is yet further appreciated that specific functions, and accordingly utilities, of GAM206 correlate with, and may be deduced from, the identity of the target genes which

GAM206 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2884] Nucleotide sequences of the GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM206 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM206 are further described hereinbelow with reference to Table Table1.

[2885] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM206 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2886]

[2887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 207 (GAM207) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2888] GAM207 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM207 was detected is described hereinabove with reference to Figs. 2-8.

[2889] GAM207 gene, herein designated GAM GENE, and GAM207 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2890] GAM207 gene, herein designated GAM GENE, encodes a GAM207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM207 precursor RNA is designated SEQ ID:3004, and is provided hereinbelow with reference to the sequence listing part.

[2891] GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[2892] An enzyme complex designated DICER COMPLEX, dices the GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM207 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 26%) nucleotide sequence of GAM207 RNA is designated SEQ ID:3005, and is provided hereinbelow with reference to the sequence listing part.

[2893] GAM207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM207 target RNA, herein designated GAM TARGET RNA.
GAM207 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2894] GAM207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM207 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM207 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM207 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2895] The complementary binding of GAM207 RNA, herein designated GAM RNA, to target binding sites on GAM207 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM207 target RNA, herein desig-

nated GAM TARGET RNA, into GAM207 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2896] It is appreciated that GAM207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM207 target genes. The mRNA of each one of this plurality of GAM207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM207 RNA, herein designated GAM RNA, and which when bound by GAM207 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM207 target proteins.

[2897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM207 gene, herein designated GAM GENE, on one or more GAM207 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM207 correlate with, and may be deduced from, the identity of the target genes which GAM207 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2899] Nucleotide sequences of the GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM207 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM207 are further described hereinbelow with reference to Table Table1.

[2900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM207 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[2901]

[2902] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 208 (GAM208) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2903] GAM208 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM208 was detected is described hereinabove with reference to Figs. 2-8.

[2904] GAM208 gene, herein designated GAM GENE, and GAM208 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2905] GAM208 gene, herein designated GAM GENE, encodes a GAM208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM208 precursor RNA is designated SEQ ID:3021, and is provided hereinbelow with ref-

erence to the sequence listing part.

[2906] GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2907] An enzyme complex designated DICER COMPLEX, dices the GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM208 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM208 RNA is designated SEQ ID:3022, and is provided hereinbelow with reference to the sequence listing part.

[2908] GAM208 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM208 target RNA, herein designated GAM TARGET RNA.

GAM208 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2909] GAM208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM208 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM208 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM208 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2910] The complementary binding of GAM208 RNA, herein designated GAM RNA, to target binding sites on GAM208 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM208 target RNA, herein designated GAM TARGET RNA, into GAM208 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2911] It is appreciated that GAM208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM208 target genes. The mRNA of each one of this plurality of GAM208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM208 RNA, herein designated GAM RNA, and which when bound by GAM208 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM208 target proteins.

[2912] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM208 gene, herein designated GAM GENE, on one or more GAM208 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2913] It is yet further appreciated that specific functions, and accordingly utilities, of GAM208 correlate with, and may be deduced from, the identity of the target genes which GAM208 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2914] Nucleotide sequences of the GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM208 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM208 are further described hereinbelow with reference to Table Table1.

[2915] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM208 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2916]

[2917] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 209 (GAM209) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2918] GAM209 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM209 was detected is described hereinabove with reference to Figs. 2-8.

[2919] GAM209 gene, herein designated GAM GENE, and GAM209 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2920] GAM209 gene, herein designated GAM GENE, encodes a GAM209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM209 precursor RNA is designated SEQ ID:3030, and is provided hereinbelow with reference to the sequence listing part.

[2921] GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2922] An enzyme complex designated DICER COMPLEX, dices the GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM209 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM209 RNA is designated SEQ ID:3031, and is provided hereinbelow with reference to the sequence listing part.

[2923] GAM209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM209 target RNA, herein designated GAM TARGET RNA. GAM209 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2924] GAM209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM209 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM209 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM209 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2925] The complementary binding of GAM209 RNA, herein designated GAM RNA, to target binding sites on GAM209 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM209 target RNA, herein designated GAM TARGET RNA, into GAM209 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2926] It is appreciated that GAM209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM209 target genes. The mRNA of each one of this plurality of GAM209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM209 RNA, herein designated GAM RNA, and which when bound by GAM209 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM209 target proteins.

[2927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM209 gene, herein designated GAM GENE, on one or more GAM209 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2928] It is yet further appreciated that specific functions, and accordingly utilities, of GAM209 correlate with, and may be deduced from, the identity of the target genes which GAM209 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2929] Nucleotide sequences of the GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM209 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM209 are further described hereinbelow with reference to Table Table1.

[2930] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM209 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2931]

[2932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

210 (GAM210) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2933] GAM210 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM210 was detected is described hereinabove with reference to Figs. 2-8.

[2934] GAM210 gene, herein designated GAM GENE, and GAM210 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2935] GAM210 gene, herein designated GAM GENE, encodes a GAM210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM210 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM210 precursor RNA is designated SEQ ID:3043, and is provided hereinbelow with reference to the sequence listing part.

[2936] GAM210 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2937] An enzyme complex designated DICER COMPLEX, dices the GAM210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM210 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM210 RNA is designated SEQ ID:3044, and is provided hereinbelow with reference to the sequence listing part.

[2938] GAM210 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM210 target RNA, herein designated GAM TARGET RNA. GAM210 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2939] GAM210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM210 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM210 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM210 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2940] The complementary binding of GAM210 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM210 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM210 target RNA, herein designated GAM TARGET RNA, into GAM210 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2941] It is appreciated that GAM210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM210 target genes. The mRNA of each one of this plurality of GAM210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM210 RNA, herein designated GAM RNA, and which when bound by GAM210 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM210 target proteins.

[2942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM210 gene, herein designated GAM GENE, on one or more GAM210 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM210 correlate with, and may be deduced from, the identity of the target genes which GAM210 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2944] Nucleotide sequences of the GAM210 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM210 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM210 are further described hereinbelow with reference to Table Table1.

[2945] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM210 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2946]

[2947] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 211 (GAM211) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2948] GAM211 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM211 was detected is described hereinabove with reference to Figs. 2-8.

[2949] GAM211 gene, herein designated GAM GENE, and GAM211 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2950] GAM211 gene, herein designated GAM GENE, encodes a GAM211 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM211 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM211 precursor RNA is designated SEQ ID:3049, and is provided hereinbelow with reference to the sequence listing part.

[2951] GAM211 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2952] An enzyme complex designated DICER COMPLEX, dices the GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM211 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 66%) nucleotide sequence of GAM211 RNA is designated SEQ ID:3050, and is provided hereinbelow with reference to the sequence listing part.

[2953] GAM211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM211 target RNA, herein designated GAM TARGET RNA. GAM211 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2954] GAM211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM211 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM211 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM211 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2955] The complementary binding of GAM211 RNA, herein designated GAM RNA, to target binding sites on GAM211 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM211 target RNA, herein designated GAM TARGET RNA, into GAM211 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2956] It is appreciated that GAM211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM211 target genes. The mRNA of each one of this plurality of GAM211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM211 RNA, herein designated GAM RNA, and which when bound by

GAM211 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM211 target proteins.

[2957] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM211 gene, herein designated GAM GENE, on one or more GAM211 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2958] It is yet further appreciated that specific functions, and accordingly utilities, of GAM211 correlate with, and may be deduced from, the identity of the target genes which GAM211 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2959] Nucleotide sequences of the GAM211 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM211 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM211 are further described hereinbelow with reference to Table Table1.

[2960] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM211 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2961]

[2962] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 212 (GAM212) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2963] GAM212 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM212 was detected is described hereinabove with reference to Figs. 2-8.

[2964] GAM212 gene, herein designated GAM GENE, and GAM212 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2965] GAM212 gene, herein designated GAM GENE, encodes a GAM212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM212 precursor RNA is designated SEQ ID:3069, and is provided hereinbelow with reference to the sequence listing part.

[2966] GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[2967] An enzyme complex designated DICER COMPLEX, dices the GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM212 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM212 RNA is designated SEQ ID:3070, and is provided hereinbelow with reference to the sequence listing part.

[2968] GAM212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM212 target RNA, herein designated GAM TARGET RNA. GAM212 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2969] GAM212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM212 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM212 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM212 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM212 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2970] The complementary binding of GAM212 RNA, herein designated GAM RNA, to target binding sites on GAM212 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM212 target RNA, herein designated GAM TARGET RNA, into GAM212 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2971] It is appreciated that GAM212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM212 target genes. The mRNA of each one of this plurality of GAM212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM212 RNA, herein designated GAM RNA, and which when bound by GAM212 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM212 target proteins.

[2972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM212 gene, herein designated GAM GENE, on one or more GAM212 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2973] It is yet further appreciated that specific functions, and accordingly utilities, of GAM212 correlate with, and may be deduced from, the identity of the target genes which GAM212 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2974] Nucleotide sequences of the GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM212 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM212 are further described hereinbelow with reference to Table Table1.

[2975] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM212 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2976]

[2977] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 213 (GAM213) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2978] GAM213 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM213 was detected is described hereinabove with reference to Figs. 2-8.

[2979] GAM213 gene, herein designated GAM GENE, and GAM213 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2980] GAM213 gene, herein designated GAM GENE, encodes a GAM213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM213 precursor RNA is designated SEQ ID:3075, and is provided hereinbelow with reference to the sequence listing part.

[2981] GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2982] An enzyme complex designated DICER COMPLEX, dices the GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM213 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM213 RNA is designated SEQ ID:3076, and is provided hereinbelow with reference to the sequence listing part.

[2983] GAM213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM213

target RNA, herein designated GAM TARGET RNA.

GAM213 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2984] GAM213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM213 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM213 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM213 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2985] The complementary binding of GAM213 RNA, herein designated GAM RNA, to target binding sites on GAM213 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM213 target RNA, herein designated GAM TARGET RNA, into GAM213 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2986] It is appreciated that GAM213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM213 target genes. The mRNA of each one of this plurality of GAM213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM213 RNA, herein designated GAM RNA, and which when bound by GAM213 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM213 target proteins.

[2987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM213 gene, herein designated GAM GENE, on one or more GAM213 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2988] It is yet further appreciated that specific functions, and accordingly utilities, of GAM213 correlate with, and may be deduced from, the identity of the target genes which GAM213 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2989] Nucleotide sequences of the GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM213 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM213 are further described hereinbelow with reference to Table Table1.

[2990] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM213 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2991]

[2992] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 214 (GAM214) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2993] GAM214 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM214 was detected is described hereinabove with reference to Figs. 2-8.

[2994] GAM214 gene, herein designated GAM GENE, and GAM214 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2995] GAM214 gene, herein designated GAM GENE, encodes a GAM214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM214 precursor RNA is designated SEQ ID:3081, and is provided hereinbelow with reference to the sequence listing part.

[2996] GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2997] An enzyme complex designated DICER COMPLEX, dices the GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM214 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM214 RNA is designated SEQ ID:3082, and is provided hereinbelow with reference to the sequence listing part.

[2998] GAM214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM214 target RNA, herein designated GAM TARGET RNA. GAM214 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2999] GAM214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM214 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM214 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM214 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3000] The complementary binding of GAM214 RNA, herein designated GAM RNA, to target binding sites on GAM214 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM214 target RNA, herein designated GAM TARGET RNA, into GAM214 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3001] It is appreciated that GAM214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM214 target genes. The mRNA of each one of this plu-

rality of GAM214 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM214 RNA, herein designated GAM RNA, and which when bound by GAM214 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM214 target proteins.

[3002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM214 gene, herein designated GAM GENE, on one or more GAM214 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3003] It is yet further appreciated that specific functions, and accordingly utilities, of GAM214 correlate with, and may be deduced from, the identity of the target genes which GAM214 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3004] Nucleotide sequences of the GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM214 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM214 are further described hereinbelow with reference to Table Table1.

[3005] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM214 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3006]

[3007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 215 (GAM215) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[3008] GAM215 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM215 was detected is described hereinabove with reference to Figs. 2-8.

[3009] GAM215 gene, herein designated GAM GENE, and GAM215 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3010] GAM215 gene, herein designated GAM GENE, encodes a GAM215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM215 precursor RNA is designated SEQ ID:3101, and is provided hereinbelow with reference to the sequence listing part.

[3011] GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3012] An enzyme complex designated DICER COMPLEX, dices the GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM215 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM215 RNA is designated SEQ ID:3102, and is provided hereinbelow with reference to the sequence listing part.

[3013] GAM215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM215 target RNA, herein designated GAM TARGET RNA.
GAM215 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3014] GAM215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM215 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM215 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM215 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3015] The complementary binding of GAM215 RNA, herein designated GAM RNA, to target binding sites on GAM215 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM215 target RNA, herein designated GAM TARGET RNA, into GAM215 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3016] It is appreciated that GAM215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM215 target genes. The mRNA of each one of this plurality of GAM215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM215 RNA, herein designated GAM RNA, and which when bound by GAM215 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM215 target proteins.

[3017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM215 gene, herein designated GAM GENE, on one or more GAM215 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3018] It is yet further appreciated that specific functions, and accordingly utilities, of GAM215 correlate with, and may be deduced from, the identity of the target genes which GAM215 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3019] Nucleotide sequences of the GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM215 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM215 are further described hereinbelow with reference to Table Table1.

[3020] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM215 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3021]

[3022] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 216 (GAM216) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3023] GAM216 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM216 was detected is described hereinabove with reference to Figs. 2-8.

[3024] GAM216 gene, herein designated GAM GENE, and GAM216 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3025] GAM216 gene, herein designated GAM GENE, encodes a GAM216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM216 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM216 precursor RNA is designated SEQ ID:3118, and is provided hereinbelow with reference to the sequence listing part.

[3026] GAM216 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3027] An enzyme complex designated DICER COMPLEX, dices the GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM216 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 32%) nucleotide sequence of

GAM216 RNA is designated SEQ ID:3119, and is provided hereinbelow with reference to the sequence listing part.

[3028] GAM216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM216 target RNA, herein designated GAM TARGET RNA. GAM216 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3029] GAM216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM216 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM216 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM216 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3030] The complementary binding of GAM216 RNA, herein designated GAM RNA, to target binding sites on GAM216 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM216 target RNA, herein designated GAM TARGET RNA, into GAM216 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3031] It is appreciated that GAM216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM216 target genes. The mRNA of each one of this plurality of GAM216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM216 RNA, herein designated GAM RNA, and which when bound by GAM216 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM216 target proteins.

[3032] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM216 gene, herein designated GAM GENE, on one or more GAM216 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3033] It is yet further appreciated that specific functions, and accordingly utilities, of GAM216 correlate with, and may be deduced from, the identity of the target genes which GAM216 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3034] Nucleotide sequences of the GAM216 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM216 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM216 are further described hereinbelow with reference to Table Table1.

[3035] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM216 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3036]

[3037] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 217 (GAM217) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3038] GAM217 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM217 was detected is described hereinabove

with reference to Figs. 2-8.

[3039] GAM217 gene, herein designated GAM GENE, and GAM217 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3040] GAM217 gene, herein designated GAM GENE, encodes a GAM217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM217 precursor RNA is designated SEQ ID:3132, and is provided hereinbelow with reference to the sequence listing part.

[3041] GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3042] An enzyme complex designated DICER COMPLEX, dices the GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM217 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM217 RNA is designated SEQ ID:3133, and is provided hereinbelow with reference to the sequence listing part.

[3043] GAM217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM217 target RNA, herein designated GAM TARGET RNA. GAM217 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3044] GAM217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM217 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM217 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM217 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM217 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3045] The complementary binding of GAM217 RNA, herein designated GAM RNA, to target binding sites on GAM217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM217 target RNA, herein designated GAM TARGET RNA, into GAM217 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3046] It is appreciated that GAM217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM217 target genes. The mRNA of each one of this plurality of GAM217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM217 RNA, herein designated GAM RNA, and which when bound by GAM217 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM217 target proteins.

[3047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM217 gene, herein designated GAM GENE, on one or more GAM217 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3048] It is yet further appreciated that specific functions, and accordingly utilities, of GAM217 correlate with, and may be deduced from, the identity of the target genes which GAM217 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3049] Nucleotide sequences of the GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM217 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM217 are further described hereinbelow with reference to Table Table1.

[3050] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM217 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3051]

[3052] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 218 (GAM218) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3053] GAM218 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM218 was detected is described hereinabove with reference to Figs. 2-8.

[3054] GAM218 gene, herein designated GAM GENE, and GAM218 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3055] GAM218 gene, herein designated GAM GENE, encodes a GAM218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM218 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM218 precursor RNA is designated SEQ ID:3172, and is provided hereinbelow with reference to the sequence listing part.

[3056] GAM218 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3057] An enzyme complex designated DICER COMPLEX, dices the GAM218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM218 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM218 RNA is designated SEQ ID:3173, and is provided hereinbelow with reference to the sequence listing part.

[3058] GAM218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM218 target RNA, herein designated GAM TARGET RNA.

GAM218 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3059] GAM218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM218 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM218 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM218 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3060] The complementary binding of GAM218 RNA, herein designated GAM RNA, to target binding sites on GAM218 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM218 target RNA, herein designated GAM TARGET RNA, into GAM218 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3061] It is appreciated that GAM218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM218 target genes. The mRNA of each one of this plurality of GAM218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM218 RNA, herein designated GAM RNA, and which when bound by GAM218 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM218 target proteins.

[3062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM218 gene, herein designated GAM GENE, on one or more GAM218 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3063] It is yet further appreciated that specific functions, and accordingly utilities, of GAM218 correlate with, and may be deduced from, the identity of the target genes which GAM218 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3064] Nucleotide sequences of the GAM218 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM218 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM218 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM218 are further described hereinbelow with reference to Table Table1.

[3065] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM218 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3066]

[3067] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 219 (GAM219) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3068] GAM219 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM219 was detected is described hereinabove with reference to Figs. 2-8.

[3069] GAM219 gene, herein designated GAM GENE, and GAM219 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3070] GAM219 gene, herein designated GAM GENE, encodes a

GAM219 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM219 precursor RNA is designated SEQ ID:3204, and is provided hereinbelow with reference to the sequence listing part.

[3071] GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3072] An enzyme complex designated DICER COMPLEX, dices the GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM219 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM219 RNA is designated SEQ ID:3205, and is provided hereinbelow with reference to the sequence listing part.

[3073] GAM219 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM219 target RNA, herein designated GAM TARGET RNA. GAM219 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3074] GAM219 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM219 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM219 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM219 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM219

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3075] The complementary binding of GAM219 RNA, herein designated GAM RNA, to target binding sites on GAM219 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM219 target RNA, herein designated GAM TARGET RNA, into GAM219 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3076] It is appreciated that GAM219 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM219 target genes. The mRNA of each one of this plurality of GAM219 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM219 RNA, herein designated GAM RNA, and which when bound by GAM219 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM219 target proteins.

[3077] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM219 gene, herein designated GAM GENE, on one or more GAM219 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3078] It is yet further appreciated that specific functions, and accordingly utilities, of GAM219 correlate with, and may be deduced from, the identity of the target genes which GAM219 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3079] Nucleotide sequences of the GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM219 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM219 are further described hereinbelow with reference to Table Table1.

[3080] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM219 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3081]

[3082] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 220 (GAM220) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3083] GAM220 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM220 was detected is described hereinabove with reference to Figs. 2-8.

[3084] GAM220 gene, herein designated GAM GENE, and

GAM220 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3085] GAM220 gene, herein designated GAM GENE, encodes a GAM220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM220 precursor RNA is designated SEQ ID:3210, and is provided hereinbelow with reference to the sequence listing part.

[3086] GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3087] An enzyme complex designated DICER COMPLEX, dices the GAM220 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM220 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM220 RNA is designated SEQ ID:3211, and is provided hereinbelow with reference to the sequence listing part.

[3088] GAM220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM220 target RNA, herein designated GAM TARGET RNA. GAM220 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3089] GAM220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM220 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM220 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM220 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3090] The complementary binding of GAM220 RNA, herein designated GAM RNA, to target binding sites on GAM220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM220 target RNA, herein designated GAM TARGET RNA, into GAM220 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3091] It is appreciated that GAM220 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM220 target genes. The mRNA of each one of this plurality of GAM220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM220 RNA, herein designated GAM RNA, and which when bound by GAM220 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM220 target proteins.

[3092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM220 gene, herein designated GAM GENE, on one or more GAM220 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3093] It is yet further appreciated that specific functions, and accordingly utilities, of GAM220 correlate with, and may be deduced from, the identity of the target genes which GAM220 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3094] Nucleotide sequences of the GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM220 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM220 are further described hereinbelow with reference to Table Table1.

[3095] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM220 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3096]

[3097] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 221 (GAM221) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3098] GAM221 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM221 was detected is described hereinabove with reference to Figs. 2-8.

[3099] GAM221 gene, herein designated GAM GENE, and GAM221 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3100] GAM221 gene, herein designated GAM GENE, encodes a GAM221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM221 precursor RNA is designated SEQ ID:3247, and is provided hereinbelow with reference to the sequence listing part.

[3101] GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3102] An enzyme complex designated DICER COMPLEX, dices the GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM221 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 33%) nucleotide sequence of GAM221 RNA is designated SEQ ID:3248, and is provided hereinbelow with reference to the sequence listing part.

[3103] GAM221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM221 target RNA, herein designated GAM TARGET RNA. GAM221 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3104] GAM221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM221 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM221 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM221 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3105] The complementary binding of GAM221 RNA, herein designated GAM RNA, to target binding sites on GAM221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM221 target RNA, herein designated GAM TARGET RNA, into GAM221 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3106] It is appreciated that GAM221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM221 target genes. The mRNA of each one of this plurality of GAM221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM221 RNA, herein designated GAM RNA, and which when bound by GAM221 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM221 target proteins.

[3107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM221 gene, herein designated GAM GENE, on one or more GAM221 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3108] It is yet further appreciated that specific functions, and accordingly utilities, of GAM221 correlate with, and may be deduced from, the identity of the target genes which GAM221 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3109] Nucleotide sequences of the GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM221 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM221 are further described hereinbelow with reference to Table Table1.

[3110] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM221 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3111]

[3112] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 222 (GAM222) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3113] GAM222 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM222 was detected is described hereinabove with reference to Figs. 2-8.

[3114] GAM222 gene, herein designated GAM GENE, and GAM222 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3115] GAM222 gene, herein designated GAM GENE, encodes a GAM222 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM222 precursor RNA is designated SEQ ID:3266, and is provided hereinbelow with reference to the sequence listing part.

[3116] GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3117] An enzyme complex designated DICER COMPLEX, dices the GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM222 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 36%) nucleotide sequence of GAM222 RNA is designated SEQ ID:3267, and is provided hereinbelow with reference to the sequence listing part.

[3118] GAM222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM222 target RNA, herein designated GAM TARGET RNA. GAM222 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3119] GAM222 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM222 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM222 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM222 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM222 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3120] The complementary binding of GAM222 RNA, herein designated GAM RNA, to target binding sites on GAM222 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM222 target RNA, herein designated GAM TARGET RNA, into GAM222 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3121] It is appreciated that GAM222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM222 target genes. The mRNA of each one of this plurality of GAM222 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM222 RNA,

herein designated GAM RNA, and which when bound by GAM222 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM222 target proteins.

[3122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM222 gene, herein designated GAM GENE, on one or more GAM222 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3123] It is yet further appreciated that specific functions, and accordingly utilities, of GAM222 correlate with, and may be deduced from, the identity of the target genes which

GAM222 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3124] Nucleotide sequences of the GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM222 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM222 are further described hereinbelow with reference to Table Table1.

[3125] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM222 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3126]

[3127] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 223 (GAM223) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3128] GAM223 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM223 was detected is described hereinabove with reference to Figs. 2-8.

[3129] GAM223 gene, herein designated GAM GENE, and GAM223 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3130] GAM223 gene, herein designated GAM GENE, encodes a GAM223 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM223 precursor RNA is designated SEQ ID:3279, and is provided hereinbelow with reference to the sequence listing part.

[3131] GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3132] An enzyme complex designated DICER COMPLEX, dices the GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM223 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM223 RNA is designated SEQ ID:3280, and is provided hereinbelow with reference to the sequence listing part.

[3133] GAM223 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM223 target RNA, herein designated GAM TARGET RNA.
GAM223 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3134] GAM223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM223 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM223 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM223 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3135] The complementary binding of GAM223 RNA, herein designated GAM RNA, to target binding sites on GAM223 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM223 target RNA, herein desig-

nated GAM TARGET RNA, into GAM223 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3136] It is appreciated that GAM223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM223 target genes. The mRNA of each one of this plurality of GAM223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM223 RNA, herein designated GAM RNA, and which when bound by GAM223 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM223 target proteins.

[3137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM223 gene, herein designated GAM GENE, on one or more GAM223 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3138] It is yet further appreciated that specific functions, and accordingly utilities, of GAM223 correlate with, and may be deduced from, the identity of the target genes which GAM223 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3139] Nucleotide sequences of the GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM223 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM223 are further described hereinbelow with reference to Table Table1.

[3140] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM223 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3141]

[3142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 224 (GAM224) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3143] GAM224 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM224 was detected is described hereinabove with reference to Figs. 2-8.

[3144] GAM224 gene, herein designated GAM GENE, and GAM224 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3145] GAM224 gene, herein designated GAM GENE, encodes a GAM224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM224 precursor RNA is designated SEQ ID:3287, and is provided hereinbelow with ref-

erence to the sequence listing part.

[3146] GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3147] An enzyme complex designated DICER COMPLEX, dices the GAM224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM224 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM224 RNA is designated SEQ ID:3288, and is provided hereinbelow with reference to the sequence listing part.

[3148] GAM224 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM224 target RNA, herein designated GAM TARGET RNA.

GAM224 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3149] GAM224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM224 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM224 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM224 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3150] The complementary binding of GAM224 RNA, herein designated GAM RNA, to target binding sites on GAM224 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM224 target RNA, herein designated GAM TARGET RNA, into GAM224 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3151] It is appreciated that GAM224 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM224 target genes. The mRNA of each one of this plurality of GAM224 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM224 RNA, herein designated GAM RNA, and which when bound by GAM224 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM224 target proteins.

[3152] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM224 gene, herein designated GAM GENE, on one or more GAM224 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM224 correlate with, and may be deduced from, the identity of the target genes which GAM224 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3154] Nucleotide sequences of the GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM224 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM224 are further described hereinbelow with reference to Table Table1.

[3155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM224 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3156]

[3157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 225 (GAM225) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3158] GAM225 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM225 was detected is described hereinabove with reference to Figs. 2-8.

[3159] GAM225 gene, herein designated GAM GENE, and GAM225 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3160] GAM225 gene, herein designated GAM GENE, encodes a GAM225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM225 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM225 precursor RNA is designated SEQ ID:3306, and is provided hereinbelow with reference to the sequence listing part.

[3161] GAM225 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3162] An enzyme complex designated DICER COMPLEX, dices the GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM225 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM225 RNA is designated SEQ ID:3307, and is provided hereinbelow with reference to the sequence listing part.

[3163] GAM225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM225 target RNA, herein designated GAM TARGET RNA. GAM225 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3164] GAM225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM225 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM225 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM225 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM225 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3165] The complementary binding of GAM225 RNA, herein designated GAM RNA, to target binding sites on GAM225 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM225 target RNA, herein designated GAM TARGET RNA, into GAM225 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3166] It is appreciated that GAM225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM225 target genes. The mRNA of each one of this plurality of GAM225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM225 RNA, herein designated GAM RNA, and which when bound by GAM225 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM225 target proteins.

[3167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM225 gene, herein designated GAM GENE, on one or more GAM225 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[3168] It is yet further appreciated that specific functions, and accordingly utilities, of GAM225 correlate with, and may be deduced from, the identity of the target genes which GAM225 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3169] Nucleotide sequences of the GAM225 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM225 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM225 are further described hereinbelow with reference to Table Table1.

[3170] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM225 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3171]

[3172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

226 (GAM226) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3173] GAM226 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM226 was detected is described hereinabove with reference to Figs. 2-8.

[3174] GAM226 gene, herein designated GAM GENE, and GAM226 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3175] GAM226 gene, herein designated GAM GENE, encodes a GAM226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM226 precursor RNA is designated SEQ ID:3315, and is provided hereinbelow with reference to the sequence listing part.

[3176] GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3177] An enzyme complex designated DICER COMPLEX, dices the GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM226 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM226 RNA is designated SEQ ID:3316, and is provided hereinbelow with reference to the sequence listing part.

[3178] GAM226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM226 target RNA, herein designated GAM TARGET RNA. GAM226 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3179] GAM226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM226 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM226 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM226 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM226 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3180] The complementary binding of GAM226 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM226 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM226 target RNA, herein designated GAM TARGET RNA, into GAM226 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3181] It is appreciated that GAM226 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM226 target genes. The mRNA of each one of this plurality of GAM226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM226 RNA, herein designated GAM RNA, and which when bound by GAM226 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM226 target proteins.

[3182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM226 gene, herein designated GAM GENE, on one or more GAM226 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM226 correlate with, and may be deduced from, the identity of the target genes which GAM226 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3184] Nucleotide sequences of the GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM226 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM226 are further described hereinbelow with reference to Table Table1.

[3185] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM226 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3186]

[3187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 227 (GAM227) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3188] GAM227 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM227 was detected is described hereinabove with reference to Figs. 2-8.

[3189] GAM227 gene, herein designated GAM GENE, and GAM227 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3190] GAM227 gene, herein designated GAM GENE, encodes a GAM227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM227 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM227 precursor RNA is designated SEQ ID:3343, and is provided hereinbelow with reference to the sequence listing part.

[3191] GAM227 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3192] An enzyme complex designated DICER COMPLEX, dices the GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM227 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 56%) nucleotide sequence of GAM227 RNA is designated SEQ ID:3344, and is provided hereinbelow with reference to the sequence listing part.

[3193] GAM227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM227 target RNA, herein designated GAM TARGET RNA. GAM227 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3194] GAM227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM227 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM227 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM227 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3195] The complementary binding of GAM227 RNA, herein designated GAM RNA, to target binding sites on GAM227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM227 target RNA, herein designated GAM TARGET RNA, into GAM227 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3196] It is appreciated that GAM227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM227 target genes. The mRNA of each one of this plurality of GAM227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM227 RNA, herein designated GAM RNA, and which when bound by

GAM227 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM227 target proteins.

[3197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM227 gene, herein designated GAM GENE, on one or more GAM227 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM227 correlate with, and may be deduced from, the identity of the target genes which GAM227 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3199] Nucleotide sequences of the GAM227 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM227 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM227 are further described hereinbelow with reference to Table Table1.

[3200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM227 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3201]

[3202] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 228 (GAM228) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3203] GAM228 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM228 was detected is described hereinabove with reference to Figs. 2-8.

[3204] GAM228 gene, herein designated GAM GENE, and GAM228 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3205] GAM228 gene, herein designated GAM GENE, encodes a GAM228 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM228 precursor RNA is designated SEQ ID:3350, and is provided hereinbelow with reference to the sequence listing part.

[3206] GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3207] An enzyme complex designated DICER COMPLEX, dices the GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM228 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM228 RNA is designated SEQ ID:3351, and is provided hereinbelow with reference to the sequence listing part.

[3208] GAM228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM228 target RNA, herein designated GAM TARGET RNA. GAM228 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3209] GAM228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM228 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM228 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM228 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM228 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3210] The complementary binding of GAM228 RNA, herein designated GAM RNA, to target binding sites on GAM228 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM228 target RNA, herein designated GAM TARGET RNA, into GAM228 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3211] It is appreciated that GAM228 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM228 target genes. The mRNA of each one of this plurality of GAM228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM228 RNA, herein designated GAM RNA, and which when bound by GAM228 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM228 target proteins.

[3212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM228 gene, herein designated GAM GENE, on one or more GAM228 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3213] It is yet further appreciated that specific functions, and accordingly utilities, of GAM228 correlate with, and may be deduced from, the identity of the target genes which GAM228 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3214] Nucleotide sequences of the GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM228 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM228 are further described hereinbelow with reference to Table Table1.

[3215] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM228 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3216]

[3217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 229 (GAM229) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3218] GAM229 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM229 was detected is described hereinabove with reference to Figs. 2-8.

[3219] GAM229 gene, herein designated GAM GENE, and GAM229 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3220] GAM229 gene, herein designated GAM GENE, encodes a GAM229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM229 precursor RNA is designated SEQ ID:3375, and is provided hereinbelow with reference to the sequence listing part.

[3221] GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3222] An enzyme complex designated DICER COMPLEX, dices the GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM229 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM229 RNA is designated SEQ ID:3376, and is provided hereinbelow with reference to the sequence listing part.

[3223] GAM229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM229

target RNA, herein designated GAM TARGET RNA.

GAM229 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3224] GAM229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM229 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM229 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM229 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3225] The complementary binding of GAM229 RNA, herein designated GAM RNA, to target binding sites on GAM229 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM229 target RNA, herein designated GAM TARGET RNA, into GAM229 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3226] It is appreciated that GAM229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM229 target genes. The mRNA of each one of this plurality of GAM229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM229 RNA, herein designated GAM RNA, and which when bound by GAM229 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM229 target proteins.

[3227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM229 gene, herein designated GAM GENE, on one or more GAM229 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3228] It is yet further appreciated that specific functions, and accordingly utilities, of GAM229 correlate with, and may be deduced from, the identity of the target genes which GAM229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3229] Nucleotide sequences of the GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM229 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM229 are further described hereinbelow with reference to Table Table1.

[3230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM229 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3231]

[3232] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 230 (GAM230) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3233] GAM230 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM230 was detected is described hereinabove with reference to Figs. 2-8.

[3234] GAM230 gene, herein designated GAM GENE, and GAM230 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3235] GAM230 gene, herein designated GAM GENE, encodes a GAM230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM230 precursor RNA is designated SEQ ID:3409, and is provided hereinbelow with reference to the sequence listing part.

[3236] GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3237] An enzyme complex designated DICER COMPLEX, dices the GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM230 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 93%) nucleotide sequence of GAM230 RNA is designated SEQ ID:3410, and is provided hereinbelow with reference to the sequence listing part.

[3238] GAM230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM230 target RNA, herein designated GAM TARGET RNA. GAM230 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3239] GAM230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM230 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM230 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM230 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3240] The complementary binding of GAM230 RNA, herein designated GAM RNA, to target binding sites on GAM230 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM230 target RNA, herein designated GAM TARGET RNA, into GAM230 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3241] It is appreciated that GAM230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM230 target genes. The mRNA of each one of this plu-

rality of GAM230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM230 RNA, herein designated GAM RNA, and which when bound by GAM230 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM230 target proteins.

[3242] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM230 gene, herein designated GAM GENE, on one or more GAM230 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3243] It is yet further appreciated that specific functions, and accordingly utilities, of GAM230 correlate with, and may be deduced from, the identity of the target genes which GAM230 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3244] Nucleotide sequences of the GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM230 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM230 are further described hereinbelow with reference to Table Table1.

[3245] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM230 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3246]

[3247] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 231 (GAM231) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[3248] GAM231 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM231 was detected is described hereinabove with reference to Figs. 2-8.

[3249] GAM231 gene, herein designated GAM GENE, and GAM231 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3250] GAM231 gene, herein designated GAM GENE, encodes a GAM231 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM231 precursor RNA is designated SEQ ID:3419, and is provided hereinbelow with reference to the sequence listing part.

[3251] GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3252] An enzyme complex designated DICER COMPLEX, dices the GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM231 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM231 RNA is designated SEQ ID:3420, and is provided hereinbelow with reference to the sequence listing part.

[3253] GAM231 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM231 target RNA, herein designated GAM TARGET RNA.
GAM231 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3254] GAM231 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM231 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM231 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM231 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM231 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3255] The complementary binding of GAM231 RNA, herein designated GAM RNA, to target binding sites on GAM231 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM231 target RNA, herein designated GAM TARGET RNA, into GAM231 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3256] It is appreciated that GAM231 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM231 target genes. The mRNA of each one of this plurality of GAM231 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM231 RNA, herein designated GAM RNA, and which when bound by GAM231 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM231 target proteins.

[3257] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM231 gene, herein designated GAM GENE, on one or more GAM231 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3258] It is yet further appreciated that specific functions, and accordingly utilities, of GAM231 correlate with, and may be deduced from, the identity of the target genes which GAM231 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3259] Nucleotide sequences of the GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM231 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM231 are further described hereinbelow with reference to Table Table1.

[3260] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM231 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3261]

[3262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 232 (GAM232) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3263] GAM232 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM232 was detected is described hereinabove with reference to Figs. 2-8.

[3264] GAM232 gene, herein designated GAM GENE, and GAM232 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3265] GAM232 gene, herein designated GAM GENE, encodes a GAM232 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM232 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM232 precursor RNA is designated SEQ ID:3431, and is provided hereinbelow with reference to the sequence listing part.

[3266] GAM232 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3267] An enzyme complex designated DICER COMPLEX, dices the GAM232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM232 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of

GAM232 RNA is designated SEQ ID:3432, and is provided hereinbelow with reference to the sequence listing part.

[3268] GAM232 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM232 target RNA, herein designated GAM TARGET RNA. GAM232 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3269] GAM232 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM232 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM232 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM232 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM232 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3270] The complementary binding of GAM232 RNA, herein designated GAM RNA, to target binding sites on GAM232 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM232 target RNA, herein designated GAM TARGET RNA, into GAM232 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3271] It is appreciated that GAM232 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM232 target genes. The mRNA of each one of this plurality of GAM232 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM232 RNA, herein designated GAM RNA, and which when bound by GAM232 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM232 target proteins.

[3272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM232 gene, herein designated GAM GENE, on one or more GAM232 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM232 correlate with, and may be deduced from, the identity of the target genes which GAM232 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3274] Nucleotide sequences of the GAM232 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM232 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM232 are further described hereinbelow with reference to Table Table1.

[3275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM232 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3276]

[3277] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 233 (GAM233) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3278] GAM233 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM233 was detected is described hereinabove

with reference to Figs. 2-8.

[3279] GAM233 gene, herein designated GAM GENE, and GAM233 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3280] GAM233 gene, herein designated GAM GENE, encodes a GAM233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM233 precursor RNA is designated SEQ ID:3449, and is provided hereinbelow with reference to the sequence listing part.

[3281] GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3282] An enzyme complex designated DICER COMPLEX, dices the GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM233 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM233 RNA is designated SEQ ID:3450, and is provided hereinbelow with reference to the sequence listing part.

[3283] GAM233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM233 target RNA, herein designated GAM TARGET RNA. GAM233 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3284] GAM233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM233 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM233 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM233 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM233 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3285] The complementary binding of GAM233 RNA, herein designated GAM RNA, to target binding sites on GAM233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM233 target RNA, herein designated GAM TARGET RNA, into GAM233 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3286] It is appreciated that GAM233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM233 target genes. The mRNA of each one of this plurality of GAM233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM233 RNA, herein designated GAM RNA, and which when bound by GAM233 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM233 target proteins.

[3287] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM233 gene, herein designated GAM GENE, on one or more GAM233 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3288] It is yet further appreciated that specific functions, and accordingly utilities, of GAM233 correlate with, and may be deduced from, the identity of the target genes which GAM233 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3289] Nucleotide sequences of the GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM233 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM233 are further described hereinbelow with reference to Table Table1.

[3290] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM233 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3291]

[3292] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 234 (GAM234) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3293] GAM234 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM234 was detected is described hereinabove with reference to Figs. 2-8.

[3294] GAM234 gene, herein designated GAM GENE, and GAM234 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3295] GAM234 gene, herein designated GAM GENE, encodes a GAM234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM234 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM234 precursor RNA is designated SEQ ID:3465, and is provided hereinbelow with reference to the sequence listing part.

[3296] GAM234 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3297] An enzyme complex designated DICER COMPLEX, dices the GAM234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM234 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of GAM234 RNA is designated SEQ ID:3466, and is provided hereinbelow with reference to the sequence listing part.

[3298] GAM234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM234 target RNA, herein designated GAM TARGET RNA.

GAM234 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3299] GAM234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM234 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM234 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM234 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3300] The complementary binding of GAM234 RNA, herein designated GAM RNA, to target binding sites on GAM234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM234 target RNA, herein designated GAM TARGET RNA, into GAM234 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3301] It is appreciated that GAM234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM234 target genes. The mRNA of each one of this plurality of GAM234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM234 RNA, herein designated GAM RNA, and which when bound by GAM234 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM234 target proteins.

[3302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM234 gene, herein designated GAM GENE, on one or more GAM234 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3303] It is yet further appreciated that specific functions, and accordingly utilities, of GAM234 correlate with, and may be deduced from, the identity of the target genes which GAM234 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3304] Nucleotide sequences of the GAM234 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM234 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM234 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM234 are further described hereinbelow with reference to Table Table1.

[3305] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM234 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3306]

[3307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 235 (GAM235) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3308] GAM235 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM235 was detected is described hereinabove with reference to Figs. 2-8.

[3309] GAM235 gene, herein designated GAM GENE, and GAM235 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3310] GAM235 gene, herein designated GAM GENE, encodes a

GAM235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM235 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM235 precursor RNA is designated SEQ ID:3469, and is provided hereinbelow with reference to the sequence listing part.

[3311] GAM235 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3312] An enzyme complex designated DICER COMPLEX, dices the GAM235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM235 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM235 RNA is designated SEQ ID:3470, and is provided hereinbelow with reference to the sequence listing part.

[3313] GAM235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM235 target RNA, herein designated GAM TARGET RNA. GAM235 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3314] GAM235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM235 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM235 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM235 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3315] The complementary binding of GAM235 RNA, herein designated GAM RNA, to target binding sites on GAM235 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM235 target RNA, herein designated GAM TARGET RNA, into GAM235 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3316] It is appreciated that GAM235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM235 target genes. The mRNA of each one of this plurality of GAM235 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM235 RNA, herein designated GAM RNA, and which when bound by GAM235 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM235 target proteins.

[3317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM235 gene, herein designated GAM GENE, on one or more GAM235 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3318] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM235 correlate with, and may be deduced from, the identity of the target genes which GAM235 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3319] Nucleotide sequences of the GAM235 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM235 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM235 are further described hereinbelow with reference to Table Table1.

[3320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM235 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3321]

[3322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 236 (GAM236) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[3323] GAM236 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM236 was detected is described hereinabove with reference to Figs. 2-8.

[3324] GAM236 gene, herein designated GAM GENE, and GAM236 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3325] GAM236 gene, herein designated GAM GENE, encodes a GAM236 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM236 precursor RNA is designated SEQ ID:3494, and is provided hereinbelow with reference to the sequence listing part.

[3326] GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3327] An enzyme complex designated DICER COMPLEX, dices the GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM236 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM236 RNA is designated SEQ ID:3495, and is provided hereinbelow with reference to the sequence listing part.

[3328] GAM236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM236 target RNA, herein designated GAM TARGET RNA. GAM236 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3329] GAM236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM236 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM236 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM236 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3330] The complementary binding of GAM236 RNA, herein designated GAM RNA, to target binding sites on GAM236 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM236 target RNA, herein designated GAM TARGET RNA, into GAM236 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3331] It is appreciated that GAM236 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM236 target genes. The mRNA of each one of this plurality of GAM236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM236 RNA, herein designated GAM RNA, and which when bound by GAM236 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM236 target proteins.

[3332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM236 gene, herein designated GAM GENE, on one or more GAM236 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM236 correlate with, and may be deduced from, the identity of the target genes which GAM236 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3334] Nucleotide sequences of the GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM236 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM236 are further described hereinbelow with reference to Table Table1.

[3335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM236 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3336]

[3337] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 237 (GAM237) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3338] GAM237 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM237 was detected is described hereinabove with reference to Figs. 2-8.

[3339] GAM237 gene, herein designated GAM GENE, and GAM237 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3340] GAM237 gene, herein designated GAM GENE, encodes a GAM237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM237 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM237 precursor RNA is designated SEQ ID:3506, and is provided hereinbelow with reference to the sequence listing part.

[3341] GAM237 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3342] An enzyme complex designated DICER COMPLEX, dices the GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM237 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM237 RNA is designated SEQ ID:3507, and is provided

hereinbelow with reference to the sequence listing part.

[3343] GAM237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM237 target RNA, herein designated GAM TARGET RNA. GAM237 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3344] GAM237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM237 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM237 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM237 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3345] The complementary binding of GAM237 RNA, herein designated GAM RNA, to target binding sites on GAM237 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM237 target RNA, herein designated GAM TARGET RNA, into GAM237 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3346] It is appreciated that GAM237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM237 target genes. The mRNA of each one of this plurality of GAM237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM237 RNA, herein designated GAM RNA, and which when bound by GAM237 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM237 tar-

get proteins.

[3347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM237 gene, herein designated GAM GENE, on one or more GAM237 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3348] It is yet further appreciated that specific functions, and accordingly utilities, of GAM237 correlate with, and may be deduced from, the identity of the target genes which GAM237 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3349] Nucleotide sequences of the GAM237 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM237 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM237 are further described hereinbelow with reference to Table Table1.

[3350] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM237 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3351]

[3352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 238 (GAM238) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3353] GAM238 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM238 was detected is described hereinabove with reference to Figs. 2-8.

[3354] GAM238 gene, herein designated GAM GENE, and GAM238 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3355] GAM238 gene, herein designated GAM GENE, encodes a GAM238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM238 precursor RNA is designated SEQ ID:3522, and is provided hereinbelow with reference to the sequence listing part.

[3356] GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3357] An enzyme complex designated DICER COMPLEX, dices

the GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM238 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM238 RNA is designated SEQ ID:3523, and is provided hereinbelow with reference to the sequence listing part.

[3358] GAM238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM238 target RNA, herein designated GAM TARGET RNA. GAM238 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3359] GAM238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM238

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM238 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM238 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3360] The complementary binding of GAM238 RNA, herein designated GAM RNA, to target binding sites on GAM238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM238 target RNA, herein designated GAM TARGET RNA, into GAM238 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3361] It is appreciated that GAM238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM238 target genes. The mRNA of each one of this plurality of GAM238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM238 RNA, herein designated GAM RNA, and which when bound by GAM238 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM238 target proteins.

[3362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM238 gene, herein designated GAM GENE, on one or more GAM238 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM238 correlate with, and may be deduced from, the identity of the target genes which GAM238 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3364] Nucleotide sequences of the GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM238 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM238 are further described hereinbelow with reference to Table Table1.

[3365] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM238 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3366]

[3367] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 239 (GAM239) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3368] GAM239 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM239 was detected is described hereinabove with reference to Figs. 2-8.

[3369] GAM239 gene, herein designated GAM GENE, and GAM239 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3370] GAM239 gene, herein designated GAM GENE, encodes a GAM239 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM239 precursor RNA is designated SEQ ID:3543, and is provided hereinbelow with reference to the sequence listing part.

[3371] GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM239 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3372] An enzyme complex designated DICER COMPLEX, dices the GAM239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM239 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM239 RNA is designated SEQ ID:3544, and is provided hereinbelow with reference to the sequence listing part.

[3373] GAM239 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM239 target RNA, herein designated GAM TARGET RNA. GAM239 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3374] GAM239 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM239 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM239 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM239 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM239 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[3375] The complementary binding of GAM239 RNA, herein designated GAM RNA, to target binding sites on GAM239 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM239 target RNA, herein designated GAM TARGET RNA, into GAM239 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3376] It is appreciated that GAM239 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM239 target genes. The mRNA of each one of this plurality of GAM239 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM239 RNA, herein designated GAM RNA, and which when bound by GAM239 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM239 target proteins.

[3377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM239 gene, herein designated GAM GENE, on one or

more GAM239 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3378] It is yet further appreciated that specific functions, and accordingly utilities, of GAM239 correlate with, and may be deduced from, the identity of the target genes which GAM239 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3379] Nucleotide sequences of the GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM239 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM239 are further de-

scribed hereinbelow with reference to Table Table1.

[3380] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM239 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3381]

[3382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 240 (GAM240) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3383] GAM240 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM240 was detected is described hereinabove with reference to Figs. 2-8.

[3384] GAM240 gene, herein designated GAM GENE, and GAM240 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3385] GAM240 gene, herein designated GAM GENE, encodes a GAM240 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM240 precursor RNA is designated SEQ ID:3570, and is provided hereinbelow with reference to the sequence listing part.

[3386] GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3387] An enzyme complex designated DICER COMPLEX, dices the GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM240 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM240 RNA is designated SEQ ID:3571, and is provided hereinbelow with reference to the sequence listing part.

[3388] GAM240 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM240 target RNA, herein designated GAM TARGET RNA. GAM240 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3389] GAM240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM240 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM240 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM240 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3390] The complementary binding of GAM240 RNA, herein designated GAM RNA, to target binding sites on GAM240 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM240 target RNA, herein designated GAM TARGET RNA, into GAM240 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3391] It is appreciated that GAM240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM240 target genes. The mRNA of each one of this plurality of GAM240 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM240 RNA, herein designated GAM RNA, and which when bound by GAM240 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM240 target proteins.

[3392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM240 gene, herein designated GAM GENE, on one or more GAM240 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM240 correlate with, and may

be deduced from, the identity of the target genes which GAM240 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3394] Nucleotide sequences of the GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM240 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM240 are further described hereinbelow with reference to Table Table1.

[3395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM240 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3396]

[3397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 241 (GAM241) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3398] GAM241 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM241 was detected is described hereinabove with reference to Figs. 2-8.

[3399] GAM241 gene, herein designated GAM GENE, and GAM241 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3400] GAM241 gene, herein designated GAM GENE, encodes a GAM241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM241 precursor RNA is designated SEQ ID:3578, and is provided hereinbelow with reference to the sequence listing part.

[3401] GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3402] An enzyme complex designated DICER COMPLEX, dices the GAM241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM241 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM241 RNA is designated SEQ ID:3579, and is provided hereinbelow with reference to the sequence listing part.

[3403] GAM241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM241 target RNA, herein designated GAM TARGET RNA. GAM241 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3404] GAM241 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM241 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM241 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM241 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3405] The complementary binding of GAM241 RNA, herein designated GAM RNA, to target binding sites on GAM241 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM241 target RNA, herein designated GAM TARGET RNA, into GAM241 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3406] It is appreciated that GAM241 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM241 target genes. The mRNA of each one of this plurality of GAM241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM241 RNA, herein designated GAM RNA, and which when bound by GAM241 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM241 target proteins.

[3407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM241 gene, herein designated GAM GENE, on one or more GAM241 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM241 correlate with, and may be deduced from, the identity of the target genes which GAM241 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3409] Nucleotide sequences of the GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM241 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM241 are further described hereinbelow with reference to Table Table1.

[3410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM241 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3411]

[3412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 242 (GAM242) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3413] GAM242 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM242 was detected is described hereinabove with reference to Figs. 2-8.

[3414] GAM242 gene, herein designated GAM GENE, and GAM242 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3415] GAM242 gene, herein designated GAM GENE, encodes a GAM242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM242 precursor RNA is desig-

nated SEQ ID:3584, and is provided hereinbelow with reference to the sequence listing part.

[3416] GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3417] An enzyme complex designated DICER COMPLEX, dices the GAM242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM242 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 20%) nucleotide sequence of GAM242 RNA is designated SEQ ID:3585, and is provided hereinbelow with reference to the sequence listing part.

[3418] GAM242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM242 target RNA, herein designated GAM TARGET RNA. GAM242 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3419] GAM242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM242 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM242 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM242 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM242

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3420] The complementary binding of GAM242 RNA, herein designated GAM RNA, to target binding sites on GAM242 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM242 target RNA, herein designated GAM TARGET RNA, into GAM242 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3421] It is appreciated that GAM242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM242 target genes. The mRNA of each one of this plurality of GAM242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM242 RNA, herein designated GAM RNA, and which when bound by GAM242 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM242 target proteins.

[3422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM242 gene, herein designated GAM GENE, on one or more GAM242 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM242 correlate with, and may be deduced from, the identity of the target genes which GAM242 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3424] Nucleotide sequences of the GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM242 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM242 are further described hereinbelow with reference to Table Table1.

[3425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM242 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3426]

[3427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 243 (GAM243) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3428] GAM243 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM243 was detected is described hereinabove with reference to Figs. 2-8.

[3429] GAM243 gene, herein designated GAM GENE, and

GAM243 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3430] GAM243 gene, herein designated GAM GENE, encodes a GAM243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM243 precursor RNA is designated SEQ ID:3593, and is provided hereinbelow with reference to the sequence listing part.

[3431] GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3432] An enzyme complex designated DICER COMPLEX, dices the GAM243 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM243 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of GAM243 RNA is designated SEQ ID:3594, and is provided hereinbelow with reference to the sequence listing part.

[3433] GAM243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM243 target RNA, herein designated GAM TARGET RNA. GAM243 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3434] GAM243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM243 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM243 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM243 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3435] The complementary binding of GAM243 RNA, herein designated GAM RNA, to target binding sites on GAM243 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM243 target RNA, herein designated GAM TARGET RNA, into GAM243 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3436] It is appreciated that GAM243 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM243 target genes. The mRNA of each one of this plurality of GAM243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM243 RNA, herein designated GAM RNA, and which when bound by GAM243 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM243 target proteins.

[3437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM243 gene, herein designated GAM GENE, on one or more GAM243 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM243 correlate with, and may be deduced from, the identity of the target genes which GAM243 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3439] Nucleotide sequences of the GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM243 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM243 are further described hereinbelow with reference to Table Table1.

[3440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM243 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3441]

[3442] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 244 (GAM244) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3443] GAM244 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM244 was detected is described hereinabove with reference to Figs. 2-8.

[3444] GAM244 gene, herein designated GAM GENE, and GAM244 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3445] GAM244 gene, herein designated GAM GENE, encodes a GAM244 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM244 precursor RNA is designated SEQ ID:3622, and is provided hereinbelow with reference to the sequence listing part.

[3446] GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3447] An enzyme complex designated DICER COMPLEX, dices the GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM244 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM244 RNA is designated SEQ ID:3623, and is provided hereinbelow with reference to the sequence listing part.

[3448] GAM244 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM244 target RNA, herein designated GAM TARGET RNA. GAM244 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3449] GAM244 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM244 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM244 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM244 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM244 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3450] The complementary binding of GAM244 RNA, herein designated GAM RNA, to target binding sites on GAM244 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM244 target RNA, herein designated GAM TARGET RNA, into GAM244 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3451] It is appreciated that GAM244 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM244 target genes. The mRNA of each one of this plurality of GAM244 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM244 RNA, herein designated GAM RNA, and which when bound by GAM244 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM244 target proteins.

[3452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM244 gene, herein designated GAM GENE, on one or more GAM244 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3453] It is yet further appreciated that specific functions, and accordingly utilities, of GAM244 correlate with, and may be deduced from, the identity of the target genes which GAM244 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3454] Nucleotide sequences of the GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM244 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM244 are further described hereinbelow with reference to Table Table1.

[3455] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM244 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3456]

[3457] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 245 (GAM245) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3458] GAM245 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM245 was detected is described hereinabove with reference to Figs. 2-8.

[3459] GAM245 gene, herein designated GAM GENE, and GAM245 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3460] GAM245 gene, herein designated GAM GENE, encodes a GAM245 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM245 precursor RNA is designated SEQ ID:3658, and is provided hereinbelow with reference to the sequence listing part.

[3461] GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3462] An enzyme complex designated DICER COMPLEX, dices the GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM245 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM245 RNA is designated SEQ ID:3623, and is provided hereinbelow with reference to the sequence listing part.

[3463] GAM245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM245 target RNA, herein designated GAM TARGET RNA. GAM245 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3464] GAM245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM245 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM245 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM245 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3465] The complementary binding of GAM245 RNA, herein designated GAM RNA, to target binding sites on GAM245 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM245 target RNA, herein designated GAM TARGET RNA, into GAM245 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3466] It is appreciated that GAM245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM245 target genes. The mRNA of each one of this plurality of GAM245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM245 RNA,

herein designated GAM RNA, and which when bound by GAM245 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM245 target proteins.

[3467] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM245 gene, herein designated GAM GENE, on one or more GAM245 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3468] It is yet further appreciated that specific functions, and accordingly utilities, of GAM245 correlate with, and may be deduced from, the identity of the target genes which

GAM245 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3469] Nucleotide sequences of the GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM245 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM245 are further described hereinbelow with reference to Table Table1.

[3470] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM245 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3471]

[3472] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 246 (GAM246) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3473] GAM246 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM246 was detected is described hereinabove with reference to Figs. 2-8.

[3474] GAM246 gene, herein designated GAM GENE, and GAM246 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3475] GAM246 gene, herein designated GAM GENE, encodes a GAM246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM246 precursor RNA is designated SEQ ID:3660, and is provided hereinbelow with reference to the sequence listing part.

[3476] GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3477] An enzyme complex designated DICER COMPLEX, dices the GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM246 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM246 RNA is designated SEQ ID:3661, and is provided hereinbelow with reference to the sequence listing part.

[3478] GAM246 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM246 target RNA, herein designated GAM TARGET RNA.
GAM246 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3479] GAM246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM246 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM246 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM246 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3480] The complementary binding of GAM246 RNA, herein designated GAM RNA, to target binding sites on GAM246 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM246 target RNA, herein desig-

nated GAM TARGET RNA, into GAM246 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3481] It is appreciated that GAM246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM246 target genes. The mRNA of each one of this plurality of GAM246 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM246 RNA, herein designated GAM RNA, and which when bound by GAM246 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM246 target proteins.

[3482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM246 gene, herein designated GAM GENE, on one or more GAM246 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3483] It is yet further appreciated that specific functions, and accordingly utilities, of GAM246 correlate with, and may be deduced from, the identity of the target genes which GAM246 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3484] Nucleotide sequences of the GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM246 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM246 are further described hereinbelow with reference to Table Table1.

[3485] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM246 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3486]

[3487] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 247 (GAM247) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3488] GAM247 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM247 was detected is described hereinabove with reference to Figs. 2-8.

[3489] GAM247 gene, herein designated GAM GENE, and GAM247 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3490] GAM247 gene, herein designated GAM GENE, encodes a GAM247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM247 precursor RNA is designated SEQ ID:3675, and is provided hereinbelow with ref-

erence to the sequence listing part.

[3491] GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3492] An enzyme complex designated DICER COMPLEX, dices the GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM247 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM247 RNA is designated SEQ ID:3676, and is provided hereinbelow with reference to the sequence listing part.

[3493] GAM247 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM247 target RNA, herein designated GAM TARGET RNA.

GAM247 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3494] GAM247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM247 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM247 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM247 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3495] The complementary binding of GAM247 RNA, herein designated GAM RNA, to target binding sites on GAM247 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM247 target RNA, herein designated GAM TARGET RNA, into GAM247 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3496] It is appreciated that GAM247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM247 target genes. The mRNA of each one of this plurality of GAM247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM247 RNA, herein designated GAM RNA, and which when bound by GAM247 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM247 target proteins.

[3497] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM247 gene, herein designated GAM GENE, on one or more GAM247 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3498] It is yet further appreciated that specific functions, and accordingly utilities, of GAM247 correlate with, and may be deduced from, the identity of the target genes which GAM247 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3499] Nucleotide sequences of the GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM247 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM247 are further described hereinbelow with reference to Table Table1.

[3500] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM247 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3501]

[3502] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 248 (GAM248) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3503] GAM248 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM248 was detected is described hereinabove with reference to Figs. 2-8.

[3504] GAM248 gene, herein designated GAM GENE, and GAM248 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3505] GAM248 gene, herein designated GAM GENE, encodes a GAM248 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM248 precursor RNA is designated SEQ ID:3696, and is provided hereinbelow with reference to the sequence listing part.

[3506] GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3507] An enzyme complex designated DICER COMPLEX, dices the GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM248 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM248 RNA is designated SEQ ID:3697, and is provided hereinbelow with reference to the sequence listing part.

[3508] GAM248 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM248 target RNA, herein designated GAM TARGET RNA. GAM248 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3509] GAM248 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM248 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM248 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM248 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM248 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3510] The complementary binding of GAM248 RNA, herein designated GAM RNA, to target binding sites on GAM248 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM248 target RNA, herein designated GAM TARGET RNA, into GAM248 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3511] It is appreciated that GAM248 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM248 target genes. The mRNA of each one of this plurality of GAM248 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM248 RNA, herein designated GAM RNA, and which when bound by GAM248 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM248 target proteins.

[3512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM248 gene, herein designated GAM GENE, on one or more GAM248 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[3513] It is yet further appreciated that specific functions, and accordingly utilities, of GAM248 correlate with, and may be deduced from, the identity of the target genes which GAM248 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3514] Nucleotide sequences of the GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM248 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM248 are further described hereinbelow with reference to Table Table1.

[3515] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM248 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3516]

[3517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

249 (GAM249) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3518] GAM249 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM249 was detected is described hereinabove with reference to Figs. 2-8.

[3519] GAM249 gene, herein designated GAM GENE, and GAM249 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3520] GAM249 gene, herein designated GAM GENE, encodes a GAM249 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM249 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM249 precursor RNA is designated SEQ ID:3709, and is provided hereinbelow with reference to the sequence listing part.

[3521] GAM249 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3522] An enzyme complex designated DICER COMPLEX, dices the GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM249 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM249 RNA is designated SEQ ID:3710, and is provided hereinbelow with reference to the sequence listing part.

[3523] GAM249 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM249 target RNA, herein designated GAM TARGET RNA. GAM249 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3524] GAM249 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM249 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM249 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM249 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM249 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3525] The complementary binding of GAM249 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM249 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM249 target RNA, herein designated GAM TARGET RNA, into GAM249 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3526] It is appreciated that GAM249 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM249 target genes. The mRNA of each one of this plurality of GAM249 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM249 RNA, herein designated GAM RNA, and which when bound by GAM249 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM249 target proteins.

[3527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM249 gene, herein designated GAM GENE, on one or more GAM249 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3528] It is yet further appreciated that specific functions, and accordingly utilities, of GAM249 correlate with, and may be deduced from, the identity of the target genes which GAM249 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3529] Nucleotide sequences of the GAM249 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM249 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM249 are further described hereinbelow with reference to Table Table1.

[3530] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM249 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3531]

[3532] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 250 (GAM250) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3533] GAM250 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM250 was detected is described hereinabove with reference to Figs. 2-8.

[3534] GAM250 gene, herein designated GAM GENE, and GAM250 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3535] GAM250 gene, herein designated GAM GENE, encodes a GAM250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM250 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM250 precursor RNA is designated SEQ ID:3717, and is provided hereinbelow with reference to the sequence listing part.

[3536] GAM250 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3537] An enzyme complex designated DICER COMPLEX, dices the GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM250 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 63%) nucleotide sequence of GAM250 RNA is designated SEQ ID:3718, and is provided hereinbelow with reference to the sequence listing part.

[3538] GAM250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM250 target RNA, herein designated GAM TARGET RNA. GAM250 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3539] GAM250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM250 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM250 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM250 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3540] The complementary binding of GAM250 RNA, herein designated GAM RNA, to target binding sites on GAM250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM250 target RNA, herein designated GAM TARGET RNA, into GAM250 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3541] It is appreciated that GAM250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM250 target genes. The mRNA of each one of this plurality of GAM250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM250 RNA, herein designated GAM RNA, and which when bound by

GAM250 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM250 target proteins.

[3542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM250 gene, herein designated GAM GENE, on one or more GAM250 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3543] It is yet further appreciated that specific functions, and accordingly utilities, of GAM250 correlate with, and may be deduced from, the identity of the target genes which GAM250 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3544] Nucleotide sequences of the GAM250 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM250 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM250 are further described hereinbelow with reference to Table Table1.

[3545] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM250 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3546]

[3547] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 251 (GAM251) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3548] GAM251 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM251 was detected is described hereinabove with reference to Figs. 2-8.

[3549] GAM251 gene, herein designated GAM GENE, and GAM251 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3550] GAM251 gene, herein designated GAM GENE, encodes a GAM251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM251 precursor RNA is designated SEQ ID:3735, and is provided hereinbelow with reference to the sequence listing part.

[3551] GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3552] An enzyme complex designated DICER COMPLEX, dices the GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM251 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 28%) nucleotide sequence of GAM251 RNA is designated SEQ ID:3736, and is provided hereinbelow with reference to the sequence listing part.

[3553] GAM251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM251 target RNA, herein designated GAM TARGET RNA. GAM251 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3554] GAM251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM251 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM251 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM251 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM251 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3555] The complementary binding of GAM251 RNA, herein designated GAM RNA, to target binding sites on GAM251 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM251 target RNA, herein designated GAM TARGET RNA, into GAM251 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3556] It is appreciated that GAM251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM251 target genes. The mRNA of each one of this plurality of GAM251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM251 RNA, herein designated GAM RNA, and which when bound by GAM251 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM251 target proteins.

[3557] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM251 gene, herein designated GAM GENE, on one or more GAM251 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3558] It is yet further appreciated that specific functions, and accordingly utilities, of GAM251 correlate with, and may be deduced from, the identity of the target genes which GAM251 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3559] Nucleotide sequences of the GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM251 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM251 are further described hereinbelow with reference to Table Table1.

[3560] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM251 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3561]

[3562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 252 (GAM252) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3563] GAM252 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM252 was detected is described hereinabove with reference to Figs. 2-8.

[3564] GAM252 gene, herein designated GAM GENE, and GAM252 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3565] GAM252 gene, herein designated GAM GENE, encodes a GAM252 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM252 precursor RNA is designated SEQ ID:3745, and is provided hereinbelow with reference to the sequence listing part.

[3566] GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3567] An enzyme complex designated DICER COMPLEX, dices the GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM252 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM252 RNA is designated SEQ ID:3746, and is provided hereinbelow with reference to the sequence listing part.

[3568] GAM252 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM252

target RNA, herein designated GAM TARGET RNA.

GAM252 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3569] GAM252 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM252 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM252 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM252 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM252 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3570] The complementary binding of GAM252 RNA, herein designated GAM RNA, to target binding sites on GAM252 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM252 target RNA, herein designated GAM TARGET RNA, into GAM252 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3571] It is appreciated that GAM252 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM252 target genes. The mRNA of each one of this plurality of GAM252 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM252 RNA, herein designated GAM RNA, and which when bound by GAM252 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM252 target proteins.

[3572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM252 gene, herein designated GAM GENE, on one or more GAM252 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM252 correlate with, and may be deduced from, the identity of the target genes which GAM252 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3574] Nucleotide sequences of the GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM252 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM252 are further described hereinbelow with reference to Table Table1.

[3575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM252 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3576]

[3577] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 253 (GAM253) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3578] GAM253 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM253 was detected is described hereinabove with reference to Figs. 2-8.

[3579] GAM253 gene, herein designated GAM GENE, and GAM253 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3580] GAM253 gene, herein designated GAM GENE, encodes a GAM253 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM253 precursor RNA is designated SEQ ID:3761, and is provided hereinbelow with reference to the sequence listing part.

[3581] GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3582] An enzyme complex designated DICER COMPLEX, dices the GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM253 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM253 RNA is designated SEQ ID:3762, and is provided hereinbelow with reference to the sequence listing part.

[3583] GAM253 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM253 target RNA, herein designated GAM TARGET RNA. GAM253 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3584] GAM253 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM253 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM253 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM253 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM253 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3585] The complementary binding of GAM253 RNA, herein designated GAM RNA, to target binding sites on GAM253 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM253 target RNA, herein designated GAM TARGET RNA, into GAM253 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3586] It is appreciated that GAM253 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM253 target genes. The mRNA of each one of this plu-

rality of GAM253 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM253 RNA, herein designated GAM RNA, and which when bound by GAM253 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM253 target proteins.

[3587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM253 gene, herein designated GAM GENE, on one or more GAM253 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3588] It is yet further appreciated that specific functions, and accordingly utilities, of GAM253 correlate with, and may be deduced from, the identity of the target genes which GAM253 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3589] Nucleotide sequences of the GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM253 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM253 are further described hereinbelow with reference to Table Table1.

[3590] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM253 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3591]

[3592] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 254 (GAM254) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[3593] GAM254 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM254 was detected is described hereinabove with reference to Figs. 2-8.

[3594] GAM254 gene, herein designated GAM GENE, and GAM254 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3595] GAM254 gene, herein designated GAM GENE, encodes a GAM254 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM254 precursor RNA is designated SEQ ID:3779, and is provided hereinbelow with reference to the sequence listing part.

[3596] GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3597] An enzyme complex designated DICER COMPLEX, dices the GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM254 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM254 RNA is designated SEQ ID:3780, and is provided hereinbelow with reference to the sequence listing part.

[3598] GAM254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM254 target RNA, herein designated GAM TARGET RNA.
GAM254 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3599] GAM254 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM254 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM254 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM254 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3600] The complementary binding of GAM254 RNA, herein designated GAM RNA, to target binding sites on GAM254 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM254 target RNA, herein designated GAM TARGET RNA, into GAM254 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3601] It is appreciated that GAM254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM254 target genes. The mRNA of each one of this plurality of GAM254 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM254 RNA, herein designated GAM RNA, and which when bound by GAM254 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM254 target proteins.

[3602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM254 gene, herein designated GAM GENE, on one or more GAM254 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3603] It is yet further appreciated that specific functions, and accordingly utilities, of GAM254 correlate with, and may be deduced from, the identity of the target genes which GAM254 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3604] Nucleotide sequences of the GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM254 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM254 are further described hereinbelow with reference to Table Table1.

[3605] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM254 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3606]

[3607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 255 (GAM255) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3608] GAM255 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM255 was detected is described hereinabove with reference to Figs. 2-8.

[3609] GAM255 gene, herein designated GAM GENE, and GAM255 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3610] GAM255 gene, herein designated GAM GENE, encodes a GAM255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM255 precursor RNA is designated SEQ ID:3815, and is provided hereinbelow with reference to the sequence listing part.

[3611] GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3612] An enzyme complex designated DICER COMPLEX, dices the GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM255 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of

GAM255 RNA is designated SEQ ID:3816, and is provided hereinbelow with reference to the sequence listing part.

[3613] GAM255 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM255 target RNA, herein designated GAM TARGET RNA. GAM255 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3614] GAM255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM255 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM255 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM255 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3615] The complementary binding of GAM255 RNA, herein designated GAM RNA, to target binding sites on GAM255 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM255 target RNA, herein designated GAM TARGET RNA, into GAM255 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3616] It is appreciated that GAM255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM255 target genes. The mRNA of each one of this plurality of GAM255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM255 RNA, herein designated GAM RNA, and which when bound by GAM255 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM255 target proteins.

[3617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM255 gene, herein designated GAM GENE, on one or more GAM255 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM255 correlate with, and may be deduced from, the identity of the target genes which GAM255 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3619] Nucleotide sequences of the GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM255 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM255 are further described hereinbelow with reference to Table Table1.

[3620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM255 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3621]

[3622] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 256 (GAM256) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3623] GAM256 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM256 was detected is described hereinabove

with reference to Figs. 2-8.

[3624] GAM256 gene, herein designated GAM GENE, and GAM256 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3625] GAM256 gene, herein designated GAM GENE, encodes a GAM256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM256 precursor RNA is designated SEQ ID:3848, and is provided hereinbelow with reference to the sequence listing part.

[3626] GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3627] An enzyme complex designated DICER COMPLEX, dices the GAM256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM256 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM256 RNA is designated SEQ ID:3849, and is provided hereinbelow with reference to the sequence listing part.

[3628] GAM256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM256 target RNA, herein designated GAM TARGET RNA. GAM256 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3629] GAM256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM256 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM256 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM256 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM256 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3630] The complementary binding of GAM256 RNA, herein designated GAM RNA, to target binding sites on GAM256 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM256 target RNA, herein designated GAM TARGET RNA, into GAM256 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3631] It is appreciated that GAM256 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM256 target genes. The mRNA of each one of this plurality of GAM256 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM256 RNA, herein designated GAM RNA, and which when bound by GAM256 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM256 target proteins.

[3632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM256 gene, herein designated GAM GENE, on one or more GAM256 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM256 correlate with, and may be deduced from, the identity of the target genes which GAM256 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3634] Nucleotide sequences of the GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM256 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM256 are further described hereinbelow with reference to Table Table1.

[3635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM256 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3636]

[3637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 257 (GAM257) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3638] GAM257 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM257 was detected is described hereinabove with reference to Figs. 2-8.

[3639] GAM257 gene, herein designated GAM GENE, and GAM257 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3640] GAM257 gene, herein designated GAM GENE, encodes a GAM257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM257 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM257 precursor RNA is designated SEQ ID:3858, and is provided hereinbelow with reference to the sequence listing part.

[3641] GAM257 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3642] An enzyme complex designated DICER COMPLEX, dices the GAM257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM257 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 32%) nucleotide sequence of GAM257 RNA is designated SEQ ID:3859, and is provided hereinbelow with reference to the sequence listing part.

[3643] GAM257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM257 target RNA, herein designated GAM TARGET RNA.

GAM257 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3644] GAM257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM257 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM257 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM257 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3645] The complementary binding of GAM257 RNA, herein designated GAM RNA, to target binding sites on GAM257 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM257 target RNA, herein designated GAM TARGET RNA, into GAM257 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3646] It is appreciated that GAM257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM257 target genes. The mRNA of each one of this plurality of GAM257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM257 RNA, herein designated GAM RNA, and which when bound by GAM257 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM257 target proteins.

[3647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM257 gene, herein designated GAM GENE, on one or more GAM257 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM257 correlate with, and may be deduced from, the identity of the target genes which GAM257 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3649] Nucleotide sequences of the GAM257 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM257 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM257 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM257 are further described hereinbelow with reference to Table Table1.

[3650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM257 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3651]

[3652] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 258 (GAM258) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3653] GAM258 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM258 was detected is described hereinabove with reference to Figs. 2-8.

[3654] GAM258 gene, herein designated GAM GENE, and GAM258 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3655] GAM258 gene, herein designated GAM GENE, encodes a

GAM258 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM258 precursor RNA is designated SEQ ID:3884, and is provided hereinbelow with reference to the sequence listing part.

[3656] GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3657] An enzyme complex designated DICER COMPLEX, dices the GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM258 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM258 RNA is designated SEQ ID:3885, and is provided hereinbelow with reference to the sequence listing part.

[3658] GAM258 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM258 target RNA, herein designated GAM TARGET RNA. GAM258 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3659] GAM258 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM258 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM258 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM258 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM258 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3660] The complementary binding of GAM258 RNA, herein designated GAM RNA, to target binding sites on GAM258 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM258 target RNA, herein designated GAM TARGET RNA, into GAM258 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3661] It is appreciated that GAM258 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM258 target genes. The mRNA of each one of this plurality of GAM258 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM258 RNA, herein designated GAM RNA, and which when bound by GAM258 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM258 target proteins.

[3662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM258 gene, herein designated GAM GENE, on one or more GAM258 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3663] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM258 correlate with, and may be deduced from, the identity of the target genes which GAM258 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3664] Nucleotide sequences of the GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM258 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM258 are further described hereinbelow with reference to Table Table1.

[3665] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM258 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3666]

[3667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 259 (GAM259) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[3668] GAM259 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM259 was detected is described hereinabove with reference to Figs. 2-8.

[3669] GAM259 gene, herein designated GAM GENE, and GAM259 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3670] GAM259 gene, herein designated GAM GENE, encodes a GAM259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM259 precursor RNA is designated SEQ ID:3899, and is provided hereinbelow with reference to the sequence listing part.

[3671] GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3672] An enzyme complex designated DICER COMPLEX, dices the GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM259 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM259 RNA is designated SEQ ID:3900, and is provided hereinbelow with reference to the sequence listing part.

[3673] GAM259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM259 target RNA, herein designated GAM TARGET RNA. GAM259 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3674] GAM259 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM259 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM259 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM259 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3675] The complementary binding of GAM259 RNA, herein designated GAM RNA, to target binding sites on GAM259 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM259 target RNA, herein designated GAM TARGET RNA, into GAM259 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3676] It is appreciated that GAM259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM259 target genes. The mRNA of each one of this plurality of GAM259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM259 RNA, herein designated GAM RNA, and which when bound by GAM259 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM259 target proteins.

[3677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM259 gene, herein designated GAM GENE, on one or more GAM259 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM259 correlate with, and may be deduced from, the identity of the target genes which GAM259 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3679] Nucleotide sequences of the GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM259 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM259 are further described hereinbelow with reference to Table Table1.

[3680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM259 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3681]

[3682] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 260 (GAM260) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3683] GAM260 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM260 was detected is described hereinabove with reference to Figs. 2-8.

[3684] GAM260 gene, herein designated GAM GENE, and GAM260 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3685] GAM260 gene, herein designated GAM GENE, encodes a GAM260 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM260 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM260 precursor RNA is designated SEQ ID:3909, and is provided hereinbelow with reference to the sequence listing part.

[3686] GAM260 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3687] An enzyme complex designated DICER COMPLEX, dices the GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM260 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM260 RNA is designated SEQ ID:3910, and is provided

hereinbelow with reference to the sequence listing part.

[3688] GAM260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM260 target RNA, herein designated GAM TARGET RNA.
GAM260 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3689] GAM260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM260 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM260 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM260 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3690] The complementary binding of GAM260 RNA, herein designated GAM RNA, to target binding sites on GAM260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM260 target RNA, herein designated GAM TARGET RNA, into GAM260 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3691] It is appreciated that GAM260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM260 target genes. The mRNA of each one of this plurality of GAM260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM260 RNA, herein designated GAM RNA, and which when bound by GAM260 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM260 tar-

get proteins.

[3692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM260 gene, herein designated GAM GENE, on one or more GAM260 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3693] It is yet further appreciated that specific functions, and accordingly utilities, of GAM260 correlate with, and may be deduced from, the identity of the target genes which GAM260 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3694] Nucleotide sequences of the GAM260 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM260 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM260 are further described hereinbelow with reference to Table Table1.

[3695] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM260 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3696]

[3697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 261 (GAM261) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3698] GAM261 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM261 was detected is described hereinabove with reference to Figs. 2-8.

[3699] GAM261 gene, herein designated GAM GENE, and GAM261 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3700] GAM261 gene, herein designated GAM GENE, encodes a GAM261 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM261 precursor RNA is designated SEQ ID:3917, and is provided hereinbelow with reference to the sequence listing part.

[3701] GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3702] An enzyme complex designated DICER COMPLEX, dices

the GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM261 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM261 RNA is designated SEQ ID:3918, and is provided hereinbelow with reference to the sequence listing part.

[3703] GAM261 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM261 target RNA, herein designated GAM TARGET RNA. GAM261 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3704] GAM261 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM261 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM261

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM261 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM261 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3705] The complementary binding of GAM261 RNA, herein designated GAM RNA, to target binding sites on GAM261 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM261 target RNA, herein designated GAM TARGET RNA, into GAM261 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3706] It is appreciated that GAM261 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM261 target genes. The mRNA of each one of this plurality of GAM261 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM261 RNA, herein designated GAM RNA, and which when bound by GAM261 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM261 target proteins.

[3707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM261 gene, herein designated GAM GENE, on one or more GAM261 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM261 correlate with, and may be deduced from, the identity of the target genes which GAM261 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3709] Nucleotide sequences of the GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM261 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM261 are further described hereinbelow with reference to Table Table1.

[3710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM261 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3711]

[3712] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 262 (GAM262) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3713] GAM262 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM262 was detected is described hereinabove with reference to Figs. 2-8.

[3714] GAM262 gene, herein designated GAM GENE, and GAM262 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3715] GAM262 gene, herein designated GAM GENE, encodes a GAM262 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM262 precursor RNA is designated SEQ ID:3922, and is provided hereinbelow with reference to the sequence listing part.

[3716] GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM262 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3717] An enzyme complex designated DICER COMPLEX, dices the GAM262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM262 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 28%) nucleotide sequence of GAM262 RNA is designated SEQ ID:3923, and is provided hereinbelow with reference to the sequence listing part.

[3718] GAM262 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM262 target RNA, herein designated GAM TARGET RNA. GAM262 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3719] GAM262 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM262 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM262 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM262 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM262 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[3720] The complementary binding of GAM262 RNA, herein designated GAM RNA, to target binding sites on GAM262 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM262 target RNA, herein designated GAM TARGET RNA, into GAM262 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3721] It is appreciated that GAM262 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM262 target genes. The mRNA of each one of this plurality of GAM262 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM262 RNA, herein designated GAM RNA, and which when bound by GAM262 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM262 target proteins.

[3722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM262 gene, herein designated GAM GENE, on one or

more GAM262 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3723] It is yet further appreciated that specific functions, and accordingly utilities, of GAM262 correlate with, and may be deduced from, the identity of the target genes which GAM262 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3724] Nucleotide sequences of the GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM262 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM262 are further de-

scribed hereinbelow with reference to Table Table1.

[3725] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM262 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3726]

[3727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 263 (GAM263) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3728] GAM263 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM263 was detected is described hereinabove with reference to Figs. 2-8.

[3729] GAM263 gene, herein designated GAM GENE, and GAM263 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3730] GAM263 gene, herein designated GAM GENE, encodes a GAM263 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM263 precursor RNA is designated SEQ ID:3947, and is provided hereinbelow with reference to the sequence listing part.

[3731] GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3732] An enzyme complex designated DICER COMPLEX, dices the GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM263 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM263 RNA is designated SEQ ID:3948, and is provided hereinbelow with reference to the sequence listing part.

[3733] GAM263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM263 target RNA, herein designated GAM TARGET RNA. GAM263 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3734] GAM263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM263 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM263 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM263 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3735] The complementary binding of GAM263 RNA, herein designated GAM RNA, to target binding sites on GAM263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM263 target RNA, herein designated GAM TARGET RNA, into GAM263 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3736] It is appreciated that GAM263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM263 target genes. The mRNA of each one of this plurality of GAM263 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM263 RNA, herein designated GAM RNA, and which when bound by GAM263 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM263 target proteins.

[3737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM263 gene, herein designated GAM GENE, on one or more GAM263 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM263 correlate with, and may

be deduced from, the identity of the target genes which GAM263 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3739] Nucleotide sequences of the GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM263 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM263 are further described hereinbelow with reference to Table Table1.

[3740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM263 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3741]

[3742] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 264 (GAM264) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3743] GAM264 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM264 was detected is described hereinabove with reference to Figs. 2-8.

[3744] GAM264 gene, herein designated GAM GENE, and GAM264 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3745] GAM264 gene, herein designated GAM GENE, encodes a GAM264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM264 precursor RNA is designated SEQ ID:3961, and is provided hereinbelow with reference to the sequence listing part.

[3746] GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3747] An enzyme complex designated DICER COMPLEX, dices the GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM264 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM264 RNA is designated SEQ ID:3962, and is provided hereinbelow with reference to the sequence listing part.

[3748] GAM264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM264 target RNA, herein designated GAM TARGET RNA. GAM264 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3749] GAM264 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM264 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM264 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM264 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3750] The complementary binding of GAM264 RNA, herein designated GAM RNA, to target binding sites on GAM264 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM264 target RNA, herein designated GAM TARGET RNA, into GAM264 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3751] It is appreciated that GAM264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM264 target genes. The mRNA of each one of this plurality of GAM264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM264 RNA, herein designated GAM RNA, and which when bound by GAM264 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM264 target proteins.

[3752] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM264 gene, herein designated GAM GENE, on one or more GAM264 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3753] It is yet further appreciated that specific functions, and accordingly utilities, of GAM264 correlate with, and may be deduced from, the identity of the target genes which GAM264 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3754] Nucleotide sequences of the GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM264 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM264 are further described hereinbelow with reference to Table Table1.

[3755] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM264 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3756]

[3757] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 265 (GAM265) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3758] GAM265 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM265 was detected is described hereinabove with reference to Figs. 2-8.

[3759] GAM265 gene, herein designated GAM GENE, and GAM265 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3760] GAM265 gene, herein designated GAM GENE, encodes a GAM265 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM265 precursor RNA is desig-

nated SEQ ID:3977, and is provided hereinbelow with reference to the sequence listing part.

[3761] GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3762] An enzyme complex designated DICER COMPLEX, dices the GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM265 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM265 RNA is designated SEQ ID:3978, and is provided hereinbelow with reference to the sequence listing part.

[3763] GAM265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM265 target RNA, herein designated GAM TARGET RNA. GAM265 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3764] GAM265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM265 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM265 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM265 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM265

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3765] The complementary binding of GAM265 RNA, herein designated GAM RNA, to target binding sites on GAM265 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM265 target RNA, herein designated GAM TARGET RNA, into GAM265 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3766] It is appreciated that GAM265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM265 target genes. The mRNA of each one of this plurality of GAM265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM265 RNA, herein designated GAM RNA, and which when bound by GAM265 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM265 target proteins.

[3767] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM265 gene, herein designated GAM GENE, on one or more GAM265 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3768] It is yet further appreciated that specific functions, and accordingly utilities, of GAM265 correlate with, and may be deduced from, the identity of the target genes which GAM265 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3769] Nucleotide sequences of the GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM265 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM265 are further described hereinbelow with reference to Table Table1.

[3770] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM265 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3771]

[3772] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 266 (GAM266) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3773] GAM266 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM266 was detected is described hereinabove with reference to Figs. 2-8.

[3774] GAM266 gene, herein designated GAM GENE, and

GAM266 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3775] GAM266 gene, herein designated GAM GENE, encodes a GAM266 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM266 precursor RNA is designated SEQ ID:3988, and is provided hereinbelow with reference to the sequence listing part.

[3776] GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3777] An enzyme complex designated DICER COMPLEX, dices the GAM266 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM266 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM266 RNA is designated SEQ ID:3989, and is provided hereinbelow with reference to the sequence listing part.

[3778] GAM266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM266 target RNA, herein designated GAM TARGET RNA. GAM266 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3779] GAM266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM266 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM266 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM266 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3780] The complementary binding of GAM266 RNA, herein designated GAM RNA, to target binding sites on GAM266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM266 target RNA, herein designated GAM TARGET RNA, into GAM266 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3781] It is appreciated that GAM266 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM266 target genes. The mRNA of each one of this plurality of GAM266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM266 RNA, herein designated GAM RNA, and which when bound by GAM266 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM266 target proteins.

[3782] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM266 gene, herein designated GAM GENE, on one or more GAM266 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3783] It is yet further appreciated that specific functions, and accordingly utilities, of GAM266 correlate with, and may be deduced from, the identity of the target genes which GAM266 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3784] Nucleotide sequences of the GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM266 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM266 are further described hereinbelow with reference to Table Table1.

[3785] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM266 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3786]

[3787] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 267 (GAM267) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3788] GAM267 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM267 was detected is described hereinabove with reference to Figs. 2-8.

[3789] GAM267 gene, herein designated GAM GENE, and GAM267 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3790] GAM267 gene, herein designated GAM GENE, encodes a GAM267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM267 precursor RNA is designated SEQ ID:4007, and is provided hereinbelow with reference to the sequence listing part.

[3791] GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3792] An enzyme complex designated DICER COMPLEX, dices the GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM267 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM267 RNA is designated SEQ ID:4008, and is provided hereinbelow with reference to the sequence listing part.

[3793] GAM267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM267 target RNA, herein designated GAM TARGET RNA. GAM267 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3794] GAM267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM267 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM267 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM267 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM267 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3795] The complementary binding of GAM267 RNA, herein designated GAM RNA, to target binding sites on GAM267 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM267 target RNA, herein designated GAM TARGET RNA, into GAM267 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3796] It is appreciated that GAM267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM267 target genes. The mRNA of each one of this plurality of GAM267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM267 RNA, herein designated GAM RNA, and which when bound by GAM267 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM267 target proteins.

[3797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM267 gene, herein designated GAM GENE, on one or more GAM267 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3798] It is yet further appreciated that specific functions, and accordingly utilities, of GAM267 correlate with, and may be deduced from, the identity of the target genes which GAM267 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3799] Nucleotide sequences of the GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM267 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM267 are further described hereinbelow with reference to Table Table1.

[3800] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM267 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3801]

[3802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 268 (GAM268) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3803] GAM268 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM268 was detected is described hereinabove with reference to Figs. 2-8.

[3804] GAM268 gene, herein designated GAM GENE, and GAM268 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3805] GAM268 gene, herein designated GAM GENE, encodes a GAM268 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM268 precursor RNA is designated SEQ ID:4018, and is provided hereinbelow with reference to the sequence listing part.

[3806] GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3807] An enzyme complex designated DICER COMPLEX, dices the GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM268 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of GAM268 RNA is designated SEQ ID:4019, and is provided hereinbelow with reference to the sequence listing part.

[3808] GAM268 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM268 target RNA, herein designated GAM TARGET RNA. GAM268 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3809] GAM268 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM268 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM268 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM268 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM268 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3810] The complementary binding of GAM268 RNA, herein designated GAM RNA, to target binding sites on GAM268 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM268 target RNA, herein designated GAM TARGET RNA, into GAM268 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3811] It is appreciated that GAM268 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM268 target genes. The mRNA of each one of this plurality of GAM268 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM268 RNA,

herein designated GAM RNA, and which when bound by GAM268 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM268 target proteins.

[3812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM268 gene, herein designated GAM GENE, on one or more GAM268 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3813] It is yet further appreciated that specific functions, and accordingly utilities, of GAM268 correlate with, and may be deduced from, the identity of the target genes which

GAM268 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3814] Nucleotide sequences of the GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM268 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM268 are further described hereinbelow with reference to Table Table1.

[3815] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM268 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3816]

[3817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 269 (GAM269) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3818] GAM269 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM269 was detected is described hereinabove with reference to Figs. 2-8.

[3819] GAM269 gene, herein designated GAM GENE, and GAM269 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3820] GAM269 gene, herein designated GAM GENE, encodes a GAM269 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM269 precursor RNA is designated SEQ ID:4038, and is provided hereinbelow with reference to the sequence listing part.

[3821] GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3822] An enzyme complex designated DICER COMPLEX, dices the GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM269 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM269 RNA is designated SEQ ID:4039, and is provided hereinbelow with reference to the sequence listing part.

[3823] GAM269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM269 target RNA, herein designated GAM TARGET RNA.
GAM269 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3824] GAM269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM269 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM269 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM269 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3825] The complementary binding of GAM269 RNA, herein designated GAM RNA, to target binding sites on GAM269 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM269 target RNA, herein desig-

nated GAM TARGET RNA, into GAM269 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3826] It is appreciated that GAM269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM269 target genes. The mRNA of each one of this plurality of GAM269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM269 RNA, herein designated GAM RNA, and which when bound by GAM269 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM269 target proteins.

[3827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM269 gene, herein designated GAM GENE, on one or more GAM269 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM269 correlate with, and may be deduced from, the identity of the target genes which GAM269 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3829] Nucleotide sequences of the GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM269 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM269 are further described hereinbelow with reference to Table Table1.

[3830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM269 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3831]

[3832] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 270 (GAM270) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3833] GAM270 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM270 was detected is described hereinabove with reference to Figs. 2-8.

[3834] GAM270 gene, herein designated GAM GENE, and GAM270 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3835] GAM270 gene, herein designated GAM GENE, encodes a GAM270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM270 precursor RNA is designated SEQ ID:4052, and is provided hereinbelow with ref-

erence to the sequence listing part.

[3836] GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3837] An enzyme complex designated DICER COMPLEX, dices the GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM270 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM270 RNA is designated SEQ ID:4053, and is provided hereinbelow with reference to the sequence listing part.

[3838] GAM270 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM270 target RNA, herein designated GAM TARGET RNA.

GAM270 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3839] GAM270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM270 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM270 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM270 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3840] The complementary binding of GAM270 RNA, herein designated GAM RNA, to target binding sites on GAM270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM270 target RNA, herein designated GAM TARGET RNA, into GAM270 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3841] It is appreciated that GAM270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM270 target genes. The mRNA of each one of this plurality of GAM270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM270 RNA, herein designated GAM RNA, and which when bound by GAM270 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM270 target proteins.

[3842] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM270 gene, herein designated GAM GENE, on one or more GAM270 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3843] It is yet further appreciated that specific functions, and accordingly utilities, of GAM270 correlate with, and may be deduced from, the identity of the target genes which GAM270 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3844] Nucleotide sequences of the GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM270 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM270 are further described hereinbelow with reference to Table Table1.

[3845] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM270 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3846]

[3847] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 271 (GAM271) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3848] GAM271 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM271 was detected is described hereinabove with reference to Figs. 2-8.

[3849] GAM271 gene, herein designated GAM GENE, and GAM271 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3850] GAM271 gene, herein designated GAM GENE, encodes a GAM271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM271 precursor RNA is designated SEQ ID:4068, and is provided hereinbelow with reference to the sequence listing part.

[3851] GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3852] An enzyme complex designated DICER COMPLEX, dices the GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM271 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM271 RNA is designated SEQ ID:4069, and is provided hereinbelow with reference to the sequence listing part.

[3853] GAM271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM271 target RNA, herein designated GAM TARGET RNA. GAM271 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3854] GAM271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM271 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM271 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM271 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3855] The complementary binding of GAM271 RNA, herein designated GAM RNA, to target binding sites on GAM271 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM271 target RNA, herein designated GAM TARGET RNA, into GAM271 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3856] It is appreciated that GAM271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM271 target genes. The mRNA of each one of this plurality of GAM271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM271 RNA, herein designated GAM RNA, and which when bound by GAM271 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM271 target proteins.

[3857] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM271 gene, herein designated GAM GENE, on one or more GAM271 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[3858] It is yet further appreciated that specific functions, and accordingly utilities, of GAM271 correlate with, and may be deduced from, the identity of the target genes which GAM271 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3859] Nucleotide sequences of the GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM271 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM271 are further described hereinbelow with reference to Table Table1.

[3860] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM271 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3861]

[3862] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

272 (GAM272) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3863] GAM272 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM272 was detected is described hereinabove with reference to Figs. 2-8.

[3864] GAM272 gene, herein designated GAM GENE, and GAM272 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3865] GAM272 gene, herein designated GAM GENE, encodes a GAM272 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM272 precursor RNA is designated SEQ ID:4104, and is provided hereinbelow with reference to the sequence listing part.

[3866] GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3867] An enzyme complex designated DICER COMPLEX, dices the GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM272 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM272 RNA is designated SEQ ID:4105, and is provided hereinbelow with reference to the sequence listing part.

[3868] GAM272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM272 target RNA, herein designated GAM TARGET RNA. GAM272 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3869] GAM272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM272 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM272 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM272 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3870] The complementary binding of GAM272 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM272 target RNA, herein designated GAM TARGET RNA, into GAM272 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3871] It is appreciated that GAM272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM272 target genes. The mRNA of each one of this plurality of GAM272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM272 RNA, herein designated GAM RNA, and which when bound by GAM272 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM272 target proteins.

[3872] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM272 gene, herein designated GAM GENE, on one or more GAM272 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3873] It is yet further appreciated that specific functions, and accordingly utilities, of GAM272 correlate with, and may be deduced from, the identity of the target genes which GAM272 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3874] Nucleotide sequences of the GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM272 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM272 are further described hereinbelow with reference to Table Table1.

[3875] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM272 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3876]

[3877] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 273 (GAM273) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3878] GAM273 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM273 was detected is described hereinabove with reference to Figs. 2-8.

[3879] GAM273 gene, herein designated GAM GENE, and GAM273 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3880] GAM273 gene, herein designated GAM GENE, encodes a GAM273 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM273 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM273 precursor RNA is designated SEQ ID:4125, and is provided hereinbelow with reference to the sequence listing part.

[3881] GAM273 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3882] An enzyme complex designated DICER COMPLEX, dices the GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM273 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 54%) nucleotide sequence of GAM273 RNA is designated SEQ ID:4126, and is provided hereinbelow with reference to the sequence listing part.

[3883] GAM273 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM273 target RNA, herein designated GAM TARGET RNA. GAM273 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3884] GAM273 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM273 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM273 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM273 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM273 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3885] The complementary binding of GAM273 RNA, herein designated GAM RNA, to target binding sites on GAM273 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM273 target RNA, herein designated GAM TARGET RNA, into GAM273 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3886] It is appreciated that GAM273 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM273 target genes. The mRNA of each one of this plurality of GAM273 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM273 RNA, herein designated GAM RNA, and which when bound by

GAM273 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM273 target proteins.

[3887] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM273 gene, herein designated GAM GENE, on one or more GAM273 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3888] It is yet further appreciated that specific functions, and accordingly utilities, of GAM273 correlate with, and may be deduced from, the identity of the target genes which GAM273 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3889] Nucleotide sequences of the GAM273 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM273 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM273 are further described hereinbelow with reference to Table Table1.

[3890] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM273 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3891]

[3892] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 274 (GAM274) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3893] GAM274 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM274 was detected is described hereinabove with reference to Figs. 2-8.

[3894] GAM274 gene, herein designated GAM GENE, and GAM274 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3895] GAM274 gene, herein designated GAM GENE, encodes a GAM274 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM274 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM274 precursor RNA is designated SEQ ID:4137, and is provided hereinbelow with reference to the sequence listing part.

[3896] GAM274 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3897] An enzyme complex designated DICER COMPLEX, dices the GAM274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM274 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM274 RNA is designated SEQ ID:4138, and is provided hereinbelow with reference to the sequence listing part.

[3898] GAM274 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM274 target RNA, herein designated GAM TARGET RNA. GAM274 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3899] GAM274 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM274 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM274 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM274 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM274 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3900] The complementary binding of GAM274 RNA, herein designated GAM RNA, to target binding sites on GAM274 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM274 target RNA, herein designated GAM TARGET RNA, into GAM274 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3901] It is appreciated that GAM274 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM274 target genes. The mRNA of each one of this plurality of GAM274 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM274 RNA, herein designated GAM RNA, and which when bound by GAM274 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM274 target proteins.

[3902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM274 gene, herein designated GAM GENE, on one or more GAM274 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3903] It is yet further appreciated that specific functions, and accordingly utilities, of GAM274 correlate with, and may be deduced from, the identity of the target genes which GAM274 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3904] Nucleotide sequences of the GAM274 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM274 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM274 are further described hereinbelow with reference to Table Table1.

[3905] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM274 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3906]

[3907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 275 (GAM275) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3908] GAM275 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM275 was detected is described hereinabove with reference to Figs. 2-8.

[3909] GAM275 gene, herein designated GAM GENE, and GAM275 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3910] GAM275 gene, herein designated GAM GENE, encodes a GAM275 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM275 precursor RNA is designated SEQ ID:4142, and is provided hereinbelow with reference to the sequence listing part.

[3911] GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3912] An enzyme complex designated DICER COMPLEX, dices the GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM275 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM275 RNA is designated SEQ ID:4143, and is provided hereinbelow with reference to the sequence listing part.

[3913] GAM275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM275

target RNA, herein designated GAM TARGET RNA.

GAM275 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3914] GAM275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM275 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM275 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM275 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3915] The complementary binding of GAM275 RNA, herein designated GAM RNA, to target binding sites on GAM275 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM275 target RNA, herein designated GAM TARGET RNA, into GAM275 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3916] It is appreciated that GAM275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM275 target genes. The mRNA of each one of this plurality of GAM275 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM275 RNA, herein designated GAM RNA, and which when bound by GAM275 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM275 target proteins.

[3917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM275 gene, herein designated GAM GENE, on one or more GAM275 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM275 correlate with, and may be deduced from, the identity of the target genes which GAM275 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3919] Nucleotide sequences of the GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM275 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM275 are further described hereinbelow with reference to Table Table1.

[3920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM275 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3921]

[3922] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 276 (GAM276) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3923] GAM276 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM276 was detected is described hereinabove with reference to Figs. 2-8.

[3924] GAM276 gene, herein designated GAM GENE, and GAM276 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3925] GAM276 gene, herein designated GAM GENE, encodes a GAM276 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM276 precursor RNA is designated SEQ ID:4157, and is provided hereinbelow with reference to the sequence listing part.

[3926] GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3927] An enzyme complex designated DICER COMPLEX, dices the GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM276 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of GAM276 RNA is designated SEQ ID:4158, and is provided hereinbelow with reference to the sequence listing part.

[3928] GAM276 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM276 target RNA, herein designated GAM TARGET RNA. GAM276 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3929] GAM276 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM276 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM276 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM276 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM276 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3930] The complementary binding of GAM276 RNA, herein designated GAM RNA, to target binding sites on GAM276 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM276 target RNA, herein designated GAM TARGET RNA, into GAM276 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3931] It is appreciated that GAM276 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM276 target genes. The mRNA of each one of this plu-

rality of GAM276 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM276 RNA, herein designated GAM RNA, and which when bound by GAM276 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM276 target proteins.

[3932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM276 gene, herein designated GAM GENE, on one or more GAM276 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3933] It is yet further appreciated that specific functions, and accordingly utilities, of GAM276 correlate with, and may be deduced from, the identity of the target genes which GAM276 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3934] Nucleotide sequences of the GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM276 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM276 are further described hereinbelow with reference to Table Table1.

[3935] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM276 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3936]

[3937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 277 (GAM277) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[3938] GAM277 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM277 was detected is described hereinabove with reference to Figs. 2-8.

[3939] GAM277 gene, herein designated GAM GENE, and GAM277 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3940] GAM277 gene, herein designated GAM GENE, encodes a GAM277 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM277 precursor RNA is designated SEQ ID:4177, and is provided hereinbelow with reference to the sequence listing part.

[3941] GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3942] An enzyme complex designated DICER COMPLEX, dices the GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM277 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM277 RNA is designated SEQ ID:4178, and is provided hereinbelow with reference to the sequence listing part.

[3943] GAM277 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM277 target RNA, herein designated GAM TARGET RNA. GAM277 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3944] GAM277 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM277 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM277 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM277 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM277 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3945] The complementary binding of GAM277 RNA, herein designated GAM RNA, to target binding sites on GAM277 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM277 target RNA, herein designated GAM TARGET RNA, into GAM277 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3946] It is appreciated that GAM277 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM277 target genes. The mRNA of each one of this plurality of GAM277 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM277 RNA, herein designated GAM RNA, and which when bound by GAM277 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM277 target proteins.

[3947] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM277 gene, herein designated GAM GENE, on one or more GAM277 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3948] It is yet further appreciated that specific functions, and accordingly utilities, of GAM277 correlate with, and may be deduced from, the identity of the target genes which GAM277 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3949] Nucleotide sequences of the GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM277 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM277 are further described hereinbelow with reference to Table Table1.

[3950] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM277 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3951]

[3952] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 278 (GAM278) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3953] GAM278 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM278 was detected is described hereinabove with reference to Figs. 2-8.

[3954] GAM278 gene, herein designated GAM GENE, and GAM278 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3955] GAM278 gene, herein designated GAM GENE, encodes a GAM278 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM278 precursor RNA is designated SEQ ID:4202, and is provided hereinbelow with reference to the sequence listing part.

[3956] GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3957] An enzyme complex designated DICER COMPLEX, dices the GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM278 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of

GAM278 RNA is designated SEQ ID:4203, and is provided hereinbelow with reference to the sequence listing part.

[3958] GAM278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM278 target RNA, herein designated GAM TARGET RNA. GAM278 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3959] GAM278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM278 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM278 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM278 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3960] The complementary binding of GAM278 RNA, herein designated GAM RNA, to target binding sites on GAM278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM278 target RNA, herein designated GAM TARGET RNA, into GAM278 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3961] It is appreciated that GAM278 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM278 target genes. The mRNA of each one of this plurality of GAM278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM278 RNA, herein designated GAM RNA, and which when bound by GAM278 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM278 target proteins.

[3962] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM278 gene, herein designated GAM GENE, on one or more GAM278 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3963] It is yet further appreciated that specific functions, and accordingly utilities, of GAM278 correlate with, and may be deduced from, the identity of the target genes which GAM278 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3964] Nucleotide sequences of the GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM278 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM278 are further described hereinbelow with reference to Table Table1.

[3965] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM278 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3966]

[3967] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 279 (GAM279) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3968] GAM279 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM279 was detected is described hereinabove

with reference to Figs. 2-8.

[3969] GAM279 gene, herein designated GAM GENE, and GAM279 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3970] GAM279 gene, herein designated GAM GENE, encodes a GAM279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM279 precursor RNA is designated SEQ ID:4234, and is provided hereinbelow with reference to the sequence listing part.

[3971] GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3972] An enzyme complex designated DICER COMPLEX, dices the GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM279 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM279 RNA is designated SEQ ID:4235, and is provided hereinbelow with reference to the sequence listing part.

[3973] GAM279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM279 target RNA, herein designated GAM TARGET RNA. GAM279 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3974] GAM279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM279 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM279 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM279 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM279 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3975] The complementary binding of GAM279 RNA, herein designated GAM RNA, to target binding sites on GAM279 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM279 target RNA, herein designated GAM TARGET RNA, into GAM279 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3976] It is appreciated that GAM279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM279 target genes. The mRNA of each one of this plurality of GAM279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM279 RNA, herein designated GAM RNA, and which when bound by GAM279 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM279 target proteins.

[3977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM279 gene, herein designated GAM GENE, on one or more GAM279 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3978] It is yet further appreciated that specific functions, and accordingly utilities, of GAM279 correlate with, and may be deduced from, the identity of the target genes which GAM279 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3979] Nucleotide sequences of the GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM279 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM279 are further described hereinbelow with reference to Table Table1.

[3980] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM279 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3981]

[3982] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 280 (GAM280) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3983] GAM280 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM280 was detected is described hereinabove with reference to Figs. 2-8.

[3984] GAM280 gene, herein designated GAM GENE, and GAM280 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3985] GAM280 gene, herein designated GAM GENE, encodes a GAM280 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM280 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM280 precursor RNA is designated SEQ ID:4245, and is provided hereinbelow with reference to the sequence listing part.

[3986] GAM280 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3987] An enzyme complex designated DICER COMPLEX, dices the GAM280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM280 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM280 RNA is designated SEQ ID:4246, and is provided hereinbelow with reference to the sequence listing part.

[3988] GAM280 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM280 target RNA, herein designated GAM TARGET RNA.

GAM280 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3989] GAM280 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM280 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM280 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM280 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM280 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3990] The complementary binding of GAM280 RNA, herein designated GAM RNA, to target binding sites on GAM280 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM280 target RNA, herein designated GAM TARGET RNA, into GAM280 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3991] It is appreciated that GAM280 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM280 target genes. The mRNA of each one of this plurality of GAM280 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM280 RNA, herein designated GAM RNA, and which when bound by GAM280 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM280 target proteins.

[3992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM280 gene, herein designated GAM GENE, on one or more GAM280 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3993] It is yet further appreciated that specific functions, and accordingly utilities, of GAM280 correlate with, and may be deduced from, the identity of the target genes which GAM280 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3994] Nucleotide sequences of the GAM280 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM280 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM280 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM280 are further described hereinbelow with reference to Table Table1.

[3995] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM280 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3996]

[3997] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 281 (GAM281) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3998] GAM281 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM281 was detected is described hereinabove with reference to Figs. 2-8.

[3999] GAM281 gene, herein designated GAM GENE, and GAM281 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4000] GAM281 gene, herein designated GAM GENE, encodes a

GAM281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM281 precursor RNA is designated SEQ ID:4261, and is provided hereinbelow with reference to the sequence listing part.

[4001] GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4002] An enzyme complex designated DICER COMPLEX, dices the GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM281 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 22%) nucleotide sequence of GAM281 RNA is designated SEQ ID:4262, and is provided hereinbelow with reference to the sequence listing part.

[4003] GAM281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM281 target RNA, herein designated GAM TARGET RNA. GAM281 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4004] GAM281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM281 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM281 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4005] The complementary binding of GAM281 RNA, herein designated GAM RNA, to target binding sites on GAM281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM281 target RNA, herein designated GAM TARGET RNA, into GAM281 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4006] It is appreciated that GAM281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM281 target genes. The mRNA of each one of this plurality of GAM281 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM281 RNA, herein designated GAM RNA, and which when bound by GAM281 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM281 target proteins.

[4007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM281 gene, herein designated GAM GENE, on one or more GAM281 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4008] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM281 correlate with, and may be deduced from, the identity of the target genes which GAM281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4009] Nucleotide sequences of the GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM281 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM281 are further described hereinbelow with reference to Table Table1.

[4010] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM281 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4011]

[4012] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 282 (GAM282) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4013] GAM282 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM282 was detected is described hereinabove with reference to Figs. 2-8.

[4014] GAM282 gene, herein designated GAM GENE, and GAM282 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4015] GAM282 gene, herein designated GAM GENE, encodes a GAM282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM282 precursor RNA is designated SEQ ID:4276, and is provided hereinbelow with reference to the sequence listing part.

[4016] GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4017] An enzyme complex designated DICER COMPLEX, dices the GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM282 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM282 RNA is designated SEQ ID:4277, and is provided hereinbelow with reference to the sequence listing part.

[4018] GAM282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM282 target RNA, herein designated GAM TARGET RNA. GAM282 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4019] GAM282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM282 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM282 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM282 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4020] The complementary binding of GAM282 RNA, herein designated GAM RNA, to target binding sites on GAM282 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM282 target RNA, herein designated GAM TARGET RNA, into GAM282 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4021] It is appreciated that GAM282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM282 target genes. The mRNA of each one of this plurality of GAM282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM282 RNA, herein designated GAM RNA, and which when bound by GAM282 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM282 target proteins.

[4022] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM282 gene, herein designated GAM GENE, on one or more GAM282 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4023] It is yet further appreciated that specific functions, and accordingly utilities, of GAM282 correlate with, and may be deduced from, the identity of the target genes which GAM282 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4024] Nucleotide sequences of the GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM282 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM282 are further described hereinbelow with reference to Table Table1.

[4025] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM282 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4026]

[4027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 283 (GAM283) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4028] GAM283 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM283 was detected is described hereinabove with reference to Figs. 2-8.

[4029] GAM283 gene, herein designated GAM GENE, and GAM283 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4030] GAM283 gene, herein designated GAM GENE, encodes a GAM283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM283 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM283 precursor RNA is designated SEQ ID:4290, and is provided hereinbelow with reference to the sequence listing part.

[4031] GAM283 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4032] An enzyme complex designated DICER COMPLEX, dices the GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM283 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM283 RNA is designated SEQ ID:4291, and is provided

hereinbelow with reference to the sequence listing part.

[4033] GAM283 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM283 target RNA, herein designated GAM TARGET RNA.

GAM283 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4034] GAM283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM283 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM283 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM283 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4035] The complementary binding of GAM283 RNA, herein designated GAM RNA, to target binding sites on GAM283 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM283 target RNA, herein designated GAM TARGET RNA, into GAM283 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4036] It is appreciated that GAM283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM283 target genes. The mRNA of each one of this plurality of GAM283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM283 RNA, herein designated GAM RNA, and which when bound by GAM283 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM283 tar-

get proteins.

[4037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM283 gene, herein designated GAM GENE, on one or more GAM283 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM283 correlate with, and may be deduced from, the identity of the target genes which GAM283 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4039] Nucleotide sequences of the GAM283 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM283 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM283 are further described hereinbelow with reference to Table Table1.

[4040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM283 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4041]

[4042] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 284 (GAM284) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4043] GAM284 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM284 was detected is described hereinabove with reference to Figs. 2-8.

[4044] GAM284 gene, herein designated GAM GENE, and GAM284 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4045] GAM284 gene, herein designated GAM GENE, encodes a GAM284 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM284 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM284 precursor RNA is designated SEQ ID:4301, and is provided hereinbelow with reference to the sequence listing part.

[4046] GAM284 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4047] An enzyme complex designated DICER COMPLEX, dices

the GAM284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM284 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM284 RNA is designated SEQ ID:4302, and is provided hereinbelow with reference to the sequence listing part.

[4048] GAM284 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM284 target RNA, herein designated GAM TARGET RNA. GAM284 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4049] GAM284 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM284 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM284

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM284 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM284 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4050] The complementary binding of GAM284 RNA, herein designated GAM RNA, to target binding sites on GAM284 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM284 target RNA, herein designated GAM TARGET RNA, into GAM284 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4051] It is appreciated that GAM284 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM284 target genes. The mRNA of each one of this plurality of GAM284 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM284 RNA, herein designated GAM RNA, and which when bound by GAM284 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM284 target proteins.

[4052] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM284 gene, herein designated GAM GENE, on one or more GAM284 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4053] It is yet further appreciated that specific functions, and accordingly utilities, of GAM284 correlate with, and may be deduced from, the identity of the target genes which GAM284 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4054] Nucleotide sequences of the GAM284 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM284 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM284 are further described hereinbelow with reference to Table Table1.

[4055] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM284 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4056]

[4057] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 285 (GAM285) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4058] GAM285 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM285 was detected is described hereinabove with reference to Figs. 2-8.

[4059] GAM285 gene, herein designated GAM GENE, and GAM285 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4060] GAM285 gene, herein designated GAM GENE, encodes a GAM285 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM285 precursor RNA is designated SEQ ID:4318, and is provided hereinbelow with reference to the sequence listing part.

[4061] GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM285 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4062] An enzyme complex designated DICER COMPLEX, dices the GAM285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM285 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of GAM285 RNA is designated SEQ ID:4319, and is provided hereinbelow with reference to the sequence listing part.

[4063] GAM285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM285 target RNA, herein designated GAM TARGET RNA. GAM285 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4064] GAM285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM285 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM285 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM285 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[4065] The complementary binding of GAM285 RNA, herein designated GAM RNA, to target binding sites on GAM285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM285 target RNA, herein designated GAM TARGET RNA, into GAM285 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4066] It is appreciated that GAM285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM285 target genes. The mRNA of each one of this plurality of GAM285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM285 RNA, herein designated GAM RNA, and which when bound by GAM285 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM285 target proteins.

[4067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM285 gene, herein designated GAM GENE, on one or

more GAM285 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM285 correlate with, and may be deduced from, the identity of the target genes which GAM285 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4069] Nucleotide sequences of the GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM285 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM285 are further de-

scribed hereinbelow with reference to Table Table1.

[4070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM285 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4071]

[4072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 286 (GAM286) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4073] GAM286 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM286 was detected is described hereinabove with reference to Figs. 2-8.

[4074] GAM286 gene, herein designated GAM GENE, and GAM286 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4075] GAM286 gene, herein designated GAM GENE, encodes a GAM286 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM286 precursor RNA is designated SEQ ID:4328, and is provided hereinbelow with reference to the sequence listing part.

[4076] GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4077] An enzyme complex designated DICER COMPLEX, dices the GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM286 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM286 RNA is designated SEQ ID:4329, and is provided hereinbelow with reference to the sequence listing part.

[4078] GAM286 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM286 target RNA, herein designated GAM TARGET RNA. GAM286 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4079] GAM286 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM286 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM286 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM286 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM286 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4080] The complementary binding of GAM286 RNA, herein designated GAM RNA, to target binding sites on GAM286 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM286 target RNA, herein designated GAM TARGET RNA, into GAM286 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4081] It is appreciated that GAM286 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM286 target genes. The mRNA of each one of this plurality of GAM286 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM286 RNA, herein designated GAM RNA, and which when bound by GAM286 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM286 target proteins.

[4082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM286 gene, herein designated GAM GENE, on one or more GAM286 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM286 correlate with, and may

be deduced from, the identity of the target genes which GAM286 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4084] Nucleotide sequences of the GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM286 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM286 are further described hereinbelow with reference to Table Table1.

[4085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM286 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4086]

[4087] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 287 (GAM287) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4088] GAM287 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM287 was detected is described hereinabove with reference to Figs. 2-8.

[4089] GAM287 gene, herein designated GAM GENE, and GAM287 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4090] GAM287 gene, herein designated GAM GENE, encodes a GAM287 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM287 precursor RNA is designated SEQ ID:4344, and is provided hereinbelow with reference to the sequence listing part.

[4091] GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4092] An enzyme complex designated DICER COMPLEX, dices the GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM287 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM287 RNA is designated SEQ ID:4345, and is provided hereinbelow with reference to the sequence listing part.

[4093] GAM287 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM287 target RNA, herein designated GAM TARGET RNA. GAM287 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4094] GAM287 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM287 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM287 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM287 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM287 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4095] The complementary binding of GAM287 RNA, herein designated GAM RNA, to target binding sites on GAM287 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM287 target RNA, herein designated GAM TARGET RNA, into GAM287 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4096] It is appreciated that GAM287 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM287 target genes. The mRNA of each one of this plurality of GAM287 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM287 RNA, herein designated GAM RNA, and which when bound by GAM287 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM287 target proteins.

[4097] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM287 gene, herein designated GAM GENE, on one or more GAM287 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4098] It is yet further appreciated that specific functions, and accordingly utilities, of GAM287 correlate with, and may be deduced from, the identity of the target genes which GAM287 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4099] Nucleotide sequences of the GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM287 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM287 are further described hereinbelow with reference to Table Table1.

[4100] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM287 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4101]

[4102] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 288 (GAM288) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4103] GAM288 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM288 was detected is described hereinabove with reference to Figs. 2-8.

[4104] GAM288 gene, herein designated GAM GENE, and GAM288 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4105] GAM288 gene, herein designated GAM GENE, encodes a GAM288 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM288 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM288 precursor RNA is designated SEQ ID:4353, and is provided hereinbelow with reference to the sequence listing part.

[4106] GAM288 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4107] An enzyme complex designated DICER COMPLEX, dices the GAM288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM288 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of GAM288 RNA is designated SEQ ID:4354, and is provided hereinbelow with reference to the sequence listing part.

[4108] GAM288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM288 target RNA, herein designated GAM TARGET RNA.

GAM288 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4109] GAM288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM288 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM288 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM288 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4110] The complementary binding of GAM288 RNA, herein designated GAM RNA, to target binding sites on GAM288 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM288 target RNA, herein designated GAM TARGET RNA, into GAM288 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4111] It is appreciated that GAM288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM288 target genes. The mRNA of each one of this plurality of GAM288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM288 RNA, herein designated GAM RNA, and which when bound by GAM288 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM288 target proteins.

[4112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM288 gene, herein designated GAM GENE, on one or more GAM288 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4113] It is yet further appreciated that specific functions, and accordingly utilities, of GAM288 correlate with, and may be deduced from, the identity of the target genes which GAM288 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4114] Nucleotide sequences of the GAM288 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM288 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM288 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM288 are further described hereinbelow with reference to Table Table1.

[4115] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM288 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4116]

[4117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 289 (GAM289) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4118] GAM289 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM289 was detected is described hereinabove with reference to Figs. 2-8.

[4119] GAM289 gene, herein designated GAM GENE, and GAM289 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4120] GAM289 gene, herein designated GAM GENE, encodes a

GAM289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM289 precursor RNA is designated SEQ ID:4369, and is provided hereinbelow with reference to the sequence listing part.

[4121] GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4122] An enzyme complex designated DICER COMPLEX, dices the GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM289 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM289 RNA is designated SEQ ID:4370, and is provided hereinbelow with reference to the sequence listing part.

[4123] GAM289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM289 target RNA, herein designated GAM TARGET RNA. GAM289 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4124] GAM289 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM289 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM289 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM289 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4125] The complementary binding of GAM289 RNA, herein designated GAM RNA, to target binding sites on GAM289 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM289 target RNA, herein designated GAM TARGET RNA, into GAM289 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4126] It is appreciated that GAM289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM289 target genes. The mRNA of each one of this plurality of GAM289 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM289 RNA, herein designated GAM RNA, and which when bound by GAM289 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM289 target proteins.

[4127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM289 gene, herein designated GAM GENE, on one or more GAM289 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4128] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM289 correlate with, and may be deduced from, the identity of the target genes which GAM289 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4129] Nucleotide sequences of the GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM289 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM289 are further described hereinbelow with reference to Table Table1.

[4130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM289 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4131]

[4132] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 290 (GAM290) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4133] GAM290 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM290 was detected is described hereinabove with reference to Figs. 2-8.

[4134] GAM290 gene, herein designated GAM GENE, and GAM290 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4135] GAM290 gene, herein designated GAM GENE, encodes a GAM290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM290 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM290 precursor RNA is designated SEQ ID:4378, and is provided hereinbelow with reference to the sequence listing part.

[4136] GAM290 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4137] An enzyme complex designated DICER COMPLEX, dices the GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM290 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of GAM290 RNA is designated SEQ ID:4379, and is provided hereinbelow with reference to the sequence listing part.

[4138] GAM290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM290 target RNA, herein designated GAM TARGET RNA.
GAM290 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4139] GAM290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM290 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM290 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM290 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4140] The complementary binding of GAM290 RNA, herein designated GAM RNA, to target binding sites on GAM290 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM290 target RNA, herein designated GAM TARGET RNA, into GAM290 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4141] It is appreciated that GAM290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM290 target genes. The mRNA of each one of this plurality of GAM290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM290 RNA, herein designated GAM RNA, and which when bound by GAM290 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM290 target proteins.

[4142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM290 gene, herein designated GAM GENE, on one or more GAM290 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4143] It is yet further appreciated that specific functions, and accordingly utilities, of GAM290 correlate with, and may be deduced from, the identity of the target genes which GAM290 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4144] Nucleotide sequences of the GAM290 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM290 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM290 are further described hereinbelow with reference to Table Table1.

[4145] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM290 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4146]

[4147] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 291 (GAM291) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4148] GAM291 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM291 was detected is described hereinabove with reference to Figs. 2-8.

[4149] GAM291 gene, herein designated GAM GENE, and GAM291 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4150] GAM291 gene, herein designated GAM GENE, encodes a GAM291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM291 precursor RNA is designated SEQ ID:4400, and is provided hereinbelow with reference to the sequence listing part.

[4151] GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4152] An enzyme complex designated DICER COMPLEX, dices the GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM291 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of GAM291 RNA is designated SEQ ID:4401, and is provided

hereinbelow with reference to the sequence listing part.

[4153] GAM291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM291 target RNA, herein designated GAM TARGET RNA. GAM291 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4154] GAM291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM291 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM291 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM291 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4155] The complementary binding of GAM291 RNA, herein designated GAM RNA, to target binding sites on GAM291 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM291 target RNA, herein designated GAM TARGET RNA, into GAM291 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4156] It is appreciated that GAM291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM291 target genes. The mRNA of each one of this plurality of GAM291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM291 RNA, herein designated GAM RNA, and which when bound by GAM291 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM291 tar-

get proteins.

[4157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM291 gene, herein designated GAM GENE, on one or more GAM291 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4158] It is yet further appreciated that specific functions, and accordingly utilities, of GAM291 correlate with, and may be deduced from, the identity of the target genes which GAM291 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4159] Nucleotide sequences of the GAM291 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM291 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM291 are further described hereinbelow with reference to Table Table1.

[4160] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM291 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4161]

[4162] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 292 (GAM292) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4163] GAM292 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM292 was detected is described hereinabove with reference to Figs. 2-8.

[4164] GAM292 gene, herein designated GAM GENE, and GAM292 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4165] GAM292 gene, herein designated GAM GENE, encodes a GAM292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM292 precursor RNA is designated SEQ ID:4429, and is provided hereinbelow with reference to the sequence listing part.

[4166] GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4167] An enzyme complex designated DICER COMPLEX, dices

the GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM292 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM292 RNA is designated SEQ ID:4430, and is provided hereinbelow with reference to the sequence listing part.

[4168] GAM292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM292 target RNA, herein designated GAM TARGET RNA. GAM292 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4169] GAM292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM292

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM292 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM292 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4170] The complementary binding of GAM292 RNA, herein designated GAM RNA, to target binding sites on GAM292 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM292 target RNA, herein designated GAM TARGET RNA, into GAM292 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4171] It is appreciated that GAM292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM292 target genes. The mRNA of each one of this plurality of GAM292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM292 RNA, herein designated GAM RNA, and which when bound by GAM292 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM292 target proteins.

[4172] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM292 gene, herein designated GAM GENE, on one or more GAM292 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4173] It is yet further appreciated that specific functions, and accordingly utilities, of GAM292 correlate with, and may be deduced from, the identity of the target genes which GAM292 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4174] Nucleotide sequences of the GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM292 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM292 are further described hereinbelow with reference to Table Table1.

[4175] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM292 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4176]

[4177] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 293 (GAM293) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4178] GAM293 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM293 was detected is described hereinabove with reference to Figs. 2-8.

[4179] GAM293 gene, herein designated GAM GENE, and GAM293 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4180] GAM293 gene, herein designated GAM GENE, encodes a GAM293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM293 precursor RNA is designated SEQ ID:4449, and is provided hereinbelow with reference to the sequence listing part.

[4181] GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM293 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4182] An enzyme complex designated DICER COMPLEX, dices the GAM293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM293 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM293 RNA is designated SEQ ID:4450, and is provided hereinbelow with reference to the sequence listing part.

[4183] GAM293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM293 target RNA, herein designated GAM TARGET RNA. GAM293 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4184] GAM293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM293 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM293 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM293 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[4185] The complementary binding of GAM293 RNA, herein designated GAM RNA, to target binding sites on GAM293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM293 target RNA, herein designated GAM TARGET RNA, into GAM293 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4186] It is appreciated that GAM293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM293 target genes. The mRNA of each one of this plurality of GAM293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM293 RNA, herein designated GAM RNA, and which when bound by GAM293 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM293 target proteins.

[4187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM293 gene, herein designated GAM GENE, on one or

more GAM293 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4188] It is yet further appreciated that specific functions, and accordingly utilities, of GAM293 correlate with, and may be deduced from, the identity of the target genes which GAM293 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4189] Nucleotide sequences of the GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM293 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM293 are further de-

scribed hereinbelow with reference to Table Table1.

[4190] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM293 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4191]

[4192] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 294 (GAM294) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4193] GAM294 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM294 was detected is described hereinabove with reference to Figs. 2-8.

[4194] GAM294 gene, herein designated GAM GENE, and GAM294 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4195] GAM294 gene, herein designated GAM GENE, encodes a GAM294 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM294 precursor RNA is designated SEQ ID:4458, and is provided hereinbelow with reference to the sequence listing part.

[4196] GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4197] An enzyme complex designated DICER COMPLEX, dices the GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM294 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM294 RNA is designated SEQ ID:4459, and is provided hereinbelow with reference to the sequence listing part.

[4198] GAM294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM294 target RNA, herein designated GAM TARGET RNA. GAM294 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4199] GAM294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM294 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM294 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM294 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4200] The complementary binding of GAM294 RNA, herein designated GAM RNA, to target binding sites on GAM294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM294 target RNA, herein designated GAM TARGET RNA, into GAM294 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4201] It is appreciated that GAM294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM294 target genes. The mRNA of each one of this plurality of GAM294 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM294 RNA, herein designated GAM RNA, and which when bound by GAM294 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM294 target proteins.

[4202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM294 gene, herein designated GAM GENE, on one or more GAM294 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4203] It is yet further appreciated that specific functions, and accordingly utilities, of GAM294 correlate with, and may

be deduced from, the identity of the target genes which GAM294 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4204] Nucleotide sequences of the GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM294 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM294 are further described hereinbelow with reference to Table Table1.

[4205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM294 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4206]

[4207] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 295 (GAM295) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4208] GAM295 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM295 was detected is described hereinabove with reference to Figs. 2-8.

[4209] GAM295 gene, herein designated GAM GENE, and GAM295 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4210] GAM295 gene, herein designated GAM GENE, encodes a GAM295 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM295 precursor RNA is designated SEQ ID:4462, and is provided hereinbelow with reference to the sequence listing part.

[4211] GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4212] An enzyme complex designated DICER COMPLEX, dices the GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM295 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM295 RNA is designated SEQ ID:4463, and is provided hereinbelow with reference to the sequence listing part.

[4213] GAM295 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM295 target RNA, herein designated GAM TARGET RNA. GAM295 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4214] GAM295 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM295 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM295 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM295 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM295 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4215] The complementary binding of GAM295 RNA, herein designated GAM RNA, to target binding sites on GAM295 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM295 target RNA, herein designated GAM TARGET RNA, into GAM295 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4216] It is appreciated that GAM295 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM295 target genes. The mRNA of each one of this plurality of GAM295 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM295 RNA, herein designated GAM RNA, and which when bound by GAM295 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM295 target proteins.

[4217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM295 gene, herein designated GAM GENE, on one or more GAM295 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4218] It is yet further appreciated that specific functions, and accordingly utilities, of GAM295 correlate with, and may be deduced from, the identity of the target genes which GAM295 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4219] Nucleotide sequences of the GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM295 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM295 are further described hereinbelow with reference to Table Table1.

[4220] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM295 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4221]

[4222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 296 (GAM296) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4223] GAM296 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM296 was detected is described hereinabove with reference to Figs. 2-8.

[4224] GAM296 gene, herein designated GAM GENE, and GAM296 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4225] GAM296 gene, herein designated GAM GENE, encodes a GAM296 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM296 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM296 precursor RNA is desig-

nated SEQ ID:4473, and is provided hereinbelow with reference to the sequence listing part.

[4226] GAM296 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4227] An enzyme complex designated DICER COMPLEX, dices the GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM296 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 36%) nucleotide sequence of GAM296 RNA is designated SEQ ID:4474, and is provided hereinbelow with reference to the sequence listing part.

[4228] GAM296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM296 target RNA, herein designated GAM TARGET RNA. GAM296 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4229] GAM296 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM296 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM296 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM296

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4230] The complementary binding of GAM296 RNA, herein designated GAM RNA, to target binding sites on GAM296 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM296 target RNA, herein designated GAM TARGET RNA, into GAM296 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4231] It is appreciated that GAM296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM296 target genes. The mRNA of each one of this plurality of GAM296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM296 RNA, herein designated GAM RNA, and which when bound by GAM296 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM296 target proteins.

[4232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM296 gene, herein designated GAM GENE, on one or more GAM296 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM296 correlate with, and may be deduced from, the identity of the target genes which GAM296 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4234] Nucleotide sequences of the GAM296 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM296 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM296 are further described hereinbelow with reference to Table Table1.

[4235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM296 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4236]

[4237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 297 (GAM297) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4238] GAM297 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM297 was detected is described hereinabove with reference to Figs. 2-8.

[4239] GAM297 gene, herein designated GAM GENE, and

GAM297 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4240] GAM297 gene, herein designated GAM GENE, encodes a GAM297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM297 precursor RNA is designated SEQ ID:4488, and is provided hereinbelow with reference to the sequence listing part.

[4241] GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4242] An enzyme complex designated DICER COMPLEX, dices the GAM297 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM297 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM297 RNA is designated SEQ ID:4489, and is provided hereinbelow with reference to the sequence listing part.

[4243] GAM297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM297 target RNA, herein designated GAM TARGET RNA. GAM297 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4244] GAM297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM297 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM297 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM297 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4245] The complementary binding of GAM297 RNA, herein designated GAM RNA, to target binding sites on GAM297 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM297 target RNA, herein designated GAM TARGET RNA, into GAM297 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4246] It is appreciated that GAM297 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM297 target genes. The mRNA of each one of this plurality of GAM297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM297 RNA, herein designated GAM RNA, and which when bound by GAM297 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM297 target proteins.

[4247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM297 gene, herein designated GAM GENE, on one or more GAM297 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM297 correlate with, and may be deduced from, the identity of the target genes which GAM297 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4249] Nucleotide sequences of the GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM297 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM297 are further described hereinbelow with reference to Table Table1.

[4250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM297 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4251]

[4252] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 298 (GAM298) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4253] GAM298 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM298 was detected is described hereinabove with reference to Figs. 2-8.

[4254] GAM298 gene, herein designated GAM GENE, and GAM298 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4255] GAM298 gene, herein designated GAM GENE, encodes a GAM298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM298 precursor RNA is designated SEQ ID:4508, and is provided hereinbelow with reference to the sequence listing part.

[4256] GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4257] An enzyme complex designated DICER COMPLEX, dices the GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM298 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM298 RNA is designated SEQ ID:4509, and is provided hereinbelow with reference to the sequence listing part.

[4258] GAM298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM298 target RNA, herein designated GAM TARGET RNA. GAM298 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4259] GAM298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM298 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM298 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM298 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4260] The complementary binding of GAM298 RNA, herein designated GAM RNA, to target binding sites on GAM298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM298 target RNA, herein designated GAM TARGET RNA, into GAM298 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4261] It is appreciated that GAM298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM298 target genes. The mRNA of each one of this plurality of GAM298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM298 RNA, herein designated GAM RNA, and which when bound by GAM298 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM298 target proteins.

[4262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM298 gene, herein designated GAM GENE, on one or more GAM298 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM298 correlate with, and may be deduced from, the identity of the target genes which GAM298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4264] Nucleotide sequences of the GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM298 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM298 are further described hereinbelow with reference to Table Table1.

[4265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM298 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4266]

[4267] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 299 (GAM299) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4268] GAM299 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM299 was detected is described hereinabove with reference to Figs. 2-8.

[4269] GAM299 gene, herein designated GAM GENE, and GAM299 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4270] GAM299 gene, herein designated GAM GENE, encodes a GAM299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM299 precursor RNA is designated SEQ ID:4521, and is provided hereinbelow with reference to the sequence listing part.

[4271] GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4272] An enzyme complex designated DICER COMPLEX, dices the GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM299 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM299 RNA is designated SEQ ID:4522, and is provided hereinbelow with reference to the sequence listing part.

[4273] GAM299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM299 target RNA, herein designated GAM TARGET RNA. GAM299 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4274] GAM299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM299 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM299 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM299 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4275] The complementary binding of GAM299 RNA, herein designated GAM RNA, to target binding sites on GAM299 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM299 target RNA, herein designated GAM TARGET RNA, into GAM299 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4276] It is appreciated that GAM299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM299 target genes. The mRNA of each one of this plurality of GAM299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM299 RNA,

herein designated GAM RNA, and which when bound by GAM299 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM299 target proteins.

[4277] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM299 gene, herein designated GAM GENE, on one or more GAM299 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4278] It is yet further appreciated that specific functions, and accordingly utilities, of GAM299 correlate with, and may be deduced from, the identity of the target genes which

GAM299 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4279] Nucleotide sequences of the GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM299 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM299 are further described hereinbelow with reference to Table Table1.

[4280] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM299 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4281]

[4282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 300 (GAM300) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4283] GAM300 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM300 was detected is described hereinabove with reference to Figs. 2-8.

[4284] GAM300 gene, herein designated GAM GENE, and GAM300 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4285] GAM300 gene, herein designated GAM GENE, encodes a GAM300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM300 precursor RNA is designated SEQ ID:4544, and is provided hereinbelow with reference to the sequence listing part.

[4286] GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4287] An enzyme complex designated DICER COMPLEX, dices the GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM300 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 20%) nucleotide sequence of GAM300 RNA is designated SEQ ID:4545, and is provided hereinbelow with reference to the sequence listing part.

[4288] GAM300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM300 target RNA, herein designated GAM TARGET RNA.
GAM300 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4289] GAM300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM300 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM300 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM300 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4290] The complementary binding of GAM300 RNA, herein designated GAM RNA, to target binding sites on GAM300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM300 target RNA, herein desig-

nated GAM TARGET RNA, into GAM300 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4291] It is appreciated that GAM300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM300 target genes. The mRNA of each one of this plurality of GAM300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM300 RNA, herein designated GAM RNA, and which when bound by GAM300 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM300 target proteins.

[4292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM300 gene, herein designated GAM GENE, on one or more GAM300 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM300 correlate with, and may be deduced from, the identity of the target genes which GAM300 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4294] Nucleotide sequences of the GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM300 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM300 are further described hereinbelow with reference to Table Table1.

[4295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM300 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4296]

[4297] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 301 (GAM301) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4298] GAM301 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM301 was detected is described hereinabove with reference to Figs. 2-8.

[4299] GAM301 gene, herein designated GAM GENE, and GAM301 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4300] GAM301 gene, herein designated GAM GENE, encodes a GAM301 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM301 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM301 precursor RNA is designated SEQ ID:4556, and is provided hereinbelow with ref-

erence to the sequence listing part.

[4301] GAM301 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4302] An enzyme complex designated DICER COMPLEX, dices the GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM301 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM301 RNA is designated SEQ ID:4557, and is provided hereinbelow with reference to the sequence listing part.

[4303] GAM301 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM301 target RNA, herein designated GAM TARGET RNA.

GAM301 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4304] GAM301 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM301 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM301 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM301 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM301 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4305] The complementary binding of GAM301 RNA, herein designated GAM RNA, to target binding sites on GAM301 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM301 target RNA, herein designated GAM TARGET RNA, into GAM301 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4306] It is appreciated that GAM301 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM301 target genes. The mRNA of each one of this plurality of GAM301 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM301 RNA, herein designated GAM RNA, and which when bound by GAM301 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM301 target proteins.

[4307] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM301 gene, herein designated GAM GENE, on one or more GAM301 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4308] It is yet further appreciated that specific functions, and accordingly utilities, of GAM301 correlate with, and may be deduced from, the identity of the target genes which GAM301 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4309] Nucleotide sequences of the GAM301 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM301 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM301 are further described hereinbelow with reference to Table Table1.

[4310] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM301 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4311]

[4312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 302 (GAM302) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4313] GAM302 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM302 was detected is described hereinabove with reference to Figs. 2-8.

[4314] GAM302 gene, herein designated GAM GENE, and GAM302 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4315] GAM302 gene, herein designated GAM GENE, encodes a GAM302 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM302 precursor RNA is designated SEQ ID:4578, and is provided hereinbelow with reference to the sequence listing part.

[4316] GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4317] An enzyme complex designated DICER COMPLEX, dices the GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM302 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM302 RNA is designated SEQ ID:4579, and is provided hereinbelow with reference to the sequence listing part.

[4318] GAM302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM302 target RNA, herein designated GAM TARGET RNA. GAM302 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4319] GAM302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM302 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM302 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM302 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4320] The complementary binding of GAM302 RNA, herein designated GAM RNA, to target binding sites on GAM302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM302 target RNA, herein designated GAM TARGET RNA, into GAM302 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4321] It is appreciated that GAM302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM302 target genes. The mRNA of each one of this plurality of GAM302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM302 RNA, herein designated GAM RNA, and which when bound by GAM302 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM302 target proteins.

[4322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM302 gene, herein designated GAM GENE, on one or more GAM302 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM302 correlate with, and may be deduced from, the identity of the target genes which GAM302 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4324] Nucleotide sequences of the GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM302 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM302 are further described hereinbelow with reference to Table Table1.

[4325] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM302 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4326]

[4327] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

303 (GAM303) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4328] GAM303 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM303 was detected is described hereinabove with reference to Figs. 2-8.

[4329] GAM303 gene, herein designated GAM GENE, and GAM303 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4330] GAM303 gene, herein designated GAM GENE, encodes a GAM303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM303 precursor RNA is designated SEQ ID:4591, and is provided hereinbelow with reference to the sequence listing part.

[4331] GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4332] An enzyme complex designated DICER COMPLEX, dices the GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM303 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM303 RNA is designated SEQ ID:4592, and is provided hereinbelow with reference to the sequence listing part.

[4333] GAM303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM303 target RNA, herein designated GAM TARGET RNA. GAM303 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4334] GAM303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM303 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM303 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM303 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4335] The complementary binding of GAM303 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM303 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM303 target RNA, herein designated GAM TARGET RNA, into GAM303 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4336] It is appreciated that GAM303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM303 target genes. The mRNA of each one of this plurality of GAM303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM303 RNA, herein designated GAM RNA, and which when bound by GAM303 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM303 target proteins.

[4337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM303 gene, herein designated GAM GENE, on one or more GAM303 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4338] It is yet further appreciated that specific functions, and accordingly utilities, of GAM303 correlate with, and may be deduced from, the identity of the target genes which GAM303 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4339] Nucleotide sequences of the GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM303 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM303 are further described hereinbelow with reference to Table Table1.

[4340] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM303 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4341]

[4342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 304 (GAM304) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4343] GAM304 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM304 was detected is described hereinabove with reference to Figs. 2-8.

[4344] GAM304 gene, herein designated GAM GENE, and GAM304 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4345] GAM304 gene, herein designated GAM GENE, encodes a GAM304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM304 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM304 precursor RNA is designated SEQ ID:4618, and is provided hereinbelow with reference to the sequence listing part.

[4346] GAM304 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4347] An enzyme complex designated DICER COMPLEX, dices the GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM304 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 52%) nucleotide sequence of GAM304 RNA is designated SEQ ID:4619, and is provided hereinbelow with reference to the sequence listing part.

[4348] GAM304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM304 target RNA, herein designated GAM TARGET RNA. GAM304 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4349] GAM304 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM304 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM304 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM304 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4350] The complementary binding of GAM304 RNA, herein designated GAM RNA, to target binding sites on GAM304 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM304 target RNA, herein designated GAM TARGET RNA, into GAM304 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4351] It is appreciated that GAM304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM304 target genes. The mRNA of each one of this plurality of GAM304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM304 RNA, herein designated GAM RNA, and which when bound by

GAM304 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM304 target proteins.

[4352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM304 gene, herein designated GAM GENE, on one or more GAM304 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM304 correlate with, and may be deduced from, the identity of the target genes which GAM304 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[4354] Nucleotide sequences of the GAM304 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM304 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM304 are further described hereinbelow with reference to Table Table1.

[4355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM304 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4356]

[4357] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 305 (GAM305) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4358] GAM305 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM305 was detected is described hereinabove with reference to Figs. 2-8.

[4359] GAM305 gene, herein designated GAM GENE, and GAM305 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4360] GAM305 gene, herein designated GAM GENE, encodes a GAM305 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM305 precursor RNA is designated SEQ ID:4627, and is provided hereinbelow with reference to the sequence listing part.

[4361] GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[4362] An enzyme complex designated DICER COMPLEX, dices the GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM305 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM305 RNA is designated SEQ ID:4628, and is provided hereinbelow with reference to the sequence listing part.

[4363] GAM305 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM305 target RNA, herein designated GAM TARGET RNA. GAM305 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4364] GAM305 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM305 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM305 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM305 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM305 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4365] The complementary binding of GAM305 RNA, herein designated GAM RNA, to target binding sites on GAM305 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM305 target RNA, herein designated GAM TARGET RNA, into GAM305 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4366] It is appreciated that GAM305 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM305 target genes. The mRNA of each one of this plurality of GAM305 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM305 RNA, herein designated GAM RNA, and which when bound by GAM305 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM305 target proteins.

[4367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM305 gene, herein designated GAM GENE, on one or more GAM305 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4368] It is yet further appreciated that specific functions, and accordingly utilities, of GAM305 correlate with, and may be deduced from, the identity of the target genes which GAM305 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4369] Nucleotide sequences of the GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM305 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM305 are further described hereinbelow with reference to Table Table1.

[4370] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM305 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4371]

[4372] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 306 (GAM306) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4373] GAM306 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM306 was detected is described hereinabove with reference to Figs. 2-8.

[4374] GAM306 gene, herein designated GAM GENE, and GAM306 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4375] GAM306 gene, herein designated GAM GENE, encodes a GAM306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM306 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM306 precursor RNA is designated SEQ ID:4647, and is provided hereinbelow with reference to the sequence listing part.

[4376] GAM306 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4377] An enzyme complex designated DICER COMPLEX, dices the GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM306 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM306 RNA is designated SEQ ID:2738, and is provided hereinbelow with reference to the sequence listing part.

[4378] GAM306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM306

target RNA, herein designated GAM TARGET RNA.

GAM306 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4379] GAM306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM306 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM306 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM306 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4380] The complementary binding of GAM306 RNA, herein designated GAM RNA, to target binding sites on GAM306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM306 target RNA, herein designated GAM TARGET RNA, into GAM306 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4381] It is appreciated that GAM306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM306 target genes. The mRNA of each one of this plurality of GAM306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM306 RNA, herein designated GAM RNA, and which when bound by GAM306 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM306 target proteins.

[4382] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM306 gene, herein designated GAM GENE, on one or more GAM306 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4383] It is yet further appreciated that specific functions, and accordingly utilities, of GAM306 correlate with, and may be deduced from, the identity of the target genes which GAM306 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4384] Nucleotide sequences of the GAM306 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM306 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM306 are further described hereinbelow with reference to Table Table1.

[4385] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM306 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4386]

[4387] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 307 (GAM307) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4388] GAM307 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM307 was detected is described hereinabove with reference to Figs. 2-8.

[4389] GAM307 gene, herein designated GAM GENE, and GAM307 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4390] GAM307 gene, herein designated GAM GENE, encodes a GAM307 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM307 precursor RNA is designated SEQ ID:4652, and is provided hereinbelow with reference to the sequence listing part.

[4391] GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4392] An enzyme complex designated DICER COMPLEX, dices the GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM307 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 38%) nucleotide sequence of GAM307 RNA is designated SEQ ID:4653, and is provided hereinbelow with reference to the sequence listing part.

[4393] GAM307 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM307 target RNA, herein designated GAM TARGET RNA. GAM307 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4394] GAM307 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM307 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM307 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM307 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM307 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4395] The complementary binding of GAM307 RNA, herein designated GAM RNA, to target binding sites on GAM307 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM307 target RNA, herein designated GAM TARGET RNA, into GAM307 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4396] It is appreciated that GAM307 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM307 target genes. The mRNA of each one of this plu-

rality of GAM307 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM307 RNA, herein designated GAM RNA, and which when bound by GAM307 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM307 target proteins.

[4397] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM307 gene, herein designated GAM GENE, on one or more GAM307 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4398] It is yet further appreciated that specific functions, and accordingly utilities, of GAM307 correlate with, and may be deduced from, the identity of the target genes which GAM307 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4399] Nucleotide sequences of the GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM307 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM307 are further described hereinbelow with reference to Table Table1.

[4400] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM307 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4401]

[4402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 308 (GAM308) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4403] GAM308 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM308 was detected is described hereinabove with reference to Figs. 2-8.

[4404] GAM308 gene, herein designated GAM GENE, and GAM308 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4405] GAM308 gene, herein designated GAM GENE, encodes a GAM308 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM308 precursor RNA is designated SEQ ID:4667, and is provided hereinbelow with reference to the sequence listing part.

[4406] GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4407] An enzyme complex designated DICER COMPLEX, dices the GAM308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM308 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM308 RNA is designated SEQ ID:4668, and is provided hereinbelow with reference to the sequence listing part.

[4408] GAM308 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM308 target RNA, herein designated GAM TARGET RNA.
GAM308 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[4409] GAM308 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM308 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM308 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM308 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM308 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4410] The complementary binding of GAM308 RNA, herein designated GAM RNA, to target binding sites on GAM308 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM308 target RNA, herein designated GAM TARGET RNA, into GAM308 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4411] It is appreciated that GAM308 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM308 target genes. The mRNA of each one of this plurality of GAM308 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM308 RNA, herein designated GAM RNA, and which when bound by GAM308 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM308 target proteins.

[4412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM308 gene, herein designated GAM GENE, on one or more GAM308 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM308 correlate with, and may be deduced from, the identity of the target genes which GAM308 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4414] Nucleotide sequences of the GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM308 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM308 are further described hereinbelow with reference to Table Table1.

[4415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM308 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4416]

[4417] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 309 (GAM309) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4418] GAM309 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM309 was detected is described hereinabove with reference to Figs. 2-8.

[4419] GAM309 gene, herein designated GAM GENE, and GAM309 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4420] GAM309 gene, herein designated GAM GENE, encodes a GAM309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM309 precursor RNA is designated SEQ ID:4680, and is provided hereinbelow with reference to the sequence listing part.

[4421] GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4422] An enzyme complex designated DICER COMPLEX, dices the GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM309 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 38%) nucleotide sequence of

GAM309 RNA is designated SEQ ID:4681, and is provided hereinbelow with reference to the sequence listing part.

[4423] GAM309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM309 target RNA, herein designated GAM TARGET RNA. GAM309 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4424] GAM309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM309 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM309 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM309 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4425] The complementary binding of GAM309 RNA, herein designated GAM RNA, to target binding sites on GAM309 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM309 target RNA, herein designated GAM TARGET RNA, into GAM309 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4426] It is appreciated that GAM309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM309 target genes. The mRNA of each one of this plurality of GAM309 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM309 RNA, herein designated GAM RNA, and which when bound by GAM309 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM309 target proteins.

[4427] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM309 gene, herein designated GAM GENE, on one or more GAM309 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4428] It is yet further appreciated that specific functions, and accordingly utilities, of GAM309 correlate with, and may be deduced from, the identity of the target genes which GAM309 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4429] Nucleotide sequences of the GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM309 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM309 are further described hereinbelow with reference to Table Table1.

[4430] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM309 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4431]

[4432] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 310 (GAM310) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4433] GAM310 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM310 was detected is described hereinabove

with reference to Figs. 2-8.

[4434] GAM310 gene, herein designated GAM GENE, and GAM310 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4435] GAM310 gene, herein designated GAM GENE, encodes a GAM310 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM310 precursor RNA is designated SEQ ID:4701, and is provided hereinbelow with reference to the sequence listing part.

[4436] GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4437] An enzyme complex designated DICER COMPLEX, dices the GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM310 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM310 RNA is designated SEQ ID:4702, and is provided hereinbelow with reference to the sequence listing part.

[4438] GAM310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM310 target RNA, herein designated GAM TARGET RNA. GAM310 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4439] GAM310 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM310 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM310 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM310 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM310 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4440] The complementary binding of GAM310 RNA, herein designated GAM RNA, to target binding sites on GAM310 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM310 target RNA, herein designated GAM TARGET RNA, into GAM310 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4441] It is appreciated that GAM310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM310 target genes. The mRNA of each one of this plurality of GAM310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM310 RNA, herein designated GAM RNA, and which when bound by GAM310 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM310 target proteins.

[4442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM310 gene, herein designated GAM GENE, on one or more GAM310 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4443] It is yet further appreciated that specific functions, and accordingly utilities, of GAM310 correlate with, and may be deduced from, the identity of the target genes which GAM310 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4444] Nucleotide sequences of the GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM310 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM310 are further described hereinbelow with reference to Table Table1.

[4445] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM310 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4446]

[4447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 311 (GAM311) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4448] GAM311 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM311 was detected is described hereinabove with reference to Figs. 2-8.

[4449] GAM311 gene, herein designated GAM GENE, and GAM311 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4450] GAM311 gene, herein designated GAM GENE, encodes a GAM311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM311 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM311 precursor RNA is designated SEQ ID:4719, and is provided hereinbelow with reference to the sequence listing part.

[4451] GAM311 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4452] An enzyme complex designated DICER COMPLEX, dices the GAM311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM311 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of GAM311 RNA is designated SEQ ID:4720, and is provided hereinbelow with reference to the sequence listing part.

[4453] GAM311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM311 target RNA, herein designated GAM TARGET RNA.

GAM311 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4454] GAM311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM311 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM311 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM311 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4455] The complementary binding of GAM311 RNA, herein designated GAM RNA, to target binding sites on GAM311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM311 target RNA, herein designated GAM TARGET RNA, into GAM311 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4456] It is appreciated that GAM311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM311 target genes. The mRNA of each one of this plurality of GAM311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM311 RNA, herein designated GAM RNA, and which when bound by GAM311 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM311 target proteins.

[4457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM311 gene, herein designated GAM GENE, on one or more GAM311 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4458] It is yet further appreciated that specific functions, and accordingly utilities, of GAM311 correlate with, and may be deduced from, the identity of the target genes which GAM311 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4459] Nucleotide sequences of the GAM311 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM311 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM311 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM311 are further described hereinbelow with reference to Table Table1.

[4460] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM311 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4461]

[4462] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 312 (GAM312) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4463] GAM312 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM312 was detected is described hereinabove with reference to Figs. 2-8.

[4464] GAM312 gene, herein designated GAM GENE, and GAM312 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4465] GAM312 gene, herein designated GAM GENE, encodes a

GAM312 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM312 precursor RNA is designated SEQ ID:4738, and is provided hereinbelow with reference to the sequence listing part.

[4466] GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4467] An enzyme complex designated DICER COMPLEX, dices the GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM312 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM312 RNA is designated SEQ ID:4739, and is provided hereinbelow with reference to the sequence listing part.

[4468] GAM312 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM312 target RNA, herein designated GAM TARGET RNA. GAM312 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4469] GAM312 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM312 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM312 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM312 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM312 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4470] The complementary binding of GAM312 RNA, herein designated GAM RNA, to target binding sites on GAM312 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM312 target RNA, herein designated GAM TARGET RNA, into GAM312 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4471] It is appreciated that GAM312 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM312 target genes. The mRNA of each one of this plurality of GAM312 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM312 RNA, herein designated GAM RNA, and which when bound by GAM312 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM312 target proteins.

[4472] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM312 gene, herein designated GAM GENE, on one or more GAM312 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4473] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM312 correlate with, and may be deduced from, the identity of the target genes which GAM312 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4474] Nucleotide sequences of the GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM312 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM312 are further described hereinbelow with reference to Table Table1.

[4475] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM312 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4476]

[4477] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 313 (GAM313) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4478] GAM313 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM313 was detected is described hereinabove with reference to Figs. 2-8.

[4479] GAM313 gene, herein designated GAM GENE, and GAM313 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4480] GAM313 gene, herein designated GAM GENE, encodes a GAM313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM313 precursor RNA is designated SEQ ID:4771, and is provided hereinbelow with reference to the sequence listing part.

[4481] GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4482] An enzyme complex designated DICER COMPLEX, dices the GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM313 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM313 RNA is designated SEQ ID:4772, and is provided hereinbelow with reference to the sequence listing part.

[4483] GAM313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM313 target RNA, herein designated GAM TARGET RNA. GAM313 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4484] GAM313 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM313 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM313 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM313 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4485] The complementary binding of GAM313 RNA, herein designated GAM RNA, to target binding sites on GAM313 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM313 target RNA, herein designated GAM TARGET RNA, into GAM313 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4486] It is appreciated that GAM313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM313 target genes. The mRNA of each one of this plurality of GAM313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM313 RNA, herein designated GAM RNA, and which when bound by GAM313 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM313 target proteins.

[4487] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM313 gene, herein designated GAM GENE, on one or more GAM313 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4488] It is yet further appreciated that specific functions, and accordingly utilities, of GAM313 correlate with, and may be deduced from, the identity of the target genes which GAM313 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4489] Nucleotide sequences of the GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM313 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM313 are further described hereinbelow with reference to Table Table1.

[4490] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM313 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4491]

[4492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 314 (GAM314) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4493] GAM314 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM314 was detected is described hereinabove with reference to Figs. 2-8.

[4494] GAM314 gene, herein designated GAM GENE, and GAM314 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4495] GAM314 gene, herein designated GAM GENE, encodes a GAM314 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM314 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM314 precursor RNA is designated SEQ ID:4781, and is provided hereinbelow with reference to the sequence listing part.

[4496] GAM314 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4497] An enzyme complex designated DICER COMPLEX, dices the GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM314 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 33%) nucleotide sequence of GAM314 RNA is designated SEQ ID:4782, and is provided

hereinbelow with reference to the sequence listing part.

[4498] GAM314 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM314 target RNA, herein designated GAM TARGET RNA. GAM314 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4499] GAM314 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM314 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM314 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM314 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM314 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4500] The complementary binding of GAM314 RNA, herein designated GAM RNA, to target binding sites on GAM314 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM314 target RNA, herein designated GAM TARGET RNA, into GAM314 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4501] It is appreciated that GAM314 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM314 target genes. The mRNA of each one of this plurality of GAM314 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM314 RNA, herein designated GAM RNA, and which when bound by GAM314 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM314 tar-

get proteins.

[4502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM314 gene, herein designated GAM GENE, on one or more GAM314 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4503] It is yet further appreciated that specific functions, and accordingly utilities, of GAM314 correlate with, and may be deduced from, the identity of the target genes which GAM314 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4504] Nucleotide sequences of the GAM314 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM314 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM314 are further described hereinbelow with reference to Table Table1.

[4505] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM314 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4506]

[4507] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 315 (GAM315) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4508] GAM315 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM315 was detected is described hereinabove with reference to Figs. 2-8.

[4509] GAM315 gene, herein designated GAM GENE, and GAM315 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4510] GAM315 gene, herein designated GAM GENE, encodes a GAM315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM315 precursor RNA is designated SEQ ID:4798, and is provided hereinbelow with reference to the sequence listing part.

[4511] GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4512] An enzyme complex designated DICER COMPLEX, dices

the GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM315 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM315 RNA is designated SEQ ID:4799, and is provided hereinbelow with reference to the sequence listing part.

[4513] GAM315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM315 target RNA, herein designated GAM TARGET RNA. GAM315 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4514] GAM315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM315

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM315 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM315 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4515] The complementary binding of GAM315 RNA, herein designated GAM RNA, to target binding sites on GAM315 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM315 target RNA, herein designated GAM TARGET RNA, into GAM315 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4516] It is appreciated that GAM315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM315 target genes. The mRNA of each one of this plurality of GAM315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM315 RNA, herein designated GAM RNA, and which when bound by GAM315 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM315 target proteins.

[4517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM315 gene, herein designated GAM GENE, on one or more GAM315 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4518] It is yet further appreciated that specific functions, and accordingly utilities, of GAM315 correlate with, and may be deduced from, the identity of the target genes which GAM315 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4519] Nucleotide sequences of the GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM315 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM315 are further described hereinbelow with reference to Table Table1.

[4520] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM315 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4521]

[4522] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 316 (GAM316) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4523] GAM316 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM316 was detected is described hereinabove with reference to Figs. 2-8.

[4524] GAM316 gene, herein designated GAM GENE, and GAM316 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4525] GAM316 gene, herein designated GAM GENE, encodes a GAM316 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM316 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM316 precursor RNA is designated SEQ ID:4812, and is provided hereinbelow with reference to the sequence listing part.

[4526] GAM316 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM316 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4527] An enzyme complex designated DICER COMPLEX, dices the GAM316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM316 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM316 RNA is designated SEQ ID:4813, and is provided hereinbelow with reference to the sequence listing part.

[4528] GAM316 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM316 target RNA, herein designated GAM TARGET RNA. GAM316 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4529] GAM316 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM316 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM316 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM316 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM316 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[4530] The complementary binding of GAM316 RNA, herein designated GAM RNA, to target binding sites on GAM316 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM316 target RNA, herein designated GAM TARGET RNA, into GAM316 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4531] It is appreciated that GAM316 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM316 target genes. The mRNA of each one of this plurality of GAM316 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM316 RNA, herein designated GAM RNA, and which when bound by GAM316 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM316 target proteins.

[4532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM316 gene, herein designated GAM GENE, on one or

more GAM316 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM316 correlate with, and may be deduced from, the identity of the target genes which GAM316 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4534] Nucleotide sequences of the GAM316 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM316 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM316 are further de-

scribed hereinbelow with reference to Table Table1.

[4535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM316 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4536]

[4537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 317 (GAM317) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4538] GAM317 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM317 was detected is described hereinabove with reference to Figs. 2-8.

[4539] GAM317 gene, herein designated GAM GENE, and GAM317 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4540] GAM317 gene, herein designated GAM GENE, encodes a GAM317 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM317 precursor RNA is designated SEQ ID:4819, and is provided hereinbelow with reference to the sequence listing part.

[4541] GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4542] An enzyme complex designated DICER COMPLEX, dices the GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM317 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of GAM317 RNA is designated SEQ ID:4820, and is provided hereinbelow with reference to the sequence listing part.

[4543] GAM317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM317 target RNA, herein designated GAM TARGET RNA. GAM317 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4544] GAM317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM317 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM317 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM317 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4545] The complementary binding of GAM317 RNA, herein designated GAM RNA, to target binding sites on GAM317 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM317 target RNA, herein designated GAM TARGET RNA, into GAM317 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4546] It is appreciated that GAM317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM317 target genes. The mRNA of each one of this plurality of GAM317 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM317 RNA, herein designated GAM RNA, and which when bound by GAM317 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM317 target proteins.

[4547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM317 gene, herein designated GAM GENE, on one or more GAM317 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM317 correlate with, and may

be deduced from, the identity of the target genes which GAM317 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4549] Nucleotide sequences of the GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM317 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM317 are further described hereinbelow with reference to Table Table1.

[4550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM317 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4551]

[4552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 318 (GAM318) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4553] GAM318 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM318 was detected is described hereinabove with reference to Figs. 2-8.

[4554] GAM318 gene, herein designated GAM GENE, and GAM318 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4555] GAM318 gene, herein designated GAM GENE, encodes a GAM318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM318 precursor RNA is designated SEQ ID:4843, and is provided hereinbelow with reference to the sequence listing part.

[4556] GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4557] An enzyme complex designated DICER COMPLEX, dices the GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM318 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 39%) nucleotide sequence of GAM318 RNA is designated SEQ ID:4844, and is provided hereinbelow with reference to the sequence listing part.

[4558] GAM318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM318 target RNA, herein designated GAM TARGET RNA. GAM318 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4559] GAM318 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM318 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM318 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM318 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4560] The complementary binding of GAM318 RNA, herein designated GAM RNA, to target binding sites on GAM318 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM318 target RNA, herein designated GAM TARGET RNA, into GAM318 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4561] It is appreciated that GAM318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM318 target genes. The mRNA of each one of this plurality of GAM318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM318 RNA, herein designated GAM RNA, and which when bound by GAM318 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM318 target proteins.

[4562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM318 gene, herein designated GAM GENE, on one or more GAM318 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4563] It is yet further appreciated that specific functions, and accordingly utilities, of GAM318 correlate with, and may be deduced from, the identity of the target genes which GAM318 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4564] Nucleotide sequences of the GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM318 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM318 are further described hereinbelow with reference to Table Table1.

[4565] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM318 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4566]

[4567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 319 (GAM319) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4568] GAM319 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM319 was detected is described hereinabove with reference to Figs. 2-8.

[4569] GAM319 gene, herein designated GAM GENE, and GAM319 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4570] GAM319 gene, herein designated GAM GENE, encodes a GAM319 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM319 precursor RNA is desig-

nated SEQ ID:4858, and is provided hereinbelow with reference to the sequence listing part.

[4571] GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4572] An enzyme complex designated DICER COMPLEX, dices the GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM319 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM319 RNA is designated SEQ ID:4859, and is provided hereinbelow with reference to the sequence listing part.

[4573] GAM319 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM319 target RNA, herein designated GAM TARGET RNA. GAM319 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4574] GAM319 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM319 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM319 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM319 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM319

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4575] The complementary binding of GAM319 RNA, herein designated GAM RNA, to target binding sites on GAM319 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM319 target RNA, herein designated GAM TARGET RNA, into GAM319 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4576] It is appreciated that GAM319 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM319 target genes. The mRNA of each one of this plurality of GAM319 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM319 RNA, herein designated GAM RNA, and which when bound by GAM319 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM319 target proteins.

[4577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM319 gene, herein designated GAM GENE, on one or more GAM319 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM319 correlate with, and may be deduced from, the identity of the target genes which GAM319 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4579] Nucleotide sequences of the GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM319 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM319 are further described hereinbelow with reference to Table Table1.

[4580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM319 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4581]

[4582] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 320 (GAM320) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4583] GAM320 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM320 was detected is described hereinabove with reference to Figs. 2-8.

[4584] GAM320 gene, herein designated GAM GENE, and

GAM320 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4585] GAM320 gene, herein designated GAM GENE, encodes a GAM320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM320 precursor RNA is designated SEQ ID:4873, and is provided hereinbelow with reference to the sequence listing part.

[4586] GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4587] An enzyme complex designated DICER COMPLEX, dices the GAM320 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM320 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM320 RNA is designated SEQ ID:4874, and is provided hereinbelow with reference to the sequence listing part.

[4588] GAM320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM320 target RNA, herein designated GAM TARGET RNA. GAM320 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4589] GAM320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM320 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM320 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM320 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4590] The complementary binding of GAM320 RNA, herein designated GAM RNA, to target binding sites on GAM320 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM320 target RNA, herein designated GAM TARGET RNA, into GAM320 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4591] It is appreciated that GAM320 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM320 target genes. The mRNA of each one of this plurality of GAM320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM320 RNA, herein designated GAM RNA, and which when bound by GAM320 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM320 target proteins.

[4592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM320 gene, herein designated GAM GENE, on one or more GAM320 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4593] It is yet further appreciated that specific functions, and accordingly utilities, of GAM320 correlate with, and may be deduced from, the identity of the target genes which GAM320 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4594] Nucleotide sequences of the GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM320 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM320 are further described hereinbelow with reference to Table Table1.

[4595] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM320 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4596]

[4597] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 321 (GAM321) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4598] GAM321 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM321 was detected is described hereinabove with reference to Figs. 2-8.

[4599] GAM321 gene, herein designated GAM GENE, and GAM321 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4600] GAM321 gene, herein designated GAM GENE, encodes a GAM321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM321 precursor RNA is designated SEQ ID:4918, and is provided hereinbelow with reference to the sequence listing part.

[4601] GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4602] An enzyme complex designated DICER COMPLEX, dices the GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM321 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM321 RNA is designated SEQ ID:4919, and is provided hereinbelow with reference to the sequence listing part.

[4603] GAM321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM321 target RNA, herein designated GAM TARGET RNA. GAM321 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4604] GAM321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM321 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM321 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM321 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM321 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4605] The complementary binding of GAM321 RNA, herein designated GAM RNA, to target binding sites on GAM321 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM321 target RNA, herein designated GAM TARGET RNA, into GAM321 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4606] It is appreciated that GAM321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM321 target genes. The mRNA of each one of this plurality of GAM321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM321 RNA, herein designated GAM RNA, and which when bound by GAM321 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM321 target proteins.

[4607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM321 gene, herein designated GAM GENE, on one or more GAM321 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4608] It is yet further appreciated that specific functions, and accordingly utilities, of GAM321 correlate with, and may be deduced from, the identity of the target genes which GAM321 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4609] Nucleotide sequences of the GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM321 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM321 are further described hereinbelow with reference to Table Table1.

[4610] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM321 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4611]

[4612] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 322 (GAM322) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4613] GAM322 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM322 was detected is described hereinabove with reference to Figs. 2-8.

[4614] GAM322 gene, herein designated GAM GENE, and GAM322 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4615] GAM322 gene, herein designated GAM GENE, encodes a GAM322 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM322 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM322 precursor RNA is designated SEQ ID:4923, and is provided hereinbelow with reference to the sequence listing part.

[4616] GAM322 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4617] An enzyme complex designated DICER COMPLEX, dices the GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM322 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM322 RNA is designated SEQ ID:4924, and is provided hereinbelow with reference to the sequence listing part.

[4618] GAM322 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM322 target RNA, herein designated GAM TARGET RNA. GAM322 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4619] GAM322 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM322 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM322 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM322 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM322 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4620] The complementary binding of GAM322 RNA, herein designated GAM RNA, to target binding sites on GAM322 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM322 target RNA, herein designated GAM TARGET RNA, into GAM322 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4621] It is appreciated that GAM322 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM322 target genes. The mRNA of each one of this plurality of GAM322 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM322 RNA,

herein designated GAM RNA, and which when bound by GAM322 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM322 target proteins.

[4622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM322 gene, herein designated GAM GENE, on one or more GAM322 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4623] It is yet further appreciated that specific functions, and accordingly utilities, of GAM322 correlate with, and may be deduced from, the identity of the target genes which

GAM322 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4624] Nucleotide sequences of the GAM322 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM322 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM322 are further described hereinbelow with reference to Table Table1.

[4625] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM322 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4626]

[4627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 323 (GAM323) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4628] GAM323 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM323 was detected is described hereinabove with reference to Figs. 2-8.

[4629] GAM323 gene, herein designated GAM GENE, and GAM323 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4630] GAM323 gene, herein designated GAM GENE, encodes a GAM323 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM323 precursor RNA is designated SEQ ID:4942, and is provided hereinbelow with reference to the sequence listing part.

[4631] GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4632] An enzyme complex designated DICER COMPLEX, dices the GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM323 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM323 RNA is designated SEQ ID:4943, and is provided hereinbelow with reference to the sequence listing part.

[4633] GAM323 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM323 target RNA, herein designated GAM TARGET RNA.
GAM323 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4634] GAM323 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM323 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM323 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM323 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM323 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4635] The complementary binding of GAM323 RNA, herein designated GAM RNA, to target binding sites on GAM323 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM323 target RNA, herein desig-

nated GAM TARGET RNA, into GAM323 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4636] It is appreciated that GAM323 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM323 target genes. The mRNA of each one of this plurality of GAM323 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM323 RNA, herein designated GAM RNA, and which when bound by GAM323 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM323 target proteins.

[4637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM323 gene, herein designated GAM GENE, on one or more GAM323 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM323 correlate with, and may be deduced from, the identity of the target genes which GAM323 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4639] Nucleotide sequences of the GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM323 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM323 are further described hereinbelow with reference to Table Table1.

[4640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM323 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4641]

[4642] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 324 (GAM324) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4643] GAM324 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM324 was detected is described hereinabove with reference to Figs. 2-8.

[4644] GAM324 gene, herein designated GAM GENE, and GAM324 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4645] GAM324 gene, herein designated GAM GENE, encodes a GAM324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM324 precursor RNA is designated SEQ ID:4958, and is provided hereinbelow with ref-

erence to the sequence listing part.

[4646] GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4647] An enzyme complex designated DICER COMPLEX, dices the GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM324 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM324 RNA is designated SEQ ID:4959, and is provided hereinbelow with reference to the sequence listing part.

[4648] GAM324 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM324 target RNA, herein designated GAM TARGET RNA.

GAM324 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4649] GAM324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM324 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM324 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM324 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4650] The complementary binding of GAM324 RNA, herein designated GAM RNA, to target binding sites on GAM324 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM324 target RNA, herein designated GAM TARGET RNA, into GAM324 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4651] It is appreciated that GAM324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM324 target genes. The mRNA of each one of this plurality of GAM324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM324 RNA, herein designated GAM RNA, and which when bound by GAM324 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM324 target proteins.

[4652] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM324 gene, herein designated GAM GENE, on one or more GAM324 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4653] It is yet further appreciated that specific functions, and accordingly utilities, of GAM324 correlate with, and may be deduced from, the identity of the target genes which GAM324 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4654] Nucleotide sequences of the GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM324 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM324 are further described hereinbelow with reference to Table Table1.

[4655] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM324 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4656]

[4657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 325 (GAM325) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4658] GAM325 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM325 was detected is described hereinabove with reference to Figs. 2-8.

[4659] GAM325 gene, herein designated GAM GENE, and GAM325 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4660] GAM325 gene, herein designated GAM GENE, encodes a GAM325 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM325 precursor RNA is designated SEQ ID:4970, and is provided hereinbelow with reference to the sequence listing part.

[4661] GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4662] An enzyme complex designated DICER COMPLEX, dices the GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM325 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM325 RNA is designated SEQ ID:4971, and is provided hereinbelow with reference to the sequence listing part.

[4663] GAM325 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM325 target RNA, herein designated GAM TARGET RNA. GAM325 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4664] GAM325 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM325 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM325 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM325 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM325 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4665] The complementary binding of GAM325 RNA, herein designated GAM RNA, to target binding sites on GAM325 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM325 target RNA, herein designated GAM TARGET RNA, into GAM325 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4666] It is appreciated that GAM325 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM325 target genes. The mRNA of each one of this plurality of GAM325 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM325 RNA, herein designated GAM RNA, and which when bound by GAM325 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM325 target proteins.

[4667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM325 gene, herein designated GAM GENE, on one or more GAM325 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM325 correlate with, and may be deduced from, the identity of the target genes which GAM325 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4669] Nucleotide sequences of the GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM325 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM325 are further described hereinbelow with reference to Table Table1.

[4670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM325 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4671]

[4672] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

326 (GAM326) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4673] GAM326 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM326 was detected is described hereinabove with reference to Figs. 2-8.

[4674] GAM326 gene, herein designated GAM GENE, and GAM326 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4675] GAM326 gene, herein designated GAM GENE, encodes a GAM326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM326 precursor RNA is designated SEQ ID:4974, and is provided hereinbelow with reference to the sequence listing part.

[4676] GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4677] An enzyme complex designated DICER COMPLEX, dices the GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM326 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of GAM326 RNA is designated SEQ ID:4975, and is provided hereinbelow with reference to the sequence listing part.

[4678] GAM326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM326 target RNA, herein designated GAM TARGET RNA. GAM326 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4679] GAM326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM326 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM326 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM326 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4680] The complementary binding of GAM326 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM326 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM326 target RNA, herein designated GAM TARGET RNA, into GAM326 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4681] It is appreciated that GAM326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM326 target genes. The mRNA of each one of this plurality of GAM326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM326 RNA, herein designated GAM RNA, and which when bound by GAM326 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM326 target proteins.

[4682] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM326 gene, herein designated GAM GENE, on one or more GAM326 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4683] It is yet further appreciated that specific functions, and accordingly utilities, of GAM326 correlate with, and may be deduced from, the identity of the target genes which GAM326 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4684] Nucleotide sequences of the GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM326 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM326 are further described hereinbelow with reference to Table Table1.

[4685] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM326 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4686]

[4687] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 327 (GAM327) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4688] GAM327 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM327 was detected is described hereinabove with reference to Figs. 2-8.

[4689] GAM327 gene, herein designated GAM GENE, and GAM327 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4690] GAM327 gene, herein designated GAM GENE, encodes a GAM327 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM327 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM327 precursor RNA is designated SEQ ID:4979, and is provided hereinbelow with reference to the sequence listing part.

[4691] GAM327 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4692] An enzyme complex designated DICER COMPLEX, dices the GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM327 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 51%) nucleotide sequence of GAM327 RNA is designated SEQ ID:4980, and is provided hereinbelow with reference to the sequence listing part.

[4693] GAM327 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM327 target RNA, herein designated GAM TARGET RNA. GAM327 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4694] GAM327 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM327 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM327 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM327 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM327 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4695] The complementary binding of GAM327 RNA, herein designated GAM RNA, to target binding sites on GAM327 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM327 target RNA, herein designated GAM TARGET RNA, into GAM327 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4696] It is appreciated that GAM327 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM327 target genes. The mRNA of each one of this plurality of GAM327 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM327 RNA, herein designated GAM RNA, and which when bound by

GAM327 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM327 target proteins.

[4697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM327 gene, herein designated GAM GENE, on one or more GAM327 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4698] It is yet further appreciated that specific functions, and accordingly utilities, of GAM327 correlate with, and may be deduced from, the identity of the target genes which GAM327 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[4699] Nucleotide sequences of the GAM327 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM327 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM327 are further described hereinbelow with reference to Table Table1.

[4700] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM327 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4701]

[4702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 328 (GAM328) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4703] GAM328 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM328 was detected is described hereinabove with reference to Figs. 2-8.

[4704] GAM328 gene, herein designated GAM GENE, and GAM328 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4705] GAM328 gene, herein designated GAM GENE, encodes a GAM328 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM328 precursor RNA is designated SEQ ID:4987, and is provided hereinbelow with reference to the sequence listing part.

[4706] GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[4707] An enzyme complex designated DICER COMPLEX, dices the GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM328 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM328 RNA is designated SEQ ID:4988, and is provided hereinbelow with reference to the sequence listing part.

[4708] GAM328 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM328 target RNA, herein designated GAM TARGET RNA. GAM328 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4709] GAM328 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM328 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM328 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM328 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM328 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4710] The complementary binding of GAM328 RNA, herein designated GAM RNA, to target binding sites on GAM328 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM328 target RNA, herein designated GAM TARGET RNA, into GAM328 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4711] It is appreciated that GAM328 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM328 target genes. The mRNA of each one of this plurality of GAM328 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM328 RNA, herein designated GAM RNA, and which when bound by GAM328 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM328 target proteins.

[4712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM328 gene, herein designated GAM GENE, on one or more GAM328 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM328 correlate with, and may be deduced from, the identity of the target genes which GAM328 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4714] Nucleotide sequences of the GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM328 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM328 are further described hereinbelow with reference to Table Table1.

[4715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM328 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4716]

[4717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 329 (GAM329) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4718] GAM329 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM329 was detected is described hereinabove with reference to Figs. 2-8.

[4719] GAM329 gene, herein designated GAM GENE, and GAM329 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4720] GAM329 gene, herein designated GAM GENE, encodes a GAM329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM329 precursor RNA is designated SEQ ID:5001, and is provided hereinbelow with reference to the sequence listing part.

[4721] GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4722] An enzyme complex designated DICER COMPLEX, dices the GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM329 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM329 RNA is designated SEQ ID:5002, and is provided hereinbelow with reference to the sequence listing part.

[4723] GAM329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM329

target RNA, herein designated GAM TARGET RNA.

GAM329 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4724] GAM329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM329 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM329 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM329 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4725] The complementary binding of GAM329 RNA, herein designated GAM RNA, to target binding sites on GAM329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM329 target RNA, herein designated GAM TARGET RNA, into GAM329 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4726] It is appreciated that GAM329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM329 target genes. The mRNA of each one of this plurality of GAM329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM329 RNA, herein designated GAM RNA, and which when bound by GAM329 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM329 target proteins.

[4727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM329 gene, herein designated GAM GENE, on one or more GAM329 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4728] It is yet further appreciated that specific functions, and accordingly utilities, of GAM329 correlate with, and may be deduced from, the identity of the target genes which GAM329 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4729] Nucleotide sequences of the GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM329 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM329 are further described hereinbelow with reference to Table Table1.

[4730] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM329 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4731]

[4732] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 330 (GAM330) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4733] GAM330 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM330 was detected is described hereinabove with reference to Figs. 2-8.

[4734] GAM330 gene, herein designated GAM GENE, and GAM330 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4735] GAM330 gene, herein designated GAM GENE, encodes a GAM330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM330 precursor RNA is designated SEQ ID:5006, and is provided hereinbelow with reference to the sequence listing part.

[4736] GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4737] An enzyme complex designated DICER COMPLEX, dices the GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM330 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM330 RNA is designated SEQ ID:5007, and is provided hereinbelow with reference to the sequence listing part.

[4738] GAM330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM330 target RNA, herein designated GAM TARGET RNA. GAM330 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4739] GAM330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM330 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM330 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM330 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4740] The complementary binding of GAM330 RNA, herein designated GAM RNA, to target binding sites on GAM330 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM330 target RNA, herein designated GAM TARGET RNA, into GAM330 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4741] It is appreciated that GAM330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM330 target genes. The mRNA of each one of this plu-

rality of GAM330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM330 RNA, herein designated GAM RNA, and which when bound by GAM330 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM330 target proteins.

[4742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM330 gene, herein designated GAM GENE, on one or more GAM330 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4743] It is yet further appreciated that specific functions, and accordingly utilities, of GAM330 correlate with, and may be deduced from, the identity of the target genes which GAM330 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4744] Nucleotide sequences of the GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM330 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM330 are further described hereinbelow with reference to Table Table1.

[4745] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM330 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4746]

[4747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 331 (GAM331) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4748] GAM331 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM331 was detected is described hereinabove with reference to Figs. 2-8.

[4749] GAM331 gene, herein designated GAM GENE, and GAM331 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4750] GAM331 gene, herein designated GAM GENE, encodes a GAM331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM331 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM331 precursor RNA is designated SEQ ID:5078, and is provided hereinbelow with reference to the sequence listing part.

[4751] GAM331 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4752] An enzyme complex designated DICER COMPLEX, dices the GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM331 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of GAM331 RNA is designated SEQ ID:5079, and is provided hereinbelow with reference to the sequence listing part.

[4753] GAM331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM331 target RNA, herein designated GAM TARGET RNA.
GAM331 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[4754] GAM331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM331 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM331 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM331 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4755] The complementary binding of GAM331 RNA, herein designated GAM RNA, to target binding sites on GAM331 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM331 target RNA, herein designated GAM TARGET RNA, into GAM331 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4756] It is appreciated that GAM331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM331 target genes. The mRNA of each one of this plurality of GAM331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM331 RNA, herein designated GAM RNA, and which when bound by GAM331 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM331 target proteins.

[4757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM331 gene, herein designated GAM GENE, on one or more GAM331 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM331 correlate with, and may be deduced from, the identity of the target genes which GAM331 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4759] Nucleotide sequences of the GAM331 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM331 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM331 are further described hereinbelow with reference to Table Table1.

[4760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM331 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4761]

[4762] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 332 (GAM332) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4763] GAM332 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM332 was detected is described hereinabove with reference to Figs. 2-8.

[4764] GAM332 gene, herein designated GAM GENE, and GAM332 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4765] GAM332 gene, herein designated GAM GENE, encodes a GAM332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM332 precursor RNA is designated SEQ ID:5105, and is provided hereinbelow with reference to the sequence listing part.

[4766] GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4767] An enzyme complex designated DICER COMPLEX, dices the GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM332 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of

GAM332 RNA is designated SEQ ID:5106, and is provided hereinbelow with reference to the sequence listing part.

[4768] GAM332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM332 target RNA, herein designated GAM TARGET RNA. GAM332 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4769] GAM332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM332 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM332 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM332 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM332 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4770] The complementary binding of GAM332 RNA, herein designated GAM RNA, to target binding sites on GAM332 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM332 target RNA, herein designated GAM TARGET RNA, into GAM332 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4771] It is appreciated that GAM332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM332 target genes. The mRNA of each one of this plurality of GAM332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM332 RNA, herein designated GAM RNA, and which when bound by GAM332 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM332 target proteins.

[4772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM332 gene, herein designated GAM GENE, on one or more GAM332 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4773] It is yet further appreciated that specific functions, and accordingly utilities, of GAM332 correlate with, and may be deduced from, the identity of the target genes which GAM332 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4774] Nucleotide sequences of the GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM332 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM332 are further described hereinbelow with reference to Table Table1.

[4775] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM332 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4776]

[4777] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 333 (GAM333) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4778] GAM333 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM333 was detected is described hereinabove

with reference to Figs. 2-8.

[4779] GAM333 gene, herein designated GAM GENE, and GAM333 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4780] GAM333 gene, herein designated GAM GENE, encodes a GAM333 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM333 precursor RNA is designated SEQ ID:5123, and is provided hereinbelow with reference to the sequence listing part.

[4781] GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4782] An enzyme complex designated DICER COMPLEX, dices the GAM333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM333 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 26%) nucleotide sequence of GAM333 RNA is designated SEQ ID:5124, and is provided hereinbelow with reference to the sequence listing part.

[4783] GAM333 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM333 target RNA, herein designated GAM TARGET RNA. GAM333 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4784] GAM333 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM333 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM333 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM333 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM333 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4785] The complementary binding of GAM333 RNA, herein designated GAM RNA, to target binding sites on GAM333 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM333 target RNA, herein designated GAM TARGET RNA, into GAM333 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4786] It is appreciated that GAM333 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM333 target genes. The mRNA of each one of this plurality of GAM333 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM333 RNA, herein designated GAM RNA, and which when bound by GAM333 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM333 target proteins.

[4787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM333 gene, herein designated GAM GENE, on one or more GAM333 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4788] It is yet further appreciated that specific functions, and accordingly utilities, of GAM333 correlate with, and may be deduced from, the identity of the target genes which GAM333 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4789] Nucleotide sequences of the GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM333 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM333 are further described hereinbelow with reference to Table Table1.

[4790] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM333 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4791]

[4792] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 334 (GAM334) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4793] GAM334 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM334 was detected is described hereinabove with reference to Figs. 2-8.

[4794] GAM334 gene, herein designated GAM GENE, and GAM334 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4795] GAM334 gene, herein designated GAM GENE, encodes a GAM334 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM334 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM334 precursor RNA is designated SEQ ID:5135, and is provided hereinbelow with reference to the sequence listing part.

[4796] GAM334 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4797] An enzyme complex designated DICER COMPLEX, dices the GAM334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM334 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 38%) nucleotide sequence of GAM334 RNA is designated SEQ ID:5136, and is provided hereinbelow with reference to the sequence listing part.

[4798] GAM334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM334 target RNA, herein designated GAM TARGET RNA.

GAM334 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4799] GAM334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM334 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM334 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM334 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4800] The complementary binding of GAM334 RNA, herein designated GAM RNA, to target binding sites on GAM334 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM334 target RNA, herein designated GAM TARGET RNA, into GAM334 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4801] It is appreciated that GAM334 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM334 target genes. The mRNA of each one of this plurality of GAM334 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM334 RNA, herein designated GAM RNA, and which when bound by GAM334 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM334 target proteins.

[4802] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM334 gene, herein designated GAM GENE, on one or more GAM334 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4803] It is yet further appreciated that specific functions, and accordingly utilities, of GAM334 correlate with, and may be deduced from, the identity of the target genes which GAM334 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4804] Nucleotide sequences of the GAM334 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM334 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM334 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM334 are further described hereinbelow with reference to Table Table1.

[4805] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM334 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4806]

[4807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 335 (GAM335) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4808] GAM335 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM335 was detected is described hereinabove with reference to Figs. 2-8.

[4809] GAM335 gene, herein designated GAM GENE, and GAM335 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4810] GAM335 gene, herein designated GAM GENE, encodes a

GAM335 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM335 precursor RNA is designated SEQ ID:5145, and is provided hereinbelow with reference to the sequence listing part.

[4811] GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4812] An enzyme complex designated DICER COMPLEX, dices the GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM335 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM335 RNA is designated SEQ ID:5146, and is provided hereinbelow with reference to the sequence listing part.

[4813] GAM335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM335 target RNA, herein designated GAM TARGET RNA. GAM335 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4814] GAM335 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM335 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM335 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM335 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4815] The complementary binding of GAM335 RNA, herein designated GAM RNA, to target binding sites on GAM335 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM335 target RNA, herein designated GAM TARGET RNA, into GAM335 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4816] It is appreciated that GAM335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM335 target genes. The mRNA of each one of this plurality of GAM335 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM335 RNA, herein designated GAM RNA, and which when bound by GAM335 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM335 target proteins.

[4817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM335 gene, herein designated GAM GENE, on one or more GAM335 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4818] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM335 correlate with, and may be deduced from, the identity of the target genes which GAM335 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4819] Nucleotide sequences of the GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM335 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM335 are further described hereinbelow with reference to Table Table1.

[4820] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM335 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4821]

[4822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 336 (GAM336) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4823] GAM336 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM336 was detected is described hereinabove with reference to Figs. 2-8.

[4824] GAM336 gene, herein designated GAM GENE, and GAM336 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4825] GAM336 gene, herein designated GAM GENE, encodes a GAM336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM336 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336 precursor RNA is designated SEQ ID:5161, and is provided hereinbelow with reference to the sequence listing part.

[4826] GAM336 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4827] An enzyme complex designated DICER COMPLEX, dices the GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM336 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of GAM336 RNA is designated SEQ ID:5162, and is provided hereinbelow with reference to the sequence listing part.

[4828] GAM336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336 target RNA, herein designated GAM TARGET RNA.
GAM336 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4829] GAM336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM336 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM336 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4830] The complementary binding of GAM336 RNA, herein designated GAM RNA, to target binding sites on GAM336 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336 target RNA, herein designated GAM TARGET RNA, into GAM336 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4831] It is appreciated that GAM336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336 target genes. The mRNA of each one of this plurality of GAM336 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336 RNA, herein designated GAM RNA, and which when bound by GAM336 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM336 target proteins.

[4832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM336 gene, herein designated GAM GENE, on one or more GAM336 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM336 correlate with, and may be deduced from, the identity of the target genes which GAM336 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4834] Nucleotide sequences of the GAM336 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM336 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM336 are further described hereinbelow with reference to Table Table1.

[4835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM336 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4836]

[4837] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 337 (GAM337) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4838] GAM337 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM337 was detected is described hereinabove with reference to Figs. 2-8.

[4839] GAM337 gene, herein designated GAM GENE, and GAM337 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4840] GAM337 gene, herein designated GAM GENE, encodes a GAM337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM337 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM337 precursor RNA is designated SEQ ID:5176, and is provided hereinbelow with reference to the sequence listing part.

[4841] GAM337 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4842] An enzyme complex designated DICER COMPLEX, dices the GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM337 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM337 RNA is designated SEQ ID:5177, and is provided

hereinbelow with reference to the sequence listing part.

[4843] GAM337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337 target RNA, herein designated GAM TARGET RNA.
GAM337 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4844] GAM337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM337 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM337 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4845] The complementary binding of GAM337 RNA, herein designated GAM RNA, to target binding sites on GAM337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337 target RNA, herein designated GAM TARGET RNA, into GAM337 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4846] It is appreciated that GAM337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337 target genes. The mRNA of each one of this plurality of GAM337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337 RNA, herein designated GAM RNA, and which when bound by GAM337 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM337 tar-

get proteins.

[4847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM337 gene, herein designated GAM GENE, on one or more GAM337 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4848] It is yet further appreciated that specific functions, and accordingly utilities, of GAM337 correlate with, and may be deduced from, the identity of the target genes which GAM337 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4849] Nucleotide sequences of the GAM337 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM337 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM337 are further described hereinbelow with reference to Table Table1.

[4850] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM337 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4851]

[4852] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 338 (GAM338) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4853] GAM338 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM338 was detected is described hereinabove with reference to Figs. 2-8.

[4854] GAM338 gene, herein designated GAM GENE, and GAM338 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4855] GAM338 gene, herein designated GAM GENE, encodes a GAM338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM338 precursor RNA is designated SEQ ID:5197, and is provided hereinbelow with reference to the sequence listing part.

[4856] GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4857] An enzyme complex designated DICER COMPLEX, dices

the GAM338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM338 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM338 RNA is designated SEQ ID:5198, and is provided hereinbelow with reference to the sequence listing part.

[4858] GAM338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM338 target RNA, herein designated GAM TARGET RNA. GAM338 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4859] GAM338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM338

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM338 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM338 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4860] The complementary binding of GAM338 RNA, herein designated GAM RNA, to target binding sites on GAM338 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM338 target RNA, herein designated GAM TARGET RNA, into GAM338 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4861] It is appreciated that GAM338 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM338 target genes. The mRNA of each one of this plurality of GAM338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM338 RNA, herein designated GAM RNA, and which when bound by GAM338 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM338 target proteins.

[4862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM338 gene, herein designated GAM GENE, on one or more GAM338 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4863] It is yet further appreciated that specific functions, and accordingly utilities, of GAM338 correlate with, and may be deduced from, the identity of the target genes which GAM338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4864] Nucleotide sequences of the GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM338 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM338 are further described hereinbelow with reference to Table Table1.

[4865] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM338 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4866]

[4867] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 339 (GAM339) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4868] GAM339 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM339 was detected is described hereinabove with reference to Figs. 2-8.

[4869] GAM339 gene, herein designated GAM GENE, and GAM339 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4870] GAM339 gene, herein designated GAM GENE, encodes a GAM339 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM339 precursor RNA is designated SEQ ID:5213, and is provided hereinbelow with reference to the sequence listing part.

[4871] GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM339 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4872] An enzyme complex designated DICER COMPLEX, dices the GAM339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM339 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM339 RNA is designated SEQ ID:5214, and is provided hereinbelow with reference to the sequence listing part.

[4873] GAM339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM339 target RNA, herein designated GAM TARGET RNA. GAM339 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4874] GAM339 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM339 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM339 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM339 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[4875] The complementary binding of GAM339 RNA, herein designated GAM RNA, to target binding sites on GAM339 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM339 target RNA, herein designated GAM TARGET RNA, into GAM339 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4876] It is appreciated that GAM339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM339 target genes. The mRNA of each one of this plurality of GAM339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM339 RNA, herein designated GAM RNA, and which when bound by GAM339 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM339 target proteins.

[4877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM339 gene, herein designated GAM GENE, on one or

more GAM339 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM339 correlate with, and may be deduced from, the identity of the target genes which GAM339 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4879] Nucleotide sequences of the GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM339 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM339 are further de-

scribed hereinbelow with reference to Table Table1.

[4880] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM339 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4881]

[4882] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 340 (GAM340) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4883] GAM340 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM340 was detected is described hereinabove with reference to Figs. 2-8.

[4884] GAM340 gene, herein designated GAM GENE, and GAM340 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4885] GAM340 gene, herein designated GAM GENE, encodes a GAM340 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM340 precursor RNA is designated SEQ ID:5220, and is provided hereinbelow with reference to the sequence listing part.

[4886] GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4887] An enzyme complex designated DICER COMPLEX, dices the GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM340 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM340 RNA is designated SEQ ID:5221, and is provided hereinbelow with reference to the sequence listing part.

[4888] GAM340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM340 target RNA, herein designated GAM TARGET RNA. GAM340 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4889] GAM340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM340 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM340 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM340 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4890] The complementary binding of GAM340 RNA, herein designated GAM RNA, to target binding sites on GAM340 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM340 target RNA, herein designated GAM TARGET RNA, into GAM340 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4891] It is appreciated that GAM340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM340 target genes. The mRNA of each one of this plurality of GAM340 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM340 RNA, herein designated GAM RNA, and which when bound by GAM340 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM340 target proteins.

[4892] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM340 gene, herein designated GAM GENE, on one or more GAM340 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4893] It is yet further appreciated that specific functions, and accordingly utilities, of GAM340 correlate with, and may

be deduced from, the identity of the target genes which GAM340 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4894] Nucleotide sequences of the GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM340 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM340 are further described hereinbelow with reference to Table Table1.

[4895] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM340 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4896]

[4897] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 341 (GAM341) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4898] GAM341 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM341 was detected is described hereinabove with reference to Figs. 2-8.

[4899] GAM341 gene, herein designated GAM GENE, and GAM341 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4900] GAM341 gene, herein designated GAM GENE, encodes a GAM341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM341 precursor RNA is designated SEQ ID:5228, and is provided hereinbelow with reference to the sequence listing part.

[4901] GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4902] An enzyme complex designated DICER COMPLEX, dices the GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM341 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM341 RNA is designated SEQ ID:5229, and is provided hereinbelow with reference to the sequence listing part.

[4903] GAM341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM341 target RNA, herein designated GAM TARGET RNA. GAM341 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4904] GAM341 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM341 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM341 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM341 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4905] The complementary binding of GAM341 RNA, herein designated GAM RNA, to target binding sites on GAM341 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM341 target RNA, herein designated GAM TARGET RNA, into GAM341 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4906] It is appreciated that GAM341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM341 target genes. The mRNA of each one of this plurality of GAM341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM341 RNA, herein designated GAM RNA, and which when bound by GAM341 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM341 target proteins.

[4907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM341 gene, herein designated GAM GENE, on one or more GAM341 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4908] It is yet further appreciated that specific functions, and accordingly utilities, of GAM341 correlate with, and may be deduced from, the identity of the target genes which GAM341 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4909] Nucleotide sequences of the GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM341 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM341 are further described hereinbelow with reference to Table Table1.

[4910] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM341 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4911]

[4912] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 342 (GAM342) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4913] GAM342 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM342 was detected is described hereinabove with reference to Figs. 2-8.

[4914] GAM342 gene, herein designated GAM GENE, and GAM342 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4915] GAM342 gene, herein designated GAM GENE, encodes a GAM342 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM342 precursor RNA is desig-

nated SEQ ID:5248, and is provided hereinbelow with reference to the sequence listing part.

[4916] GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4917] An enzyme complex designated DICER COMPLEX, dices the GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM342 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM342 RNA is designated SEQ ID:5249, and is provided hereinbelow with reference to the sequence listing part.

[4918] GAM342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM342 target RNA, herein designated GAM TARGET RNA. GAM342 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4919] GAM342 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM342 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM342 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM342

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4920] The complementary binding of GAM342 RNA, herein designated GAM RNA, to target binding sites on GAM342 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM342 target RNA, herein designated GAM TARGET RNA, into GAM342 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4921] It is appreciated that GAM342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM342 target genes. The mRNA of each one of this plurality of GAM342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM342 RNA, herein designated GAM RNA, and which when bound by GAM342 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM342 target proteins.

[4922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM342 gene, herein designated GAM GENE, on one or more GAM342 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4923] It is yet further appreciated that specific functions, and accordingly utilities, of GAM342 correlate with, and may be deduced from, the identity of the target genes which GAM342 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4924] Nucleotide sequences of the GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM342 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM342 are further described hereinbelow with reference to Table Table1.

[4925] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM342 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4926]

[4927] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 343 (GAM343) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4928] GAM343 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM343 was detected is described hereinabove with reference to Figs. 2-8.

[4929] GAM343 gene, herein designated GAM GENE, and

GAM343 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4930] GAM343 gene, herein designated GAM GENE, encodes a GAM343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM343 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM343 precursor RNA is designated SEQ ID:5284, and is provided hereinbelow with reference to the sequence listing part.

[4931] GAM343 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4932] An enzyme complex designated DICER COMPLEX, dices the GAM343 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM343 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM343 RNA is designated SEQ ID:5285, and is provided hereinbelow with reference to the sequence listing part.

[4933] GAM343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM343 target RNA, herein designated GAM TARGET RNA. GAM343 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4934] GAM343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM343 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM343 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM343 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM343 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4935] The complementary binding of GAM343 RNA, herein designated GAM RNA, to target binding sites on GAM343 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM343 target RNA, herein designated GAM TARGET RNA, into GAM343 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4936] It is appreciated that GAM343 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM343 target genes. The mRNA of each one of this plurality of GAM343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM343 RNA, herein designated GAM RNA, and which when bound by GAM343 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM343 target proteins.

[4937] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM343 gene, herein designated GAM GENE, on one or more GAM343 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4938] It is yet further appreciated that specific functions, and accordingly utilities, of GAM343 correlate with, and may be deduced from, the identity of the target genes which GAM343 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4939] Nucleotide sequences of the GAM343 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM343 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM343 are further described hereinbelow with reference to Table Table1.

[4940] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM343 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4941]

[4942] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 344 (GAM344) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4943] GAM344 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM344 was detected is described hereinabove with reference to Figs. 2-8.

[4944] GAM344 gene, herein designated GAM GENE, and GAM344 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4945] GAM344 gene, herein designated GAM GENE, encodes a GAM344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM344 precursor RNA is designated SEQ ID:5296, and is provided hereinbelow with reference to the sequence listing part.

[4946] GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4947] An enzyme complex designated DICER COMPLEX, dices the GAM344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM344 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM344 RNA is designated SEQ ID:5297, and is provided hereinbelow with reference to the sequence listing part.

[4948] GAM344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM344 target RNA, herein designated GAM TARGET RNA. GAM344 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4949] GAM344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM344 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM344 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM344 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4950] The complementary binding of GAM344 RNA, herein designated GAM RNA, to target binding sites on GAM344 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM344 target RNA, herein designated GAM TARGET RNA, into GAM344 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4951] It is appreciated that GAM344 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM344 target genes. The mRNA of each one of this plurality of GAM344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM344 RNA, herein designated GAM RNA, and which when bound by GAM344 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM344 target proteins.

[4952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM344 gene, herein designated GAM GENE, on one or more GAM344 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4953] It is yet further appreciated that specific functions, and accordingly utilities, of GAM344 correlate with, and may be deduced from, the identity of the target genes which GAM344 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4954] Nucleotide sequences of the GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM344 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM344 are further described hereinbelow with reference to Table Table1.

[4955] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM344 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4956]

[4957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 345 (GAM345) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4958] GAM345 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM345 was detected is described hereinabove with reference to Figs. 2-8.

[4959] GAM345 gene, herein designated GAM GENE, and GAM345 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4960] GAM345 gene, herein designated GAM GENE, encodes a GAM345 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM345 precursor RNA is designated SEQ ID:5306, and is provided hereinbelow with reference to the sequence listing part.

[4961] GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4962] An enzyme complex designated DICER COMPLEX, dices the GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM345 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM345 RNA is designated SEQ ID:5307, and is provided hereinbelow with reference to the sequence listing part.

[4963] GAM345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM345 target RNA, herein designated GAM TARGET RNA. GAM345 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4964] GAM345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM345 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM345 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM345 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4965] The complementary binding of GAM345 RNA, herein designated GAM RNA, to target binding sites on GAM345 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM345 target RNA, herein designated GAM TARGET RNA, into GAM345 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4966] It is appreciated that GAM345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM345 target genes. The mRNA of each one of this plurality of GAM345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM345 RNA,

herein designated GAM RNA, and which when bound by GAM345 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM345 target proteins.

[4967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM345 gene, herein designated GAM GENE, on one or more GAM345 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4968] It is yet further appreciated that specific functions, and accordingly utilities, of GAM345 correlate with, and may be deduced from, the identity of the target genes which

GAM345 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4969] Nucleotide sequences of the GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM345 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM345 are further described hereinbelow with reference to Table Table1.

[4970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM345 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4971]

[4972] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 346 (GAM346) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4973] GAM346 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM346 was detected is described hereinabove with reference to Figs. 2-8.

[4974] GAM346 gene, herein designated GAM GENE, and GAM346 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4975] GAM346 gene, herein designated GAM GENE, encodes a GAM346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM346 precursor RNA is designated SEQ ID:5337, and is provided hereinbelow with reference to the sequence listing part.

[4976] GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4977] An enzyme complex designated DICER COMPLEX, dices the GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM346 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM346 RNA is designated SEQ ID:5338, and is provided hereinbelow with reference to the sequence listing part.

[4978] GAM346 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM346 target RNA, herein designated GAM TARGET RNA.
GAM346 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4979] GAM346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM346 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM346 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM346 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4980] The complementary binding of GAM346 RNA, herein designated GAM RNA, to target binding sites on GAM346 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM346 target RNA, herein desig-

nated GAM TARGET RNA, into GAM346 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4981] It is appreciated that GAM346 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM346 target genes. The mRNA of each one of this plurality of GAM346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM346 RNA, herein designated GAM RNA, and which when bound by GAM346 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM346 target proteins.

[4982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM346 gene, herein designated GAM GENE, on one or more GAM346 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4983] It is yet further appreciated that specific functions, and accordingly utilities, of GAM346 correlate with, and may be deduced from, the identity of the target genes which GAM346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4984] Nucleotide sequences of the GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM346 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM346 are further described hereinbelow with reference to Table Table1.

[4985] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM346 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4986]

[4987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 347 (GAM347) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4988] GAM347 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM347 was detected is described hereinabove with reference to Figs. 2-8.

[4989] GAM347 gene, herein designated GAM GENE, and GAM347 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4990] GAM347 gene, herein designated GAM GENE, encodes a GAM347 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM347 precursor RNA is designated SEQ ID:5348, and is provided hereinbelow with ref-

erence to the sequence listing part.

[4991] GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4992] An enzyme complex designated DICER COMPLEX, dices the GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM347 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM347 RNA is designated SEQ ID:5349, and is provided hereinbelow with reference to the sequence listing part.

[4993] GAM347 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM347 target RNA, herein designated GAM TARGET RNA.

GAM347 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4994] GAM347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM347 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM347 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM347 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4995] The complementary binding of GAM347 RNA, herein designated GAM RNA, to target binding sites on GAM347 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM347 target RNA, herein designated GAM TARGET RNA, into GAM347 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4996] It is appreciated that GAM347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM347 target genes. The mRNA of each one of this plurality of GAM347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM347 RNA, herein designated GAM RNA, and which when bound by GAM347 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM347 target proteins.

[4997] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM347 gene, herein designated GAM GENE, on one or more GAM347 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM347 correlate with, and may be deduced from, the identity of the target genes which GAM347 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4999] Nucleotide sequences of the GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM347 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM347 are further described hereinbelow with reference to Table Table1.

[5000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM347 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5001]

[5002] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 348 (GAM348) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5003] GAM348 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM348 was detected is described hereinabove with reference to Figs. 2-8.

[5004] GAM348 gene, herein designated GAM GENE, and GAM348 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[5005] GAM348 gene, herein designated GAM GENE, encodes a GAM348 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM348 precursor RNA is designated SEQ ID:5360, and is provided hereinbelow with reference to the sequence listing part.

[5006] GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5007] An enzyme complex designated DICER COMPLEX, dices the GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM348 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM348 RNA is designated SEQ ID:5361, and is provided hereinbelow with reference to the sequence listing part.

[5008] GAM348 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM348 target RNA, herein designated GAM TARGET RNA. GAM348 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5009] GAM348 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM348 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM348 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM348 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM348 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5010] The complementary binding of GAM348 RNA, herein designated GAM RNA, to target binding sites on GAM348 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM348 target RNA, herein designated GAM TARGET RNA, into GAM348 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5011] It is appreciated that GAM348 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM348 target genes. The mRNA of each one of this plurality of GAM348 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM348 RNA, herein designated GAM RNA, and which when bound by GAM348 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM348 target proteins.

[5012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM348 gene, herein designated GAM GENE, on one or more GAM348 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[5013] It is yet further appreciated that specific functions, and accordingly utilities, of GAM348 correlate with, and may be deduced from, the identity of the target genes which GAM348 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5014] Nucleotide sequences of the GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM348 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM348 are further described hereinbelow with reference to Table Table1.

[5015] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM348 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5016]

[5017] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

349 (GAM349) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5018] GAM349 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM349 was detected is described hereinabove with reference to Figs. 2-8.

[5019] GAM349 gene, herein designated GAM GENE, and GAM349 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5020] GAM349 gene, herein designated GAM GENE, encodes a GAM349 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM349 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM349 precursor RNA is designated SEQ ID:5370, and is provided hereinbelow with reference to the sequence listing part.

[5021] GAM349 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5022] An enzyme complex designated DICER COMPLEX, dices the GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM349 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM349 RNA is designated SEQ ID:5371, and is provided hereinbelow with reference to the sequence listing part.

[5023] GAM349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM349 target RNA, herein designated GAM TARGET RNA. GAM349 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5024] GAM349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM349 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM349 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM349 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5025] The complementary binding of GAM349 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM349 target RNA, herein designated GAM TARGET RNA, into GAM349 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5026] It is appreciated that GAM349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM349 target genes. The mRNA of each one of this plurality of GAM349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM349 RNA, herein designated GAM RNA, and which when bound by GAM349 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM349 target proteins.

[5027] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM349 gene, herein designated GAM GENE, on one or more GAM349 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5028] It is yet further appreciated that specific functions, and accordingly utilities, of GAM349 correlate with, and may be deduced from, the identity of the target genes which GAM349 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5029] Nucleotide sequences of the GAM349 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM349 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM349 are further described hereinbelow with reference to Table Table1.

[5030] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM349 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5031]

[5032] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 350 (GAM350) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5033] GAM350 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM350 was detected is described hereinabove with reference to Figs. 2-8.

[5034] GAM350 gene, herein designated GAM GENE, and GAM350 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5035] GAM350 gene, herein designated GAM GENE, encodes a GAM350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM350 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM350 precursor RNA is designated SEQ ID:5379, and is provided hereinbelow with reference to the sequence listing part.

[5036] GAM350 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5037] An enzyme complex designated DICER COMPLEX, dices the GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM350 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 66%) nucleotide sequence of GAM350 RNA is designated SEQ ID:5380, and is provided hereinbelow with reference to the sequence listing part.

[5038] GAM350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM350 target RNA, herein designated GAM TARGET RNA. GAM350 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5039] GAM350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM350 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM350 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM350 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5040] The complementary binding of GAM350 RNA, herein designated GAM RNA, to target binding sites on GAM350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM350 target RNA, herein designated GAM TARGET RNA, into GAM350 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5041] It is appreciated that GAM350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM350 target genes. The mRNA of each one of this plurality of GAM350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM350 RNA, herein designated GAM RNA, and which when bound by

GAM350 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM350 target proteins.

[5042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM350 gene, herein designated GAM GENE, on one or more GAM350 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5043] It is yet further appreciated that specific functions, and accordingly utilities, of GAM350 correlate with, and may be deduced from, the identity of the target genes which GAM350 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[5044] Nucleotide sequences of the GAM350 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM350 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM350 are further described hereinbelow with reference to Table Table1.

[5045] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM350 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5046]

[5047] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 351 (GAM351) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5048] GAM351 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM351 was detected is described hereinabove with reference to Figs. 2-8.

[5049] GAM351 gene, herein designated GAM GENE, and GAM351 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5050] GAM351 gene, herein designated GAM GENE, encodes a GAM351 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM351 precursor RNA is designated SEQ ID:5384, and is provided hereinbelow with reference to the sequence listing part.

[5051] GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[5052] An enzyme complex designated DICER COMPLEX, dices the GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM351 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM351 RNA is designated SEQ ID:5385, and is provided hereinbelow with reference to the sequence listing part.

[5053] GAM351 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM351 target RNA, herein designated GAM TARGET RNA. GAM351 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5054] GAM351 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM351 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM351 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM351 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM351 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5055] The complementary binding of GAM351 RNA, herein designated GAM RNA, to target binding sites on GAM351 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM351 target RNA, herein designated GAM TARGET RNA, into GAM351 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5056] It is appreciated that GAM351 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM351 target genes. The mRNA of each one of this plurality of GAM351 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM351 RNA, herein designated GAM RNA, and which when bound by GAM351 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM351 target proteins.

[5057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM351 gene, herein designated GAM GENE, on one or more GAM351 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5058] It is yet further appreciated that specific functions, and accordingly utilities, of GAM351 correlate with, and may be deduced from, the identity of the target genes which GAM351 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5059] Nucleotide sequences of the GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM351 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM351 are further described hereinbelow with reference to Table Table1.

[5060] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM351 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5061]

[5062] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 352 (GAM352) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5063] GAM352 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM352 was detected is described hereinabove with reference to Figs. 2-8.

[5064] GAM352 gene, herein designated GAM GENE, and GAM352 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5065] GAM352 gene, herein designated GAM GENE, encodes a GAM352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM352 precursor RNA is designated SEQ ID:5401, and is provided hereinbelow with reference to the sequence listing part.

[5066] GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5067] An enzyme complex designated DICER COMPLEX, dices the GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM352 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM352 RNA is designated SEQ ID:5402, and is provided hereinbelow with reference to the sequence listing part.

[5068] GAM352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM352

target RNA, herein designated GAM TARGET RNA.

GAM352 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5069] GAM352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM352 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM352 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM352 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM352 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5070] The complementary binding of GAM352 RNA, herein designated GAM RNA, to target binding sites on GAM352 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM352 target RNA, herein designated GAM TARGET RNA, into GAM352 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5071] It is appreciated that GAM352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM352 target genes. The mRNA of each one of this plurality of GAM352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM352 RNA, herein designated GAM RNA, and which when bound by GAM352 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM352 target proteins.

[5072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM352 gene, herein designated GAM GENE, on one or more GAM352 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5073] It is yet further appreciated that specific functions, and accordingly utilities, of GAM352 correlate with, and may be deduced from, the identity of the target genes which GAM352 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5074] Nucleotide sequences of the GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM352 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM352 are further described hereinbelow with reference to Table Table1.

[5075] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM352 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5076]

[5077] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 353 (GAM353) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5078] GAM353 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM353 was detected is described hereinabove with reference to Figs. 2-8.

[5079] GAM353 gene, herein designated GAM GENE, and GAM353 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5080] GAM353 gene, herein designated GAM GENE, encodes a GAM353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM353 precursor RNA is designated SEQ ID:5418, and is provided hereinbelow with reference to the sequence listing part.

[5081] GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5082] An enzyme complex designated DICER COMPLEX, dices the GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM353 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM353 RNA is designated SEQ ID:5419, and is provided hereinbelow with reference to the sequence listing part.

[5083] GAM353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM353 target RNA, herein designated GAM TARGET RNA. GAM353 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5084] GAM353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM353 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM353 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM353 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5085] The complementary binding of GAM353 RNA, herein designated GAM RNA, to target binding sites on GAM353 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM353 target RNA, herein designated GAM TARGET RNA, into GAM353 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5086] It is appreciated that GAM353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM353 target genes. The mRNA of each one of this plu-

rality of GAM353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM353 RNA, herein designated GAM RNA, and which when bound by GAM353 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM353 target proteins.

[5087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM353 gene, herein designated GAM GENE, on one or more GAM353 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5088] It is yet further appreciated that specific functions, and accordingly utilities, of GAM353 correlate with, and may be deduced from, the identity of the target genes which GAM353 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5089] Nucleotide sequences of the GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM353 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM353 are further described hereinbelow with reference to Table Table1.

[5090] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM353 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5091]

[5092] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 354 (GAM354) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5093] GAM354 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM354 was detected is described hereinabove with reference to Figs. 2-8.

[5094] GAM354 gene, herein designated GAM GENE, and GAM354 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5095] GAM354 gene, herein designated GAM GENE, encodes a GAM354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM354 precursor RNA is designated SEQ ID:5459, and is provided hereinbelow with reference to the sequence listing part.

[5096] GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5097] An enzyme complex designated DICER COMPLEX, dices the GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM354 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM354 RNA is designated SEQ ID:5460, and is provided hereinbelow with reference to the sequence listing part.

[5098] GAM354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM354 target RNA, herein designated GAM TARGET RNA.
GAM354 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5099] GAM354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM354 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM354 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM354 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5100] The complementary binding of GAM354 RNA, herein designated GAM RNA, to target binding sites on GAM354 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM354 target RNA, herein designated GAM TARGET RNA, into GAM354 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5101] It is appreciated that GAM354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM354 target genes. The mRNA of each one of this plurality of GAM354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM354 RNA, herein designated GAM RNA, and which when bound by GAM354 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM354 target proteins.

[5102] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM354 gene, herein designated GAM GENE, on one or more GAM354 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5103] It is yet further appreciated that specific functions, and accordingly utilities, of GAM354 correlate with, and may be deduced from, the identity of the target genes which GAM354 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5104] Nucleotide sequences of the GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM354 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM354 are further described hereinbelow with reference to Table Table1.

[5105] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM354 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5106]

[5107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 355 (GAM355) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5108] GAM355 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM355 was detected is described hereinabove with reference to Figs. 2-8.

[5109] GAM355 gene, herein designated GAM GENE, and GAM355 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5110] GAM355 gene, herein designated GAM GENE, encodes a GAM355 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM355 precursor RNA is designated SEQ ID:5469, and is provided hereinbelow with reference to the sequence listing part.

[5111] GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5112] An enzyme complex designated DICER COMPLEX, dices the GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM355 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM355 RNA is designated SEQ ID:5470, and is provided hereinbelow with reference to the sequence listing part.

[5113] GAM355 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM355

target RNA, herein designated GAM TARGET RNA.

GAM355 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5114] GAM355 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM355 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM355 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM355 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM355 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5115] The complementary binding of GAM355 RNA, herein designated GAM RNA, to target binding sites on GAM355 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM355 target RNA, herein designated GAM TARGET RNA, into GAM355 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5116] It is appreciated that GAM355 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM355 target genes. The mRNA of each one of this plurality of GAM355 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM355 RNA, herein designated GAM RNA, and which when bound by GAM355 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM355 target proteins.

[5117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM355 gene, herein designated GAM GENE, on one or more GAM355 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5118] It is yet further appreciated that specific functions, and accordingly utilities, of GAM355 correlate with, and may be deduced from, the identity of the target genes which GAM355 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5119] Nucleotide sequences of the GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM355 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM355 are further described hereinbelow with reference to Table Table1.

[5120] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM355 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5121]

[5122] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 356 (GAM356) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5123] GAM356 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM356 was detected is described hereinabove with reference to Figs. 2-8.

[5124] GAM356 gene, herein designated GAM GENE, and GAM356 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5125] GAM356 gene, herein designated GAM GENE, encodes a GAM356 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM356 precursor RNA is designated SEQ ID:5507, and is provided hereinbelow with reference to the sequence listing part.

[5126] GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5127] An enzyme complex designated DICER COMPLEX, dices the GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM356 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM356 RNA is designated SEQ ID:5508, and is provided hereinbelow with reference to the sequence listing part.

[5128] GAM356 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM356 target RNA, herein designated GAM TARGET RNA. GAM356 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5129] GAM356 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM356 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM356 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM356 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM356 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5130] The complementary binding of GAM356 RNA, herein designated GAM RNA, to target binding sites on GAM356 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM356 target RNA, herein designated GAM TARGET RNA, into GAM356 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5131] It is appreciated that GAM356 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM356 target genes. The mRNA of each one of this plu-

rality of GAM356 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM356 RNA, herein designated GAM RNA, and which when bound by GAM356 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM356 target proteins.

[5132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM356 gene, herein designated GAM GENE, on one or more GAM356 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM356 correlate with, and may be deduced from, the identity of the target genes which GAM356 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5134] Nucleotide sequences of the GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM356 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM356 are further described hereinbelow with reference to Table Table1.

[5135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM356 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5136]

[5137] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 357 (GAM357) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5138] GAM357 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM357 was detected is described hereinabove with reference to Figs. 2-8.

[5139] GAM357 gene, herein designated GAM GENE, and GAM357 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5140] GAM357 gene, herein designated GAM GENE, encodes a GAM357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM357 precursor RNA is designated SEQ ID:5514, and is provided hereinbelow with reference to the sequence listing part.

[5141] GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5142] An enzyme complex designated DICER COMPLEX, dices the GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM357 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM357 RNA is designated SEQ ID:5515, and is provided hereinbelow with reference to the sequence listing part.

[5143] GAM357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM357 target RNA, herein designated GAM TARGET RNA. GAM357 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5144] GAM357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM357 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM357 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM357 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM357 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5145] The complementary binding of GAM357 RNA, herein designated GAM RNA, to target binding sites on GAM357 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM357 target RNA, herein designated GAM TARGET RNA, into GAM357 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5146] It is appreciated that GAM357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM357 target genes. The mRNA of each one of this plurality of GAM357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM357 RNA, herein designated GAM RNA, and which when bound by GAM357 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM357 target proteins.

[5147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM357 gene, herein designated GAM GENE, on one or more GAM357 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5148] It is yet further appreciated that specific functions, and accordingly utilities, of GAM357 correlate with, and may be deduced from, the identity of the target genes which GAM357 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5149] Nucleotide sequences of the GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM357 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM357 are further described hereinbelow with reference to Table Table1.

[5150] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM357 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5151]

[5152] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 358 (GAM358) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5153] GAM358 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM358 was detected is described hereinabove with reference to Figs. 2-8.

[5154] GAM358 gene, herein designated GAM GENE, and GAM358 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5155] GAM358 gene, herein designated GAM GENE, encodes a GAM358 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM358 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM358 precursor RNA is designated SEQ ID:5522, and is provided hereinbelow with reference to the sequence listing part.

[5156] GAM358 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5157] An enzyme complex designated DICER COMPLEX, dices the GAM358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM358 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of

GAM358 RNA is designated SEQ ID:5523, and is provided hereinbelow with reference to the sequence listing part.

[5158] GAM358 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM358 target RNA, herein designated GAM TARGET RNA. GAM358 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5159] GAM358 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM358 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM358 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM358 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM358 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5160] The complementary binding of GAM358 RNA, herein designated GAM RNA, to target binding sites on GAM358 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM358 target RNA, herein designated GAM TARGET RNA, into GAM358 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5161] It is appreciated that GAM358 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM358 target genes. The mRNA of each one of this plurality of GAM358 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM358 RNA, herein designated GAM RNA, and which when bound by GAM358 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM358 target proteins.

[5162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM358 gene, herein designated GAM GENE, on one or more GAM358 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5163] It is yet further appreciated that specific functions, and accordingly utilities, of GAM358 correlate with, and may be deduced from, the identity of the target genes which GAM358 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5164] Nucleotide sequences of the GAM358 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM358 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM358 are further described hereinbelow with reference to Table Table1.

[5165] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM358 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5166]

[5167] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 359 (GAM359) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5168] GAM359 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM359 was detected is described hereinabove

with reference to Figs. 2-8.

[5169] GAM359 gene, herein designated GAM GENE, and GAM359 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5170] GAM359 gene, herein designated GAM GENE, encodes a GAM359 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM359 precursor RNA is designated SEQ ID:5541, and is provided hereinbelow with reference to the sequence listing part.

[5171] GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5172] An enzyme complex designated DICER COMPLEX, dices the GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM359 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 22%) nucleotide sequence of GAM359 RNA is designated SEQ ID:5542, and is provided hereinbelow with reference to the sequence listing part.

[5173] GAM359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM359 target RNA, herein designated GAM TARGET RNA. GAM359 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5174] GAM359 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM359 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM359 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM359 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM359 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5175] The complementary binding of GAM359 RNA, herein designated GAM RNA, to target binding sites on GAM359 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM359 target RNA, herein designated GAM TARGET RNA, into GAM359 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5176] It is appreciated that GAM359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM359 target genes. The mRNA of each one of this plurality of GAM359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM359 RNA, herein designated GAM RNA, and which when bound by GAM359 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM359 target proteins.

[5177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM359 gene, herein designated GAM GENE, on one or more GAM359 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM359 correlate with, and may be deduced from, the identity of the target genes which GAM359 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5179] Nucleotide sequences of the GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM359 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM359 are further described hereinbelow with reference to Table Table1.

[5180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM359 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5181]

[5182] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 360 (GAM360) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5183] GAM360 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM360 was detected is described hereinabove with reference to Figs. 2-8.

[5184] GAM360 gene, herein designated GAM GENE, and GAM360 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5185] GAM360 gene, herein designated GAM GENE, encodes a GAM360 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM360 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM360 precursor RNA is designated SEQ ID:5556, and is provided hereinbelow with reference to the sequence listing part.

[5186] GAM360 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5187] An enzyme complex designated DICER COMPLEX, dices the GAM360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM360 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM360 RNA is designated SEQ ID:5557, and is provided hereinbelow with reference to the sequence listing part.

[5188] GAM360 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM360 target RNA, herein designated GAM TARGET RNA.

GAM360 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5189] GAM360 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM360 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM360 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM360 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM360 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5190] The complementary binding of GAM360 RNA, herein designated GAM RNA, to target binding sites on GAM360 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM360 target RNA, herein designated GAM TARGET RNA, into GAM360 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5191] It is appreciated that GAM360 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM360 target genes. The mRNA of each one of this plurality of GAM360 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM360 RNA, herein designated GAM RNA, and which when bound by GAM360 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM360 target proteins.

[5192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM360 gene, herein designated GAM GENE, on one or more GAM360 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5193] It is yet further appreciated that specific functions, and accordingly utilities, of GAM360 correlate with, and may be deduced from, the identity of the target genes which GAM360 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5194] Nucleotide sequences of the GAM360 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM360 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM360 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM360 are further described hereinbelow with reference to Table Table1.

[5195] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM360 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5196]

[5197] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 361 (GAM361) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5198] GAM361 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM361 was detected is described hereinabove with reference to Figs. 2-8.

[5199] GAM361 gene, herein designated GAM GENE, and GAM361 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5200] GAM361 gene, herein designated GAM GENE, encodes a

GAM361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM361 precursor RNA is designated SEQ ID:5566, and is provided hereinbelow with reference to the sequence listing part.

[5201] GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5202] An enzyme complex designated DICER COMPLEX, dices the GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM361 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM361 RNA is designated SEQ ID:5567, and is provided hereinbelow with reference to the sequence listing part.

[5203] GAM361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM361 target RNA, herein designated GAM TARGET RNA. GAM361 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5204] GAM361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM361 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM361 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM361 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5205] The complementary binding of GAM361 RNA, herein designated GAM RNA, to target binding sites on GAM361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM361 target RNA, herein designated GAM TARGET RNA, into GAM361 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5206] It is appreciated that GAM361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM361 target genes. The mRNA of each one of this plurality of GAM361 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM361 RNA, herein designated GAM RNA, and which when bound by GAM361 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM361 target proteins.

[5207] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM361 gene, herein designated GAM GENE, on one or more GAM361 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5208] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM361 correlate with, and may be deduced from, the identity of the target genes which GAM361 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5209] Nucleotide sequences of the GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM361 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM361 are further described hereinbelow with reference to Table Table1.

[5210] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM361 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5211]

[5212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 362 (GAM362) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[5213] GAM362 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM362 was detected is described hereinabove with reference to Figs. 2-8.

[5214] GAM362 gene, herein designated GAM GENE, and GAM362 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5215] GAM362 gene, herein designated GAM GENE, encodes a GAM362 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM362 precursor RNA is designated SEQ ID:5577, and is provided hereinbelow with reference to the sequence listing part.

[5216] GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5217] An enzyme complex designated DICER COMPLEX, dices the GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM362 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM362 RNA is designated SEQ ID:5578, and is provided hereinbelow with reference to the sequence listing part.

[5218] GAM362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM362 target RNA, herein designated GAM TARGET RNA.
GAM362 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5219] GAM362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM362 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM362 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM362 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5220] The complementary binding of GAM362 RNA, herein designated GAM RNA, to target binding sites on GAM362 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM362 target RNA, herein designated GAM TARGET RNA, into GAM362 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5221] It is appreciated that GAM362 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM362 target genes. The mRNA of each one of this plurality of GAM362 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM362 RNA, herein designated GAM RNA, and which when bound by GAM362 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM362 target proteins.

[5222] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM362 gene, herein designated GAM GENE, on one or more GAM362 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM362 correlate with, and may be deduced from, the identity of the target genes which GAM362 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5224] Nucleotide sequences of the GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM362 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM362 are further described hereinbelow with reference to Table Table1.

[5225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM362 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5226]

[5227] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 363 (GAM363) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5228] GAM363 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM363 was detected is described hereinabove with reference to Figs. 2-8.

[5229] GAM363 gene, herein designated GAM GENE, and GAM363 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5230] GAM363 gene, herein designated GAM GENE, encodes a GAM363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM363 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM363 precursor RNA is designated SEQ ID:5609, and is provided hereinbelow with reference to the sequence listing part.

[5231] GAM363 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5232] An enzyme complex designated DICER COMPLEX, dices the GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM363 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM363 RNA is designated SEQ ID:5610, and is provided

hereinbelow with reference to the sequence listing part.

[5233] GAM363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM363 target RNA, herein designated GAM TARGET RNA.

GAM363 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5234] GAM363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM363 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM363 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM363 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5235] The complementary binding of GAM363 RNA, herein designated GAM RNA, to target binding sites on GAM363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM363 target RNA, herein designated GAM TARGET RNA, into GAM363 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5236] It is appreciated that GAM363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM363 target genes. The mRNA of each one of this plurality of GAM363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM363 RNA, herein designated GAM RNA, and which when bound by GAM363 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM363 tar-

get proteins.

[5237] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM363 gene, herein designated GAM GENE, on one or more GAM363 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5238] It is yet further appreciated that specific functions, and accordingly utilities, of GAM363 correlate with, and may be deduced from, the identity of the target genes which GAM363 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5239] Nucleotide sequences of the GAM363 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM363 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM363 are further described hereinbelow with reference to Table Table1.

[5240] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM363 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5241]

[5242] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 364 (GAM364) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5243] GAM364 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM364 was detected is described hereinabove with reference to Figs. 2-8.

[5244] GAM364 gene, herein designated GAM GENE, and GAM364 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5245] GAM364 gene, herein designated GAM GENE, encodes a GAM364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM364 precursor RNA is designated SEQ ID:5617, and is provided hereinbelow with reference to the sequence listing part.

[5246] GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5247] An enzyme complex designated DICER COMPLEX, dices

the GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM364 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM364 RNA is designated SEQ ID:5618, and is provided hereinbelow with reference to the sequence listing part.

[5248] GAM364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM364 target RNA, herein designated GAM TARGET RNA. GAM364 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5249] GAM364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM364

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM364 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM364 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5250] The complementary binding of GAM364 RNA, herein designated GAM RNA, to target binding sites on GAM364 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM364 target RNA, herein designated GAM TARGET RNA, into GAM364 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5251] It is appreciated that GAM364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM364 target genes. The mRNA of each one of this plurality of GAM364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM364 RNA, herein designated GAM RNA, and which when bound by GAM364 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM364 target proteins.

[5252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM364 gene, herein designated GAM GENE, on one or more GAM364 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5253] It is yet further appreciated that specific functions, and accordingly utilities, of GAM364 correlate with, and may be deduced from, the identity of the target genes which GAM364 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5254] Nucleotide sequences of the GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM364 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM364 are further described hereinbelow with reference to Table Table1.

[5255] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM364 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5256]

[5257] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 365 (GAM365) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5258] GAM365 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM365 was detected is described hereinabove with reference to Figs. 2-8.

[5259] GAM365 gene, herein designated GAM GENE, and GAM365 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5260] GAM365 gene, herein designated GAM GENE, encodes a GAM365 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM365 precursor RNA is designated SEQ ID:5631, and is provided hereinbelow with reference to the sequence listing part.

[5261] GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM365 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5262] An enzyme complex designated DICER COMPLEX, dices the GAM365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM365 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM365 RNA is designated SEQ ID:5632, and is provided hereinbelow with reference to the sequence listing part.

[5263] GAM365 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM365 target RNA, herein designated GAM TARGET RNA. GAM365 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5264] GAM365 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM365 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM365 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM365 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM365 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5265] The complementary binding of GAM365 RNA, herein designated GAM RNA, to target binding sites on GAM365 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM365 target RNA, herein designated GAM TARGET RNA, into GAM365 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5266] It is appreciated that GAM365 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM365 target genes. The mRNA of each one of this plurality of GAM365 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM365 RNA, herein designated GAM RNA, and which when bound by GAM365 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM365 target proteins.

[5267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM365 gene, herein designated GAM GENE, on one or

more GAM365 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5268] It is yet further appreciated that specific functions, and accordingly utilities, of GAM365 correlate with, and may be deduced from, the identity of the target genes which GAM365 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5269] Nucleotide sequences of the GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM365 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM365 are further de-

scribed hereinbelow with reference to Table Table1.

[5270] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM365 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5271]

[5272] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 366 (GAM366) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5273] GAM366 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM366 was detected is described hereinabove with reference to Figs. 2-8.

[5274] GAM366 gene, herein designated GAM GENE, and GAM366 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5275] GAM366 gene, herein designated GAM GENE, encodes a GAM366 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM366 precursor RNA is designated SEQ ID:5639, and is provided hereinbelow with reference to the sequence listing part.

[5276] GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5277] An enzyme complex designated DICER COMPLEX, dices the GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM366 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM366 RNA is designated SEQ ID:5640, and is provided hereinbelow with reference to the sequence listing part.

[5278] GAM366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM366 target RNA, herein designated GAM TARGET RNA. GAM366 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5279] GAM366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM366 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM366 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM366 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5280] The complementary binding of GAM366 RNA, herein designated GAM RNA, to target binding sites on GAM366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM366 target RNA, herein designated GAM TARGET RNA, into GAM366 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5281] It is appreciated that GAM366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM366 target genes. The mRNA of each one of this plurality of GAM366 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM366 RNA, herein designated GAM RNA, and which when bound by GAM366 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM366 target proteins.

[5282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM366 gene, herein designated GAM GENE, on one or more GAM366 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5283] It is yet further appreciated that specific functions, and accordingly utilities, of GAM366 correlate with, and may

be deduced from, the identity of the target genes which GAM366 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5284] Nucleotide sequences of the GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM366 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM366 are further described hereinbelow with reference to Table Table1.

[5285] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM366 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5286]

[5287] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 367 (GAM367) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5288] GAM367 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM367 was detected is described hereinabove with reference to Figs. 2-8.

[5289] GAM367 gene, herein designated GAM GENE, and GAM367 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5290] GAM367 gene, herein designated GAM GENE, encodes a GAM367 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM367 precursor RNA is designated SEQ ID:5660, and is provided hereinbelow with reference to the sequence listing part.

[5291] GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5292] An enzyme complex designated DICER COMPLEX, dices the GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM367 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM367 RNA is designated SEQ ID:5661, and is provided hereinbelow with reference to the sequence listing part.

[5293] GAM367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM367 target RNA, herein designated GAM TARGET RNA. GAM367 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5294] GAM367 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM367 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM367 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM367 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5295] The complementary binding of GAM367 RNA, herein designated GAM RNA, to target binding sites on GAM367 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM367 target RNA, herein designated GAM TARGET RNA, into GAM367 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5296] It is appreciated that GAM367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM367 target genes. The mRNA of each one of this plurality of GAM367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM367 RNA, herein designated GAM RNA, and which when bound by GAM367 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM367 target proteins.

[5297] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM367 gene, herein designated GAM GENE, on one or more GAM367 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5298] It is yet further appreciated that specific functions, and accordingly utilities, of GAM367 correlate with, and may be deduced from, the identity of the target genes which GAM367 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5299] Nucleotide sequences of the GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM367 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM367 are further described hereinbelow with reference to Table Table1.

[5300] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM367 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5301]

[5302] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 368 (GAM368) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5303] GAM368 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM368 was detected is described hereinabove with reference to Figs. 2-8.

[5304] GAM368 gene, herein designated GAM GENE, and GAM368 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5305] GAM368 gene, herein designated GAM GENE, encodes a GAM368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM368 precursor RNA is desig-

nated SEQ ID:5676, and is provided hereinbelow with reference to the sequence listing part.

[5306] GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5307] An enzyme complex designated DICER COMPLEX, dices the GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM368 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM368 RNA is designated SEQ ID:5677, and is provided hereinbelow with reference to the sequence listing part.

[5308] GAM368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM368 target RNA, herein designated GAM TARGET RNA. GAM368 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5309] GAM368 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM368 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM368 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM368

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5310] The complementary binding of GAM368 RNA, herein designated GAM RNA, to target binding sites on GAM368 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM368 target RNA, herein designated GAM TARGET RNA, into GAM368 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5311] It is appreciated that GAM368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM368 target genes. The mRNA of each one of this plurality of GAM368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM368 RNA, herein designated GAM RNA, and which when bound by GAM368 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM368 target proteins.

[5312] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM368 gene, herein designated GAM GENE, on one or more GAM368 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5313] It is yet further appreciated that specific functions, and accordingly utilities, of GAM368 correlate with, and may be deduced from, the identity of the target genes which GAM368 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5314] Nucleotide sequences of the GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM368 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM368 are further described hereinbelow with reference to Table Table1.

[5315] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM368 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5316]

[5317] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 369 (GAM369) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5318] GAM369 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM369 was detected is described hereinabove with reference to Figs. 2-8.

[5319] GAM369 gene, herein designated GAM GENE, and

GAM369 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5320] GAM369 gene, herein designated GAM GENE, encodes a GAM369 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM369 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM369 precursor RNA is designated SEQ ID:5703, and is provided hereinbelow with reference to the sequence listing part.

[5321] GAM369 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5322] An enzyme complex designated DICER COMPLEX, dices the GAM369 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM369 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM369 RNA is designated SEQ ID:5704, and is provided hereinbelow with reference to the sequence listing part.

[5323] GAM369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM369 target RNA, herein designated GAM TARGET RNA. GAM369 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5324] GAM369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM369 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM369 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM369 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5325] The complementary binding of GAM369 RNA, herein designated GAM RNA, to target binding sites on GAM369 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM369 target RNA, herein designated GAM TARGET RNA, into GAM369 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5326] It is appreciated that GAM369 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM369 target genes. The mRNA of each one of this plurality of GAM369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM369 RNA, herein designated GAM RNA, and which when bound by GAM369 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM369 target proteins.

[5327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM369 gene, herein designated GAM GENE, on one or more GAM369 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5328] It is yet further appreciated that specific functions, and accordingly utilities, of GAM369 correlate with, and may be deduced from, the identity of the target genes which GAM369 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5329] Nucleotide sequences of the GAM369 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM369 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM369 are further described hereinbelow with reference to Table Table1.

[5330] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM369 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5331]

[5332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 370 (GAM370) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5333] GAM370 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM370 was detected is described hereinabove with reference to Figs. 2-8.

[5334] GAM370 gene, herein designated GAM GENE, and GAM370 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5335] GAM370 gene, herein designated GAM GENE, encodes a GAM370 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM370 precursor RNA is designated SEQ ID:5719, and is provided hereinbelow with reference to the sequence listing part.

[5336] GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5337] An enzyme complex designated DICER COMPLEX, dices the GAM370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM370 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 27%) nucleotide sequence of GAM370 RNA is designated SEQ ID:5720, and is provided hereinbelow with reference to the sequence listing part.

[5338] GAM370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM370 target RNA, herein designated GAM TARGET RNA. GAM370 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5339] GAM370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM370 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM370 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM370 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5340] The complementary binding of GAM370 RNA, herein designated GAM RNA, to target binding sites on GAM370 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM370 target RNA, herein designated GAM TARGET RNA, into GAM370 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5341] It is appreciated that GAM370 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM370 target genes. The mRNA of each one of this plurality of GAM370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM370 RNA, herein designated GAM RNA, and which when bound by GAM370 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM370 target proteins.

[5342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM370 gene, herein designated GAM GENE, on one or more GAM370 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5343] It is yet further appreciated that specific functions, and accordingly utilities, of GAM370 correlate with, and may be deduced from, the identity of the target genes which GAM370 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5344] Nucleotide sequences of the GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM370 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM370 are further described hereinbelow with reference to Table Table1.

[5345] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM370 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5346]

[5347] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 371 (GAM371) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5348] GAM371 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM371 was detected is described hereinabove with reference to Figs. 2-8.

[5349] GAM371 gene, herein designated GAM GENE, and GAM371 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5350] GAM371 gene, herein designated GAM GENE, encodes a GAM371 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM371 precursor RNA is designated SEQ ID:5729, and is provided hereinbelow with reference to the sequence listing part.

[5351] GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5352] An enzyme complex designated DICER COMPLEX, dices the GAM371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM371 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM371 RNA is designated SEQ ID:5730, and is provided hereinbelow with reference to the sequence listing part.

[5353] GAM371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM371 target RNA, herein designated GAM TARGET RNA. GAM371 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5354] GAM371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM371 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM371 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM371 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5355] The complementary binding of GAM371 RNA, herein designated GAM RNA, to target binding sites on GAM371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM371 target RNA, herein designated GAM TARGET RNA, into GAM371 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5356] It is appreciated that GAM371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM371 target genes. The mRNA of each one of this plurality of GAM371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM371 RNA,

herein designated GAM RNA, and which when bound by GAM371 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM371 target proteins.

[5357] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM371 gene, herein designated GAM GENE, on one or more GAM371 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5358] It is yet further appreciated that specific functions, and accordingly utilities, of GAM371 correlate with, and may be deduced from, the identity of the target genes which

GAM371 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5359] Nucleotide sequences of the GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM371 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM371 are further described hereinbelow with reference to Table Table1.

[5360] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM371 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5361]

[5362] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 372 (GAM372) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5363] GAM372 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM372 was detected is described hereinabove with reference to Figs. 2-8.

[5364] GAM372 gene, herein designated GAM GENE, and GAM372 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5365] GAM372 gene, herein designated GAM GENE, encodes a GAM372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM372 precursor RNA is designated SEQ ID:5747, and is provided hereinbelow with reference to the sequence listing part.

[5366] GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[5367] An enzyme complex designated DICER COMPLEX, dices the GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM372 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM372 RNA is designated SEQ ID:5748, and is provided hereinbelow with reference to the sequence listing part.

[5368] GAM372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM372 target RNA, herein designated GAM TARGET RNA.
GAM372 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5369] GAM372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM372 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM372 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM372 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5370] The complementary binding of GAM372 RNA, herein designated GAM RNA, to target binding sites on GAM372 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM372 target RNA, herein desig-

nated GAM TARGET RNA, into GAM372 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5371] It is appreciated that GAM372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM372 target genes. The mRNA of each one of this plurality of GAM372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM372 RNA, herein designated GAM RNA, and which when bound by GAM372 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM372 target proteins.

[5372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM372 gene, herein designated GAM GENE, on one or more GAM372 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5373] It is yet further appreciated that specific functions, and accordingly utilities, of GAM372 correlate with, and may be deduced from, the identity of the target genes which GAM372 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5374] Nucleotide sequences of the GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM372 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM372 are further described hereinbelow with reference to Table Table1.

[5375] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM372 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[5376]

[5377] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 373 (GAM373) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5378] GAM373 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM373 was detected is described hereinabove with reference to Figs. 2-8.

[5379] GAM373 gene, herein designated GAM GENE, and GAM373 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5380] GAM373 gene, herein designated GAM GENE, encodes a GAM373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM373 precursor RNA is designated SEQ ID:5765, and is provided hereinbelow with ref-

erence to the sequence listing part.

[5381] GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5382] An enzyme complex designated DICER COMPLEX, dices the GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM373 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM373 RNA is designated SEQ ID:5766, and is provided hereinbelow with reference to the sequence listing part.

[5383] GAM373 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM373 target RNA, herein designated GAM TARGET RNA.

GAM373 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5384] GAM373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM373 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM373 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM373 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5385] The complementary binding of GAM373 RNA, herein designated GAM RNA, to target binding sites on GAM373 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM373 target RNA, herein designated GAM TARGET RNA, into GAM373 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5386] It is appreciated that GAM373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM373 target genes. The mRNA of each one of this plurality of GAM373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM373 RNA, herein designated GAM RNA, and which when bound by GAM373 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM373 target proteins.

[5387] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM373 gene, herein designated GAM GENE, on one or more GAM373 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5388] It is yet further appreciated that specific functions, and accordingly utilities, of GAM373 correlate with, and may be deduced from, the identity of the target genes which GAM373 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5389] Nucleotide sequences of the GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM373 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM373 are further described hereinbelow with reference to Table Table1.

[5390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM373 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5391]

[5392] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 374 (GAM374) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5393] GAM374 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM374 was detected is described hereinabove with reference to Figs. 2-8.

[5394] GAM374 gene, herein designated GAM GENE, and GAM374 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[5395] GAM374 gene, herein designated GAM GENE, encodes a GAM374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM374 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM374 precursor RNA is designated SEQ ID:5800, and is provided hereinbelow with reference to the sequence listing part.

[5396] GAM374 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5397] An enzyme complex designated DICER COMPLEX, dices the GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM374 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM374 RNA is designated SEQ ID:5801, and is provided hereinbelow with reference to the sequence listing part.

[5398] GAM374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM374 target RNA, herein designated GAM TARGET RNA. GAM374 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5399] GAM374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM374 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM374 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM374 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5400] The complementary binding of GAM374 RNA, herein designated GAM RNA, to target binding sites on GAM374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM374 target RNA, herein designated GAM TARGET RNA, into GAM374 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5401] It is appreciated that GAM374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM374 target genes. The mRNA of each one of this plurality of GAM374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM374 RNA, herein designated GAM RNA, and which when bound by GAM374 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM374 target proteins.

[5402] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM374 gene, herein designated GAM GENE, on one or more GAM374 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[5403] It is yet further appreciated that specific functions, and accordingly utilities, of GAM374 correlate with, and may be deduced from, the identity of the target genes which GAM374 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5404] Nucleotide sequences of the GAM374 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM374 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM374 are further described hereinbelow with reference to Table Table1.

[5405] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM374 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5406]

[5407] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

375 (GAM375) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5408] GAM375 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM375 was detected is described hereinabove with reference to Figs. 2-8.

[5409] GAM375 gene, herein designated GAM GENE, and GAM375 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5410] GAM375 gene, herein designated GAM GENE, encodes a GAM375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM375 precursor RNA is designated SEQ ID:5813, and is provided hereinbelow with reference to the sequence listing part.

[5411] GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5412] An enzyme complex designated DICER COMPLEX, dices the GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM375 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM375 RNA is designated SEQ ID:5814, and is provided hereinbelow with reference to the sequence listing part.

[5413] GAM375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM375 target RNA, herein designated GAM TARGET RNA. GAM375 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5414] GAM375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM375 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM375 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM375 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM375 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5415] The complementary binding of GAM375 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM375 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM375 target RNA, herein designated GAM TARGET RNA, into GAM375 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5416] It is appreciated that GAM375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM375 target genes. The mRNA of each one of this plurality of GAM375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM375 RNA, herein designated GAM RNA, and which when bound by GAM375 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM375 target proteins.

[5417] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM375 gene, herein designated GAM GENE, on one or more GAM375 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5418] It is yet further appreciated that specific functions, and accordingly utilities, of GAM375 correlate with, and may be deduced from, the identity of the target genes which GAM375 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5419] Nucleotide sequences of the GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM375 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM375 are further described hereinbelow with reference to Table Table1.

[5420] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM375 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5421]

[5422] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 376 (GAM376) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5423] GAM376 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM376 was detected is described hereinabove with reference to Figs. 2-8.

[5424] GAM376 gene, herein designated GAM GENE, and GAM376 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5425] GAM376 gene, herein designated GAM GENE, encodes a GAM376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM376 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM376 precursor RNA is designated SEQ ID:5837, and is provided hereinbelow with reference to the sequence listing part.

[5426] GAM376 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5427] An enzyme complex designated DICER COMPLEX, dices the GAM376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM376 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 68%) nucleotide sequence of GAM376 RNA is designated SEQ ID:5838, and is provided hereinbelow with reference to the sequence listing part.

[5428] GAM376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM376 target RNA, herein designated GAM TARGET RNA. GAM376 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5429] GAM376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM376 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM376 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM376 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5430] The complementary binding of GAM376 RNA, herein designated GAM RNA, to target binding sites on GAM376 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM376 target RNA, herein designated GAM TARGET RNA, into GAM376 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5431] It is appreciated that GAM376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM376 target genes. The mRNA of each one of this plurality of GAM376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM376 RNA, herein designated GAM RNA, and which when bound by

GAM376 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM376 target proteins.

[5432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM376 gene, herein designated GAM GENE, on one or more GAM376 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5433] It is yet further appreciated that specific functions, and accordingly utilities, of GAM376 correlate with, and may be deduced from, the identity of the target genes which GAM376 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[5434] Nucleotide sequences of the GAM376 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM376 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM376 are further described hereinbelow with reference to Table Table1.

[5435] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM376 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5436]

[5437] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 377 (GAM377) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5438] GAM377 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM377 was detected is described hereinabove with reference to Figs. 2-8.

[5439] GAM377 gene, herein designated GAM GENE, and GAM377 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5440] GAM377 gene, herein designated GAM GENE, encodes a GAM377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM377 precursor RNA is designated SEQ ID:5849, and is provided hereinbelow with reference to the sequence listing part.

[5441] GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[5442] An enzyme complex designated DICER COMPLEX, dices the GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM377 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM377 RNA is designated SEQ ID:5850, and is provided hereinbelow with reference to the sequence listing part.

[5443] GAM377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM377 target RNA, herein designated GAM TARGET RNA. GAM377 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5444] GAM377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM377 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM377 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM377 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM377 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5445] The complementary binding of GAM377 RNA, herein designated GAM RNA, to target binding sites on GAM377 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM377 target RNA, herein designated GAM TARGET RNA, into GAM377 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5446] It is appreciated that GAM377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM377 target genes. The mRNA of each one of this plurality of GAM377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM377 RNA, herein designated GAM RNA, and which when bound by GAM377 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM377 target proteins.

[5447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM377 gene, herein designated GAM GENE, on one or more GAM377 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5448] It is yet further appreciated that specific functions, and accordingly utilities, of GAM377 correlate with, and may be deduced from, the identity of the target genes which GAM377 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5449] Nucleotide sequences of the GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM377 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM377 are further described hereinbelow with reference to Table Table1.

[5450] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM377 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5451]

[5452] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 378 (GAM378) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5453] GAM378 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM378 was detected is described hereinabove with reference to Figs. 2-8.

[5454] GAM378 gene, herein designated GAM GENE, and GAM378 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5455] GAM378 gene, herein designated GAM GENE, encodes a GAM378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM378 precursor RNA is designated SEQ ID:5853, and is provided hereinbelow with reference to the sequence listing part.

[5456] GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5457] An enzyme complex designated DICER COMPLEX, dices the GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM378 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM378 RNA is designated SEQ ID:5854, and is provided hereinbelow with reference to the sequence listing part.

[5458] GAM378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM378

target RNA, herein designated GAM TARGET RNA.

GAM378 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5459] GAM378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM378 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM378 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM378 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM378 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5460] The complementary binding of GAM378 RNA, herein designated GAM RNA, to target binding sites on GAM378 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM378 target RNA, herein designated GAM TARGET RNA, into GAM378 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5461] It is appreciated that GAM378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM378 target genes. The mRNA of each one of this plurality of GAM378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM378 RNA, herein designated GAM RNA, and which when bound by GAM378 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM378 target proteins.

[5462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM378 gene, herein designated GAM GENE, on one or more GAM378 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5463] It is yet further appreciated that specific functions, and accordingly utilities, of GAM378 correlate with, and may be deduced from, the identity of the target genes which GAM378 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5464] Nucleotide sequences of the GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM378 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM378 are further described hereinbelow with reference to Table Table1.

[5465] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM378 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5466]

[5467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 379 (GAM379) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5468] GAM379 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM379 was detected is described hereinabove with reference to Figs. 2-8.

[5469] GAM379 gene, herein designated GAM GENE, and GAM379 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5470] GAM379 gene, herein designated GAM GENE, encodes a GAM379 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM379 precursor RNA is designated SEQ ID:5876, and is provided hereinbelow with reference to the sequence listing part.

[5471] GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5472] An enzyme complex designated DICER COMPLEX, dices the GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM379 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM379 RNA is designated SEQ ID:2525, and is provided hereinbelow with reference to the sequence listing part.

[5473] GAM379 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM379 target RNA, herein designated GAM TARGET RNA. GAM379 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5474] GAM379 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM379 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM379 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM379 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM379 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5475] The complementary binding of GAM379 RNA, herein designated GAM RNA, to target binding sites on GAM379 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM379 target RNA, herein designated GAM TARGET RNA, into GAM379 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5476] It is appreciated that GAM379 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM379 target genes. The mRNA of each one of this plu-

rality of GAM379 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM379 RNA, herein designated GAM RNA, and which when bound by GAM379 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM379 target proteins.

[5477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM379 gene, herein designated GAM GENE, on one or more GAM379 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM379 correlate with, and may be deduced from, the identity of the target genes which GAM379 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5479] Nucleotide sequences of the GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM379 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM379 are further described hereinbelow with reference to Table Table1.

[5480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM379 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5481]

[5482] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 380 (GAM380) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5483] GAM380 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM380 was detected is described hereinabove with reference to Figs. 2-8.

[5484] GAM380 gene, herein designated GAM GENE, and GAM380 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5485] GAM380 gene, herein designated GAM GENE, encodes a GAM380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM380 precursor RNA is designated SEQ ID:5879, and is provided hereinbelow with reference to the sequence listing part.

[5486] GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5487] An enzyme complex designated DICER COMPLEX, dices the GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM380 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 26%) nucleotide sequence of GAM380 RNA is designated SEQ ID:5880, and is provided hereinbelow with reference to the sequence listing part.

[5488] GAM380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM380 target RNA, herein designated GAM TARGET RNA.
GAM380 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5489] GAM380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM380 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM380 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM380 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5490] The complementary binding of GAM380 RNA, herein designated GAM RNA, to target binding sites on GAM380 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM380 target RNA, herein designated GAM TARGET RNA, into GAM380 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5491] It is appreciated that GAM380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM380 target genes. The mRNA of each one of this plurality of GAM380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM380 RNA, herein designated GAM RNA, and which when bound by GAM380 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM380 target proteins.

[5492] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM380 gene, herein designated GAM GENE, on one or more GAM380 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5493] It is yet further appreciated that specific functions, and accordingly utilities, of GAM380 correlate with, and may be deduced from, the identity of the target genes which GAM380 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5494] Nucleotide sequences of the GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM380 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM380 are further described hereinbelow with reference to Table Table1.

[5495] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM380 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5496]

[5497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 381 (GAM381) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5498] GAM381 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM381 was detected is described hereinabove with reference to Figs. 2-8.

[5499] GAM381 gene, herein designated GAM GENE, and GAM381 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5500] GAM381 gene, herein designated GAM GENE, encodes a GAM381 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM381 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM381 precursor RNA is designated SEQ ID:5892, and is provided hereinbelow with reference to the sequence listing part.

[5501] GAM381 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5502] An enzyme complex designated DICER COMPLEX, dices the GAM381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM381 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of

GAM381 RNA is designated SEQ ID:5893, and is provided hereinbelow with reference to the sequence listing part.

[5503] GAM381 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM381 target RNA, herein designated GAM TARGET RNA. GAM381 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5504] GAM381 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM381 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM381 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM381 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM381 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5505] The complementary binding of GAM381 RNA, herein designated GAM RNA, to target binding sites on GAM381 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM381 target RNA, herein designated GAM TARGET RNA, into GAM381 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5506] It is appreciated that GAM381 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM381 target genes. The mRNA of each one of this plurality of GAM381 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM381 RNA, herein designated GAM RNA, and which when bound by GAM381 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM381 target proteins.

[5507] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM381 gene, herein designated GAM GENE, on one or more GAM381 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM381 correlate with, and may be deduced from, the identity of the target genes which GAM381 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5509] Nucleotide sequences of the GAM381 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM381 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM381 are further described hereinbelow with reference to Table Table1.

[5510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM381 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5511]

[5512] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 382 (GAM382) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5513] GAM382 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM382 was detected is described hereinabove

with reference to Figs. 2-8.

[5514] GAM382 gene, herein designated GAM GENE, and GAM382 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5515] GAM382 gene, herein designated GAM GENE, encodes a GAM382 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM382 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM382 precursor RNA is designated SEQ ID:5913, and is provided hereinbelow with reference to the sequence listing part.

[5516] GAM382 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5517] An enzyme complex designated DICER COMPLEX, dices the GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM382 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM382 RNA is designated SEQ ID:5914, and is provided hereinbelow with reference to the sequence listing part.

[5518] GAM382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM382 target RNA, herein designated GAM TARGET RNA. GAM382 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5519] GAM382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM382 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM382 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM382 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM382 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5520] The complementary binding of GAM382 RNA, herein designated GAM RNA, to target binding sites on GAM382 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM382 target RNA, herein designated GAM TARGET RNA, into GAM382 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5521] It is appreciated that GAM382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM382 target genes. The mRNA of each one of this plurality of GAM382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM382 RNA, herein designated GAM RNA, and which when bound by GAM382 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM382 target proteins.

[5522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM382 gene, herein designated GAM GENE, on one or more GAM382 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5523] It is yet further appreciated that specific functions, and accordingly utilities, of GAM382 correlate with, and may be deduced from, the identity of the target genes which GAM382 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5524] Nucleotide sequences of the GAM382 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM382 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM382 are further described hereinbelow with reference to Table Table1.

[5525] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM382 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5526]

[5527] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 383 (GAM383) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5528] GAM383 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM383 was detected is described hereinabove with reference to Figs. 2-8.

[5529] GAM383 gene, herein designated GAM GENE, and GAM383 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5530] GAM383 gene, herein designated GAM GENE, encodes a GAM383 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM383 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM383 precursor RNA is designated SEQ ID:5924, and is provided hereinbelow with reference to the sequence listing part.

[5531] GAM383 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5532] An enzyme complex designated DICER COMPLEX, dices the GAM383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM383 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM383 RNA is designated SEQ ID:5925, and is provided hereinbelow with reference to the sequence listing part.

[5533] GAM383 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM383 target RNA, herein designated GAM TARGET RNA.

GAM383 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5534] GAM383 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM383 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM383 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM383 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM383 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5535] The complementary binding of GAM383 RNA, herein designated GAM RNA, to target binding sites on GAM383 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM383 target RNA, herein designated GAM TARGET RNA, into GAM383 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5536] It is appreciated that GAM383 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM383 target genes. The mRNA of each one of this plurality of GAM383 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM383 RNA, herein designated GAM RNA, and which when bound by GAM383 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM383 target proteins.

[5537] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM383 gene, herein designated GAM GENE, on one or more GAM383 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5538] It is yet further appreciated that specific functions, and accordingly utilities, of GAM383 correlate with, and may be deduced from, the identity of the target genes which GAM383 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5539] Nucleotide sequences of the GAM383 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM383 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM383 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM383 are further described hereinbelow with reference to Table Table1.

[5540] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM383 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5541]

[5542] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 384 (GAM384) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5543] GAM384 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM384 was detected is described hereinabove with reference to Figs. 2-8.

[5544] GAM384 gene, herein designated GAM GENE, and GAM384 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5545] GAM384 gene, herein designated GAM GENE, encodes a

GAM384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM384 precursor RNA is designated SEQ ID:5945, and is provided hereinbelow with reference to the sequence listing part.

[5546] GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5547] An enzyme complex designated DICER COMPLEX, dices the GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM384 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of GAM384 RNA is designated SEQ ID:5946, and is provided hereinbelow with reference to the sequence listing part.

[5548] GAM384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM384 target RNA, herein designated GAM TARGET RNA. GAM384 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5549] GAM384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM384 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM384 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM384 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5550] The complementary binding of GAM384 RNA, herein designated GAM RNA, to target binding sites on GAM384 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM384 target RNA, herein designated GAM TARGET RNA, into GAM384 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5551] It is appreciated that GAM384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM384 target genes. The mRNA of each one of this plurality of GAM384 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM384 RNA, herein designated GAM RNA, and which when bound by GAM384 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM384 target proteins.

[5552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM384 gene, herein designated GAM GENE, on one or more GAM384 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5553] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM384 correlate with, and may be deduced from, the identity of the target genes which GAM384 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5554] Nucleotide sequences of the GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM384 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM384 are further described hereinbelow with reference to Table Table1.

[5555] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM384 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5556]

[5557] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 385 (GAM385) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[5558] GAM385 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM385 was detected is described hereinabove with reference to Figs. 2-8.

[5559] GAM385 gene, herein designated GAM GENE, and GAM385 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5560] GAM385 gene, herein designated GAM GENE, encodes a GAM385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM385 precursor RNA is designated SEQ ID:5969, and is provided hereinbelow with reference to the sequence listing part.

[5561] GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5562] An enzyme complex designated DICER COMPLEX, dices the GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM385 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM385 RNA is designated SEQ ID:5970, and is provided hereinbelow with reference to the sequence listing part.

[5563] GAM385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM385 target RNA, herein designated GAM TARGET RNA. GAM385 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5564] GAM385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM385 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM385 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM385 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5565] The complementary binding of GAM385 RNA, herein designated GAM RNA, to target binding sites on GAM385 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM385 target RNA, herein designated GAM TARGET RNA, into GAM385 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5566] It is appreciated that GAM385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM385 target genes. The mRNA of each one of this plurality of GAM385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM385 RNA, herein designated GAM RNA, and which when bound by GAM385 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM385 target proteins.

[5567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM385 gene, herein designated GAM GENE, on one or more GAM385 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM385 correlate with, and may be deduced from, the identity of the target genes which GAM385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5569] Nucleotide sequences of the GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM385 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM385 are further described hereinbelow with reference to Table Table1.

[5570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM385 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5571]

[5572] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 386 (GAM386) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5573] GAM386 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM386 was detected is described hereinabove with reference to Figs. 2-8.

[5574] GAM386 gene, herein designated GAM GENE, and GAM386 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5575] GAM386 gene, herein designated GAM GENE, encodes a GAM386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM386 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM386 precursor RNA is designated SEQ ID:5975, and is provided hereinbelow with reference to the sequence listing part.

[5576] GAM386 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5577] An enzyme complex designated DICER COMPLEX, dices the GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM386 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM386 RNA is designated SEQ ID:5976, and is provided

hereinbelow with reference to the sequence listing part.

[5578] GAM386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM386 target RNA, herein designated GAM TARGET RNA.

GAM386 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5579] GAM386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM386 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM386 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM386 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5580] The complementary binding of GAM386 RNA, herein designated GAM RNA, to target binding sites on GAM386 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM386 target RNA, herein designated GAM TARGET RNA, into GAM386 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5581] It is appreciated that GAM386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM386 target genes. The mRNA of each one of this plurality of GAM386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM386 RNA, herein designated GAM RNA, and which when bound by GAM386 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM386 tar-

get proteins.

[5582] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM386 gene, herein designated GAM GENE, on one or more GAM386 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5583] It is yet further appreciated that specific functions, and accordingly utilities, of GAM386 correlate with, and may be deduced from, the identity of the target genes which GAM386 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5584] Nucleotide sequences of the GAM386 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM386 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM386 are further described hereinbelow with reference to Table Table1.

[5585] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM386 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5586]

[5587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 387 (GAM387) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5588] GAM387 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM387 was detected is described hereinabove with reference to Figs. 2-8.

[5589] GAM387 gene, herein designated GAM GENE, and GAM387 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5590] GAM387 gene, herein designated GAM GENE, encodes a GAM387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM387 precursor RNA is designated SEQ ID:5985, and is provided hereinbelow with reference to the sequence listing part.

[5591] GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5592] An enzyme complex designated DICER COMPLEX, dices

the GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM387 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM387 RNA is designated SEQ ID:5986, and is provided hereinbelow with reference to the sequence listing part.

[5593] GAM387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM387 target RNA, herein designated GAM TARGET RNA. GAM387 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5594] GAM387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM387

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM387 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM387 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5595] The complementary binding of GAM387 RNA, herein designated GAM RNA, to target binding sites on GAM387 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM387 target RNA, herein designated GAM TARGET RNA, into GAM387 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5596] It is appreciated that GAM387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM387 target genes. The mRNA of each one of this plurality of GAM387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM387 RNA, herein designated GAM RNA, and which when bound by GAM387 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM387 target proteins.

[5597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM387 gene, herein designated GAM GENE, on one or more GAM387 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM387 correlate with, and may be deduced from, the identity of the target genes which GAM387 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5599] Nucleotide sequences of the GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM387 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM387 are further described hereinbelow with reference to Table Table1.

[5600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM387 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5601]

[5602] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 388 (GAM388) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5603] GAM388 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM388 was detected is described hereinabove with reference to Figs. 2-8.

[5604] GAM388 gene, herein designated GAM GENE, and GAM388 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5605] GAM388 gene, herein designated GAM GENE, encodes a GAM388 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM388 precursor RNA is designated SEQ ID:6007, and is provided hereinbelow with reference to the sequence listing part.

[5606] GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM388 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5607] An enzyme complex designated DICER COMPLEX, dices the GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM388 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM388 RNA is designated SEQ ID:6008, and is provided hereinbelow with reference to the sequence listing part.

[5608] GAM388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM388 target RNA, herein designated GAM TARGET RNA. GAM388 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5609] GAM388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM388 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM388 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM388 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5610] The complementary binding of GAM388 RNA, herein designated GAM RNA, to target binding sites on GAM388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM388 target RNA, herein designated GAM TARGET RNA, into GAM388 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5611] It is appreciated that GAM388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM388 target genes. The mRNA of each one of this plurality of GAM388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM388 RNA, herein designated GAM RNA, and which when bound by GAM388 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM388 target proteins.

[5612] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM388 gene, herein designated GAM GENE, on one or

more GAM388 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5613] It is yet further appreciated that specific functions, and accordingly utilities, of GAM388 correlate with, and may be deduced from, the identity of the target genes which GAM388 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5614] Nucleotide sequences of the GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM388 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM388 are further de-

scribed hereinbelow with reference to Table Table1.

[5615] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM388 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5616]

[5617] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 389 (GAM389) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5618] GAM389 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM389 was detected is described hereinabove with reference to Figs. 2-8.

[5619] GAM389 gene, herein designated GAM GENE, and GAM389 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5620] GAM389 gene, herein designated GAM GENE, encodes a GAM389 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM389 precursor RNA is designated SEQ ID:6019, and is provided hereinbelow with reference to the sequence listing part.

[5621] GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5622] An enzyme complex designated DICER COMPLEX, dices the GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM389 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM389 RNA is designated SEQ ID:6020, and is provided hereinbelow with reference to the sequence listing part.

[5623] GAM389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM389 target RNA, herein designated GAM TARGET RNA. GAM389 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5624] GAM389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM389 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM389 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM389 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5625] The complementary binding of GAM389 RNA, herein designated GAM RNA, to target binding sites on GAM389 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM389 target RNA, herein designated GAM TARGET RNA, into GAM389 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5626] It is appreciated that GAM389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM389 target genes. The mRNA of each one of this plurality of GAM389 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM389 RNA, herein designated GAM RNA, and which when bound by GAM389 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM389 target proteins.

[5627] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM389 gene, herein designated GAM GENE, on one or more GAM389 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5628] It is yet further appreciated that specific functions, and accordingly utilities, of GAM389 correlate with, and may

be deduced from, the identity of the target genes which GAM389 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5629] Nucleotide sequences of the GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM389 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM389 are further described hereinbelow with reference to Table Table1.

[5630] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM389 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5631]

[5632] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 390 (GAM390) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5633] GAM390 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM390 was detected is described hereinabove with reference to Figs. 2-8.

[5634] GAM390 gene, herein designated GAM GENE, and GAM390 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5635] GAM390 gene, herein designated GAM GENE, encodes a GAM390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM390 precursor RNA is designated SEQ ID:6033, and is provided hereinbelow with reference to the sequence listing part.

[5636] GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5637] An enzyme complex designated DICER COMPLEX, dices the GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM390 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM390 RNA is designated SEQ ID:6034, and is provided hereinbelow with reference to the sequence listing part.

[5638] GAM390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM390 target RNA, herein designated GAM TARGET RNA. GAM390 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5639] GAM390 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM390 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM390 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM390 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM390 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5640] The complementary binding of GAM390 RNA, herein designated GAM RNA, to target binding sites on GAM390 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM390 target RNA, herein designated GAM TARGET RNA, into GAM390 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5641] It is appreciated that GAM390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM390 target genes. The mRNA of each one of this plurality of GAM390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM390 RNA, herein designated GAM RNA, and which when bound by GAM390 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM390 target proteins.

[5642] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM390 gene, herein designated GAM GENE, on one or more GAM390 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5643] It is yet further appreciated that specific functions, and accordingly utilities, of GAM390 correlate with, and may be deduced from, the identity of the target genes which GAM390 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5644] Nucleotide sequences of the GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM390 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM390 are further described hereinbelow with reference to Table Table1.

[5645] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM390 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5646]

[5647] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 391 (GAM391) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5648] GAM391 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM391 was detected is described hereinabove with reference to Figs. 2-8.

[5649] GAM391 gene, herein designated GAM GENE, and GAM391 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5650] GAM391 gene, herein designated GAM GENE, encodes a GAM391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM391 precursor RNA is desig-

nated SEQ ID:6044, and is provided hereinbelow with reference to the sequence listing part.

[5651] GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5652] An enzyme complex designated DICER COMPLEX, dices the GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM391 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of GAM391 RNA is designated SEQ ID:6045, and is provided hereinbelow with reference to the sequence listing part.

[5653] GAM391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM391 target RNA, herein designated GAM TARGET RNA. GAM391 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5654] GAM391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM391 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM391

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5655] The complementary binding of GAM391 RNA, herein designated GAM RNA, to target binding sites on GAM391 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM391 target RNA, herein designated GAM TARGET RNA, into GAM391 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5656] It is appreciated that GAM391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM391 target genes. The mRNA of each one of this plurality of GAM391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM391 RNA, herein designated GAM RNA, and which when bound by GAM391 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM391 target proteins.

[5657] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM391 gene, herein designated GAM GENE, on one or more GAM391 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5658] It is yet further appreciated that specific functions, and accordingly utilities, of GAM391 correlate with, and may be deduced from, the identity of the target genes which GAM391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5659] Nucleotide sequences of the GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM391 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM391 are further described hereinbelow with reference to Table Table1.

[5660] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM391 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5661]

[5662] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 392 (GAM392) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5663] GAM392 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM392 was detected is described hereinabove with reference to Figs. 2-8.

[5664] GAM392 gene, herein designated GAM GENE, and

GAM392 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5665] GAM392 gene, herein designated GAM GENE, encodes a GAM392 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM392 precursor RNA is designated SEQ ID:6066, and is provided hereinbelow with reference to the sequence listing part.

[5666] GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5667] An enzyme complex designated DICER COMPLEX, dices the GAM392 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM392 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of GAM392 RNA is designated SEQ ID:6067, and is provided hereinbelow with reference to the sequence listing part.

[5668] GAM392 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM392 target RNA, herein designated GAM TARGET RNA. GAM392 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5669] GAM392 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM392 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM392 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM392 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM392 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5670] The complementary binding of GAM392 RNA, herein designated GAM RNA, to target binding sites on GAM392 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM392 target RNA, herein designated GAM TARGET RNA, into GAM392 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5671] It is appreciated that GAM392 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM392 target genes. The mRNA of each one of this plurality of GAM392 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM392 RNA, herein designated GAM RNA, and which when bound by GAM392 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM392 target proteins.

[5672] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM392 gene, herein designated GAM GENE, on one or more GAM392 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5673] It is yet further appreciated that specific functions, and accordingly utilities, of GAM392 correlate with, and may be deduced from, the identity of the target genes which GAM392 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5674] Nucleotide sequences of the GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM392 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM392 are further described hereinbelow with reference to Table Table1.

[5675] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM392 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5676]

[5677] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 393 (GAM393) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5678] GAM393 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM393 was detected is described hereinabove with reference to Figs. 2-8.

[5679] GAM393 gene, herein designated GAM GENE, and GAM393 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5680] GAM393 gene, herein designated GAM GENE, encodes a GAM393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM393 precursor RNA is designated SEQ ID:6072, and is provided hereinbelow with reference to the sequence listing part.

[5681] GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5682] An enzyme complex designated DICER COMPLEX, dices the GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM393 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM393 RNA is designated SEQ ID:6073, and is provided hereinbelow with reference to the sequence listing part.

[5683] GAM393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM393 target RNA, herein designated GAM TARGET RNA. GAM393 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5684] GAM393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM393 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM393 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM393 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5685] The complementary binding of GAM393 RNA, herein designated GAM RNA, to target binding sites on GAM393 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM393 target RNA, herein designated GAM TARGET RNA, into GAM393 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5686] It is appreciated that GAM393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM393 target genes. The mRNA of each one of this plurality of GAM393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM393 RNA, herein designated GAM RNA, and which when bound by GAM393 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM393 target proteins.

[5687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM393 gene, herein designated GAM GENE, on one or more GAM393 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5688] It is yet further appreciated that specific functions, and accordingly utilities, of GAM393 correlate with, and may be deduced from, the identity of the target genes which GAM393 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5689] Nucleotide sequences of the GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM393 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM393 are further described hereinbelow with reference to Table Table1.

[5690] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM393 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5691]

[5692] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 394 (GAM394) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5693] GAM394 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM394 was detected is described hereinabove with reference to Figs. 2-8.

[5694] GAM394 gene, herein designated GAM GENE, and GAM394 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5695] GAM394 gene, herein designated GAM GENE, encodes a GAM394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM394 precursor RNA is designated SEQ ID:6089, and is provided hereinbelow with reference to the sequence listing part.

[5696] GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5697] An enzyme complex designated DICER COMPLEX, dices the GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM394 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM394 RNA is designated SEQ ID:6090, and is provided hereinbelow with reference to the sequence listing part.

[5698] GAM394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM394 target RNA, herein designated GAM TARGET RNA. GAM394 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5699] GAM394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM394 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM394 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM394 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5700] The complementary binding of GAM394 RNA, herein designated GAM RNA, to target binding sites on GAM394 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM394 target RNA, herein designated GAM TARGET RNA, into GAM394 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5701] It is appreciated that GAM394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM394 target genes. The mRNA of each one of this plurality of GAM394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM394 RNA,

herein designated GAM RNA, and which when bound by GAM394 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM394 target proteins.

[5702] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM394 gene, herein designated GAM GENE, on one or more GAM394 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5703] It is yet further appreciated that specific functions, and accordingly utilities, of GAM394 correlate with, and may be deduced from, the identity of the target genes which

GAM394 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5704] Nucleotide sequences of the GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM394 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM394 are further described hereinbelow with reference to Table Table1.

[5705] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM394 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5706]

[5707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 395 (GAM395) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5708] GAM395 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM395 was detected is described hereinabove with reference to Figs. 2-8.

[5709] GAM395 gene, herein designated GAM GENE, and GAM395 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5710] GAM395 gene, herein designated GAM GENE, encodes a GAM395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM395 precursor RNA is designated SEQ ID:6103, and is provided hereinbelow with reference to the sequence listing part.

[5711] GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[5712] An enzyme complex designated DICER COMPLEX, dices the GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM395 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM395 RNA is designated SEQ ID:6104, and is provided hereinbelow with reference to the sequence listing part.

[5713] GAM395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM395 target RNA, herein designated GAM TARGET RNA.
GAM395 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5714] GAM395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM395 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM395 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM395 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5715] The complementary binding of GAM395 RNA, herein designated GAM RNA, to target binding sites on GAM395 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM395 target RNA, herein desig-

nated GAM TARGET RNA, into GAM395 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5716] It is appreciated that GAM395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM395 target genes. The mRNA of each one of this plurality of GAM395 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM395 RNA, herein designated GAM RNA, and which when bound by GAM395 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM395 target proteins.

[5717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM395 gene, herein designated GAM GENE, on one or more GAM395 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM395 correlate with, and may be deduced from, the identity of the target genes which GAM395 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5719] Nucleotide sequences of the GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM395 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM395 are further described hereinbelow with reference to Table Table1.

[5720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM395 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[5721]

[5722] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 396 (GAM396) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5723] GAM396 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM396 was detected is described hereinabove with reference to Figs. 2-8.

[5724] GAM396 gene, herein designated GAM GENE, and GAM396 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5725] GAM396 gene, herein designated GAM GENE, encodes a GAM396 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM396 precursor RNA is designated SEQ ID:6117, and is provided hereinbelow with ref-

erence to the sequence listing part.

[5726] GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5727] An enzyme complex designated DICER COMPLEX, dices the GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM396 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM396 RNA is designated SEQ ID:6118, and is provided hereinbelow with reference to the sequence listing part.

[5728] GAM396 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM396 target RNA, herein designated GAM TARGET RNA.

GAM396 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5729] GAM396 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM396 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM396 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM396 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM396 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5730] The complementary binding of GAM396 RNA, herein designated GAM RNA, to target binding sites on GAM396 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM396 target RNA, herein designated GAM TARGET RNA, into GAM396 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5731] It is appreciated that GAM396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM396 target genes. The mRNA of each one of this plurality of GAM396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM396 RNA, herein designated GAM RNA, and which when bound by GAM396 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM396 target proteins.

[5732] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM396 gene, herein designated GAM GENE, on one or more GAM396 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5733] It is yet further appreciated that specific functions, and accordingly utilities, of GAM396 correlate with, and may be deduced from, the identity of the target genes which GAM396 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5734] Nucleotide sequences of the GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM396 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM396 are further described hereinbelow with reference to Table Table1.

[5735] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM396 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5736]

[5737] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 397 (GAM397) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5738] GAM397 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM397 was detected is described hereinabove with reference to Figs. 2-8.

[5739] GAM397 gene, herein designated GAM GENE, and GAM397 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[5740] GAM397 gene, herein designated GAM GENE, encodes a GAM397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM397 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM397 precursor RNA is designated SEQ ID:6135, and is provided hereinbelow with reference to the sequence listing part.

[5741] GAM397 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5742] An enzyme complex designated DICER COMPLEX, dices the GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM397 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of GAM397 RNA is designated SEQ ID:6136, and is provided hereinbelow with reference to the sequence listing part.

[5743] GAM397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM397 target RNA, herein designated GAM TARGET RNA. GAM397 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5744] GAM397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM397 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM397 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM397 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM397 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5745] The complementary binding of GAM397 RNA, herein designated GAM RNA, to target binding sites on GAM397 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM397 target RNA, herein designated GAM TARGET RNA, into GAM397 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5746] It is appreciated that GAM397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM397 target genes. The mRNA of each one of this plurality of GAM397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM397 RNA, herein designated GAM RNA, and which when bound by GAM397 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM397 target proteins.

[5747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM397 gene, herein designated GAM GENE, on one or more GAM397 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[5748] It is yet further appreciated that specific functions, and accordingly utilities, of GAM397 correlate with, and may be deduced from, the identity of the target genes which GAM397 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5749] Nucleotide sequences of the GAM397 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM397 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM397 are further described hereinbelow with reference to Table Table1.

[5750] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM397 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5751]

[5752] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

398 (GAM398) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5753] GAM398 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM398 was detected is described hereinabove with reference to Figs. 2-8.

[5754] GAM398 gene, herein designated GAM GENE, and GAM398 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5755] GAM398 gene, herein designated GAM GENE, encodes a GAM398 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM398 precursor RNA is designated SEQ ID:6161, and is provided hereinbelow with reference to the sequence listing part.

[5756] GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5757] An enzyme complex designated DICER COMPLEX, dices the GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM398 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM398 RNA is designated SEQ ID:6162, and is provided hereinbelow with reference to the sequence listing part.

[5758] GAM398 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM398 target RNA, herein designated GAM TARGET RNA. GAM398 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5759] GAM398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM398 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM398 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM398 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5760] The complementary binding of GAM398 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM398 target RNA, herein designated GAM TARGET RNA, into GAM398 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5761] It is appreciated that GAM398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM398 target genes. The mRNA of each one of this plurality of GAM398 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM398 RNA, herein designated GAM RNA, and which when bound by GAM398 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM398 target proteins.

[5762] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM398 gene, herein designated GAM GENE, on one or more GAM398 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5763] It is yet further appreciated that specific functions, and accordingly utilities, of GAM398 correlate with, and may be deduced from, the identity of the target genes which GAM398 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5764] Nucleotide sequences of the GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM398 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM398 are further described hereinbelow with reference to Table Table1.

[5765] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM398 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5766]

[5767] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 399 (GAM399) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5768] GAM399 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM399 was detected is described hereinabove with reference to Figs. 2-8.

[5769] GAM399 gene, herein designated GAM GENE, and GAM399 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5770] GAM399 gene, herein designated GAM GENE, encodes a GAM399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM399 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM399 precursor RNA is designated SEQ ID:6189, and is provided hereinbelow with reference to the sequence listing part.

[5771] GAM399 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5772] An enzyme complex designated DICER COMPLEX, dices the GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM399 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 58%) nucleotide sequence of GAM399 RNA is designated SEQ ID:6190, and is provided hereinbelow with reference to the sequence listing part.

[5773] GAM399 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM399 target RNA, herein designated GAM TARGET RNA. GAM399 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5774] GAM399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM399 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM399 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM399 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5775] The complementary binding of GAM399 RNA, herein designated GAM RNA, to target binding sites on GAM399 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM399 target RNA, herein designated GAM TARGET RNA, into GAM399 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5776] It is appreciated that GAM399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM399 target genes. The mRNA of each one of this plurality of GAM399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM399 RNA, herein designated GAM RNA, and which when bound by

GAM399 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM399 target proteins.

[5777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM399 gene, herein designated GAM GENE, on one or more GAM399 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5778] It is yet further appreciated that specific functions, and accordingly utilities, of GAM399 correlate with, and may be deduced from, the identity of the target genes which GAM399 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[5779] Nucleotide sequences of the GAM399 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM399 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM399 are further described hereinbelow with reference to Table Table1.

[5780] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM399 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5781]

[5782] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 400 (GAM400) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5783] GAM400 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM400 was detected is described hereinabove with reference to Figs. 2-8.

[5784] GAM400 gene, herein designated GAM GENE, and GAM400 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5785] GAM400 gene, herein designated GAM GENE, encodes a GAM400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM400 precursor RNA is designated SEQ ID:6197, and is provided hereinbelow with reference to the sequence listing part.

[5786] GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[5787] An enzyme complex designated DICER COMPLEX, dices the GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM400 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM400 RNA is designated SEQ ID:6198, and is provided hereinbelow with reference to the sequence listing part.

[5788] GAM400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM400 target RNA, herein designated GAM TARGET RNA. GAM400 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5789] GAM400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM400 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM400 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM400 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM400 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5790] The complementary binding of GAM400 RNA, herein designated GAM RNA, to target binding sites on GAM400 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM400 target RNA, herein designated GAM TARGET RNA, into GAM400 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5791] It is appreciated that GAM400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM400 target genes. The mRNA of each one of this plurality of GAM400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM400 RNA, herein designated GAM RNA, and which when bound by GAM400 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM400 target proteins.

[5792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM400 gene, herein designated GAM GENE, on one or more GAM400 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5793] It is yet further appreciated that specific functions, and accordingly utilities, of GAM400 correlate with, and may be deduced from, the identity of the target genes which GAM400 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5794] Nucleotide sequences of the GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM400 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM400 are further described hereinbelow with reference to Table Table1.

[5795] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM400 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5796]

[5797] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 401 (GAM401) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5798] GAM401 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM401 was detected is described hereinabove with reference to Figs. 2-8.

[5799] GAM401 gene, herein designated GAM GENE, and GAM401 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5800] GAM401 gene, herein designated GAM GENE, encodes a GAM401 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM401 precursor RNA is designated SEQ ID:6201, and is provided hereinbelow with reference to the sequence listing part.

[5801] GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5802] An enzyme complex designated DICER COMPLEX, dices the GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM401 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM401 RNA is designated SEQ ID:6202, and is provided hereinbelow with reference to the sequence listing part.

[5803] GAM401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM401

target RNA, herein designated GAM TARGET RNA.

GAM401 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5804] GAM401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM401 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM401 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM401 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5805] The complementary binding of GAM401 RNA, herein designated GAM RNA, to target binding sites on GAM401 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM401 target RNA, herein designated GAM TARGET RNA, into GAM401 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5806] It is appreciated that GAM401 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM401 target genes. The mRNA of each one of this plurality of GAM401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM401 RNA, herein designated GAM RNA, and which when bound by GAM401 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM401 target proteins.

[5807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM401 gene, herein designated GAM GENE, on one or more GAM401 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5808] It is yet further appreciated that specific functions, and accordingly utilities, of GAM401 correlate with, and may be deduced from, the identity of the target genes which GAM401 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5809] Nucleotide sequences of the GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM401 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM401 are further described hereinbelow with reference to Table Table1.

[5810] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM401 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5811]

[5812] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 402 (GAM402) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5813] GAM402 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM402 was detected is described hereinabove with reference to Figs. 2-8.

[5814] GAM402 gene, herein designated GAM GENE, and GAM402 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5815] GAM402 gene, herein designated GAM GENE, encodes a GAM402 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM402 precursor RNA is designated SEQ ID:6210, and is provided hereinbelow with reference to the sequence listing part.

[5816] GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5817] An enzyme complex designated DICER COMPLEX, dices the GAM402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM402 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM402 RNA is designated SEQ ID:6211, and is provided hereinbelow with reference to the sequence listing part.

[5818] GAM402 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM402 target RNA, herein designated GAM TARGET RNA. GAM402 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5819] GAM402 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM402 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM402 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM402 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM402 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5820] The complementary binding of GAM402 RNA, herein designated GAM RNA, to target binding sites on GAM402 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM402 target RNA, herein designated GAM TARGET RNA, into GAM402 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5821] It is appreciated that GAM402 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM402 target genes. The mRNA of each one of this plu-

rality of GAM402 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM402 RNA, herein designated GAM RNA, and which when bound by GAM402 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM402 target proteins.

[5822] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM402 gene, herein designated GAM GENE, on one or more GAM402 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5823] It is yet further appreciated that specific functions, and accordingly utilities, of GAM402 correlate with, and may be deduced from, the identity of the target genes which GAM402 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5824] Nucleotide sequences of the GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM402 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM402 are further described hereinbelow with reference to Table Table1.

[5825] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM402 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5826]

[5827] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 403 (GAM403) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5828] GAM403 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM403 was detected is described hereinabove with reference to Figs. 2-8.

[5829] GAM403 gene, herein designated GAM GENE, and GAM403 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5830] GAM403 gene, herein designated GAM GENE, encodes a GAM403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM403 precursor RNA is designated SEQ ID:6262, and is provided hereinbelow with reference to the sequence listing part.

[5831] GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5832] An enzyme complex designated DICER COMPLEX, dices the GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM403 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 39%) nucleotide sequence of GAM403 RNA is designated SEQ ID:6263, and is provided hereinbelow with reference to the sequence listing part.

[5833] GAM403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM403 target RNA, herein designated GAM TARGET RNA.
GAM403 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5834] GAM403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM403 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM403 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM403 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5835] The complementary binding of GAM403 RNA, herein designated GAM RNA, to target binding sites on GAM403 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM403 target RNA, herein designated GAM TARGET RNA, into GAM403 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5836] It is appreciated that GAM403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM403 target genes. The mRNA of each one of this plurality of GAM403 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM403 RNA, herein designated GAM RNA, and which when bound by GAM403 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM403 target proteins.

[5837] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM403 gene, herein designated GAM GENE, on one or more GAM403 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5838] It is yet further appreciated that specific functions, and accordingly utilities, of GAM403 correlate with, and may be deduced from, the identity of the target genes which GAM403 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5839] Nucleotide sequences of the GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM403 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM403 are further described hereinbelow with reference to Table Table1.

[5840] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM403 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5841]

[5842] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 404 (GAM404) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5843] GAM404 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM404 was detected is described hereinabove with reference to Figs. 2-8.

[5844] GAM404 gene, herein designated GAM GENE, and GAM404 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5845] GAM404 gene, herein designated GAM GENE, encodes a GAM404 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM404 precursor RNA is designated SEQ ID:6289, and is provided hereinbelow with reference to the sequence listing part.

[5846] GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5847] An enzyme complex designated DICER COMPLEX, dices the GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM404 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of

GAM404 RNA is designated SEQ ID:6290, and is provided hereinbelow with reference to the sequence listing part.

[5848] GAM404 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM404 target RNA, herein designated GAM TARGET RNA. GAM404 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5849] GAM404 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM404 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM404 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM404 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM404 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5850] The complementary binding of GAM404 RNA, herein designated GAM RNA, to target binding sites on GAM404 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM404 target RNA, herein designated GAM TARGET RNA, into GAM404 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5851] It is appreciated that GAM404 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM404 target genes. The mRNA of each one of this plurality of GAM404 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM404 RNA, herein designated GAM RNA, and which when bound by GAM404 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM404 target proteins.

[5852] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM404 gene, herein designated GAM GENE, on one or more GAM404 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5853] It is yet further appreciated that specific functions, and accordingly utilities, of GAM404 correlate with, and may be deduced from, the identity of the target genes which GAM404 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5854] Nucleotide sequences of the GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM404 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM404 are further described hereinbelow with reference to Table Table1.

[5855] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM404 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5856]

[5857] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 405 (GAM405) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5858] GAM405 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM405 was detected is described hereinabove

with reference to Figs. 2-8.

[5859] GAM405 gene, herein designated GAM GENE, and GAM405 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5860] GAM405 gene, herein designated GAM GENE, encodes a GAM405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM405 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM405 precursor RNA is designated SEQ ID:6304, and is provided hereinbelow with reference to the sequence listing part.

[5861] GAM405 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5862] An enzyme complex designated DICER COMPLEX, dices the GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM405 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 22%) nucleotide sequence of GAM405 RNA is designated SEQ ID:6305, and is provided hereinbelow with reference to the sequence listing part.

[5863] GAM405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM405 target RNA, herein designated GAM TARGET RNA. GAM405 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5864] GAM405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM405 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM405 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM405 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM405 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5865] The complementary binding of GAM405 RNA, herein designated GAM RNA, to target binding sites on GAM405 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM405 target RNA, herein designated GAM TARGET RNA, into GAM405 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5866] It is appreciated that GAM405 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM405 target genes. The mRNA of each one of this plurality of GAM405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM405 RNA, herein designated GAM RNA, and which when bound by GAM405 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM405 target proteins.

[5867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM405 gene, herein designated GAM GENE, on one or more GAM405 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM405 correlate with, and may be deduced from, the identity of the target genes which GAM405 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5869] Nucleotide sequences of the GAM405 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM405 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM405 are further described hereinbelow with reference to Table Table1.

[5870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM405 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5871]

[5872] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 406 (GAM406) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5873] GAM406 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM406 was detected is described hereinabove with reference to Figs. 2-8.

[5874] GAM406 gene, herein designated GAM GENE, and GAM406 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5875] GAM406 gene, herein designated GAM GENE, encodes a GAM406 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM406 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM406 precursor RNA is designated SEQ ID:6311, and is provided hereinbelow with reference to the sequence listing part.

[5876] GAM406 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5877] An enzyme complex designated DICER COMPLEX, dices the GAM406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM406 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM406 RNA is designated SEQ ID:6312, and is provided hereinbelow with reference to the sequence listing part.

[5878] GAM406 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM406 target RNA, herein designated GAM TARGET RNA.

GAM406 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5879] GAM406 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM406 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM406 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM406 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM406 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5880] The complementary binding of GAM406 RNA, herein designated GAM RNA, to target binding sites on GAM406 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM406 target RNA, herein designated GAM TARGET RNA, into GAM406 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5881] It is appreciated that GAM406 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM406 target genes. The mRNA of each one of this plurality of GAM406 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM406 RNA, herein designated GAM RNA, and which when bound by GAM406 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM406 target proteins.

[5882] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM406 gene, herein designated GAM GENE, on one or more GAM406 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5883] It is yet further appreciated that specific functions, and accordingly utilities, of GAM406 correlate with, and may be deduced from, the identity of the target genes which GAM406 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5884] Nucleotide sequences of the GAM406 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM406 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM406 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM406 are further described hereinbelow with reference to Table Table1.

[5885] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM406 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5886]

[5887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 407 (GAM407) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5888] GAM407 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM407 was detected is described hereinabove with reference to Figs. 2-8.

[5889] GAM407 gene, herein designated GAM GENE, and GAM407 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5890] GAM407 gene, herein designated GAM GENE, encodes a

GAM407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM407 precursor RNA is designated SEQ ID:6329, and is provided hereinbelow with reference to the sequence listing part.

[5891] GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5892] An enzyme complex designated DICER COMPLEX, dices the GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM407 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM407 RNA is designated SEQ ID:6330, and is provided hereinbelow with reference to the sequence listing part.

[5893] GAM407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM407 target RNA, herein designated GAM TARGET RNA. GAM407 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5894] GAM407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM407 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM407 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM407 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5895] The complementary binding of GAM407 RNA, herein designated GAM RNA, to target binding sites on GAM407 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM407 target RNA, herein designated GAM TARGET RNA, into GAM407 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5896] It is appreciated that GAM407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM407 target genes. The mRNA of each one of this plurality of GAM407 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM407 RNA, herein designated GAM RNA, and which when bound by GAM407 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM407 target proteins.

[5897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM407 gene, herein designated GAM GENE, on one or more GAM407 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5898] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM407 correlate with, and may be deduced from, the identity of the target genes which GAM407 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5899] Nucleotide sequences of the GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM407 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM407 are further described hereinbelow with reference to Table Table1.

[5900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM407 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5901]

[5902] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 408 (GAM408) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[5903] GAM408 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM408 was detected is described hereinabove with reference to Figs. 2-8.

[5904] GAM408 gene, herein designated GAM GENE, and GAM408 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5905] GAM408 gene, herein designated GAM GENE, encodes a GAM408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM408 precursor RNA is designated SEQ ID:6357, and is provided hereinbelow with reference to the sequence listing part.

[5906] GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5907] An enzyme complex designated DICER COMPLEX, dices the GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM408 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM408 RNA is designated SEQ ID:6358, and is provided hereinbelow with reference to the sequence listing part.

[5908] GAM408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM408 target RNA, herein designated GAM TARGET RNA. GAM408 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5909] GAM408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM408 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM408 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM408 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5910] The complementary binding of GAM408 RNA, herein designated GAM RNA, to target binding sites on GAM408 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM408 target RNA, herein designated GAM TARGET RNA, into GAM408 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5911] It is appreciated that GAM408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM408 target genes. The mRNA of each one of this plurality of GAM408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM408 RNA, herein designated GAM RNA, and which when bound by GAM408 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM408 target proteins.

[5912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM408 gene, herein designated GAM GENE, on one or more GAM408 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5913] It is yet further appreciated that specific functions, and accordingly utilities, of GAM408 correlate with, and may be deduced from, the identity of the target genes which GAM408 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5914] Nucleotide sequences of the GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM408 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM408 are further described hereinbelow with reference to Table Table1.

[5915] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM408 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5916]

[5917] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 409 (GAM409) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5918] GAM409 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM409 was detected is described hereinabove with reference to Figs. 2-8.

[5919] GAM409 gene, herein designated GAM GENE, and GAM409 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5920] GAM409 gene, herein designated GAM GENE, encodes a GAM409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM409 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM409 precursor RNA is designated SEQ ID:6372, and is provided hereinbelow with reference to the sequence listing part.

[5921] GAM409 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5922] An enzyme complex designated DICER COMPLEX, dices the GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM409 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM409 RNA is designated SEQ ID:6373, and is provided

hereinbelow with reference to the sequence listing part.

[5923] GAM409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM409 target RNA, herein designated GAM TARGET RNA.
GAM409 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5924] GAM409 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM409 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM409 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM409 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5925] The complementary binding of GAM409 RNA, herein designated GAM RNA, to target binding sites on GAM409 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM409 target RNA, herein designated GAM TARGET RNA, into GAM409 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5926] It is appreciated that GAM409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM409 target genes. The mRNA of each one of this plurality of GAM409 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM409 RNA, herein designated GAM RNA, and which when bound by GAM409 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM409 tar-

get proteins.

[5927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM409 gene, herein designated GAM GENE, on one or more GAM409 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5928] It is yet further appreciated that specific functions, and accordingly utilities, of GAM409 correlate with, and may be deduced from, the identity of the target genes which GAM409 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5929] Nucleotide sequences of the GAM409 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM409 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM409 are further described hereinbelow with reference to Table Table1.

[5930] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM409 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5931]

[5932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 410 (GAM410) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5933] GAM410 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM410 was detected is described hereinabove with reference to Figs. 2-8.

[5934] GAM410 gene, herein designated GAM GENE, and GAM410 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5935] GAM410 gene, herein designated GAM GENE, encodes a GAM410 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM410 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM410 precursor RNA is designated SEQ ID:6380, and is provided hereinbelow with reference to the sequence listing part.

[5936] GAM410 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5937] An enzyme complex designated DICER COMPLEX, dices

the GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM410 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM410 RNA is designated SEQ ID:6381, and is provided hereinbelow with reference to the sequence listing part.

[5938] GAM410 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM410 target RNA, herein designated GAM TARGET RNA. GAM410 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5939] GAM410 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM410 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM410

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM410 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM410 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5940] The complementary binding of GAM410 RNA, herein designated GAM RNA, to target binding sites on GAM410 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM410 target RNA, herein designated GAM TARGET RNA, into GAM410 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5941] It is appreciated that GAM410 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM410 target genes. The mRNA of each one of this plurality of GAM410 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM410 RNA, herein designated GAM RNA, and which when bound by GAM410 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM410 target proteins.

[5942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM410 gene, herein designated GAM GENE, on one or more GAM410 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM410 correlate with, and may be deduced from, the identity of the target genes which GAM410 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5944] Nucleotide sequences of the GAM410 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM410 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM410 are further described hereinbelow with reference to Table Table1.

[5945] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM410 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5946]

[5947] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 411 (GAM411) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5948] GAM411 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM411 was detected is described hereinabove with reference to Figs. 2-8.

[5949] GAM411 gene, herein designated GAM GENE, and GAM411 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5950] GAM411 gene, herein designated GAM GENE, encodes a GAM411 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM411 precursor RNA is designated SEQ ID:6419, and is provided hereinbelow with reference to the sequence listing part.

[5951] GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM411 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5952] An enzyme complex designated DICER COMPLEX, dices the GAM411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM411 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM411 RNA is designated SEQ ID:6420, and is provided hereinbelow with reference to the sequence listing part.

[5953] GAM411 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM411 target RNA, herein designated GAM TARGET RNA. GAM411 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5954] GAM411 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM411 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM411 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM411 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM411 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5955] The complementary binding of GAM411 RNA, herein designated GAM RNA, to target binding sites on GAM411 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM411 target RNA, herein designated GAM TARGET RNA, into GAM411 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5956] It is appreciated that GAM411 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM411 target genes. The mRNA of each one of this plurality of GAM411 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM411 RNA, herein designated GAM RNA, and which when bound by GAM411 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM411 target proteins.

[5957] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM411 gene, herein designated GAM GENE, on one or

more GAM411 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5958] It is yet further appreciated that specific functions, and accordingly utilities, of GAM411 correlate with, and may be deduced from, the identity of the target genes which GAM411 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5959] Nucleotide sequences of the GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM411 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM411 are further de-

scribed hereinbelow with reference to Table Table1.

[5960] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM411 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5961]

[5962] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 412 (GAM412) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5963] GAM412 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM412 was detected is described hereinabove with reference to Figs. 2-8.

[5964] GAM412 gene, herein designated GAM GENE, and GAM412 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5965] GAM412 gene, herein designated GAM GENE, encodes a GAM412 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM412 precursor RNA is designated SEQ ID:6436, and is provided hereinbelow with reference to the sequence listing part.

[5966] GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5967] An enzyme complex designated DICER COMPLEX, dices the GAM412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM412 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM412 RNA is designated SEQ ID:6437, and is provided hereinbelow with reference to the sequence listing part.

[5968] GAM412 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM412 target RNA, herein designated GAM TARGET RNA. GAM412 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5969] GAM412 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM412 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM412 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM412 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM412 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5970] The complementary binding of GAM412 RNA, herein designated GAM RNA, to target binding sites on GAM412 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM412 target RNA, herein designated GAM TARGET RNA, into GAM412 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5971] It is appreciated that GAM412 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM412 target genes. The mRNA of each one of this plurality of GAM412 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM412 RNA, herein designated GAM RNA, and which when bound by GAM412 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM412 target proteins.

[5972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM412 gene, herein designated GAM GENE, on one or more GAM412 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5973] It is yet further appreciated that specific functions, and accordingly utilities, of GAM412 correlate with, and may

be deduced from, the identity of the target genes which GAM412 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5974] Nucleotide sequences of the GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM412 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM412 are further described hereinbelow with reference to Table Table1.

[5975] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM412 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5976]

[5977] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 413 (GAM413) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5978] GAM413 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM413 was detected is described hereinabove with reference to Figs. 2-8.

[5979] GAM413 gene, herein designated GAM GENE, and GAM413 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5980] GAM413 gene, herein designated GAM GENE, encodes a GAM413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM413 precursor RNA is designated SEQ ID:6452, and is provided hereinbelow with reference to the sequence listing part.

[5981] GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5982] An enzyme complex designated DICER COMPLEX, dices the GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM413 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of GAM413 RNA is designated SEQ ID:6453, and is provided hereinbelow with reference to the sequence listing part.

[5983] GAM413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM413 target RNA, herein designated GAM TARGET RNA. GAM413 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5984] GAM413 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM413 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM413 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM413 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5985] The complementary binding of GAM413 RNA, herein designated GAM RNA, to target binding sites on GAM413 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM413 target RNA, herein designated GAM TARGET RNA, into GAM413 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5986] It is appreciated that GAM413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM413 target genes. The mRNA of each one of this plurality of GAM413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM413 RNA, herein designated GAM RNA, and which when bound by GAM413 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM413 target proteins.

[5987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM413 gene, herein designated GAM GENE, on one or more GAM413 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5988] It is yet further appreciated that specific functions, and accordingly utilities, of GAM413 correlate with, and may be deduced from, the identity of the target genes which GAM413 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5989] Nucleotide sequences of the GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM413 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM413 are further described hereinbelow with reference to Table Table1.

[5990] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM413 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5991]

[5992] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 414 (GAM414) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5993] GAM414 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM414 was detected is described hereinabove with reference to Figs. 2-8.

[5994] GAM414 gene, herein designated GAM GENE, and GAM414 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5995] GAM414 gene, herein designated GAM GENE, encodes a GAM414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM414 precursor RNA is desig-

nated SEQ ID:6474, and is provided hereinbelow with reference to the sequence listing part.

[5996] GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5997] An enzyme complex designated DICER COMPLEX, dices the GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM414 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM414 RNA is designated SEQ ID:6475, and is provided hereinbelow with reference to the sequence listing part.

[5998] GAM414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM414 target RNA, herein designated GAM TARGET RNA. GAM414 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5999] GAM414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM414 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM414 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM414

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6000] The complementary binding of GAM414 RNA, herein designated GAM RNA, to target binding sites on GAM414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM414 target RNA, herein designated GAM TARGET RNA, into GAM414 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6001] It is appreciated that GAM414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM414 target genes. The mRNA of each one of this plurality of GAM414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM414 RNA, herein designated GAM RNA, and which when bound by GAM414 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM414 target proteins.

[6002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM414 gene, herein designated GAM GENE, on one or more GAM414 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6003] It is yet further appreciated that specific functions, and accordingly utilities, of GAM414 correlate with, and may be deduced from, the identity of the target genes which GAM414 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6004] Nucleotide sequences of the GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM414 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM414 are further described hereinbelow with reference to Table Table1.

[6005] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM414 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6006]

[6007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 415 (GAM415) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6008] GAM415 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM415 was detected is described hereinabove with reference to Figs. 2-8.

[6009] GAM415 gene, herein designated GAM GENE, and

GAM415 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6010] GAM415 gene, herein designated GAM GENE, encodes a GAM415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM415 precursor RNA is designated SEQ ID:6489, and is provided hereinbelow with reference to the sequence listing part.

[6011] GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6012] An enzyme complex designated DICER COMPLEX, dices the GAM415 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM415 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM415 RNA is designated SEQ ID:6490, and is provided hereinbelow with reference to the sequence listing part.

[6013] GAM415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM415 target RNA, herein designated GAM TARGET RNA. GAM415 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6014] GAM415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM415 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM415 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM415 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6015] The complementary binding of GAM415 RNA, herein designated GAM RNA, to target binding sites on GAM415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM415 target RNA, herein designated GAM TARGET RNA, into GAM415 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6016] It is appreciated that GAM415 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM415 target genes. The mRNA of each one of this plurality of GAM415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM415 RNA, herein designated GAM RNA, and which when bound by GAM415 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM415 target proteins.

[6017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM415 gene, herein designated GAM GENE, on one or more GAM415 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6018] It is yet further appreciated that specific functions, and accordingly utilities, of GAM415 correlate with, and may be deduced from, the identity of the target genes which GAM415 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6019] Nucleotide sequences of the GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM415 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM415 are further described hereinbelow with reference to Table Table1.

[6020] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM415 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6021]

[6022] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 416 (GAM416) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6023] GAM416 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM416 was detected is described hereinabove with reference to Figs. 2-8.

[6024] GAM416 gene, herein designated GAM GENE, and GAM416 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6025] GAM416 gene, herein designated GAM GENE, encodes a GAM416 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM416 precursor RNA is designated SEQ ID:6500, and is provided hereinbelow with reference to the sequence listing part.

[6026] GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6027] An enzyme complex designated DICER COMPLEX, dices the GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM416 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM416 RNA is designated SEQ ID:6501, and is provided hereinbelow with reference to the sequence listing part.

[6028] GAM416 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM416 target RNA, herein designated GAM TARGET RNA. GAM416 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6029] GAM416 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM416 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM416 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM416 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM416 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6030] The complementary binding of GAM416 RNA, herein designated GAM RNA, to target binding sites on GAM416 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM416 target RNA, herein designated GAM TARGET RNA, into GAM416 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6031] It is appreciated that GAM416 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM416 target genes. The mRNA of each one of this plurality of GAM416 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM416 RNA, herein designated GAM RNA, and which when bound by GAM416 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM416 target proteins.

[6032] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM416 gene, herein designated GAM GENE, on one or more GAM416 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6033] It is yet further appreciated that specific functions, and accordingly utilities, of GAM416 correlate with, and may be deduced from, the identity of the target genes which GAM416 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6034] Nucleotide sequences of the GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM416 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM416 are further described hereinbelow with reference to Table Table1.

[6035] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM416 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6036]

[6037] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 417 (GAM417) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6038] GAM417 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM417 was detected is described hereinabove with reference to Figs. 2-8.

[6039] GAM417 gene, herein designated GAM GENE, and GAM417 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6040] GAM417 gene, herein designated GAM GENE, encodes a GAM417 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM417 precursor RNA is designated SEQ ID:6514, and is provided hereinbelow with reference to the sequence listing part.

[6041] GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6042] An enzyme complex designated DICER COMPLEX, dices the GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM417 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM417 RNA is designated SEQ ID:6515, and is provided hereinbelow with reference to the sequence listing part.

[6043] GAM417 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM417 target RNA, herein designated GAM TARGET RNA. GAM417 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6044] GAM417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM417 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM417 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM417 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6045] The complementary binding of GAM417 RNA, herein designated GAM RNA, to target binding sites on GAM417 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM417 target RNA, herein designated GAM TARGET RNA, into GAM417 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6046] It is appreciated that GAM417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM417 target genes. The mRNA of each one of this plurality of GAM417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM417 RNA,

herein designated GAM RNA, and which when bound by GAM417 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM417 target proteins.

[6047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM417 gene, herein designated GAM GENE, on one or more GAM417 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6048] It is yet further appreciated that specific functions, and accordingly utilities, of GAM417 correlate with, and may be deduced from, the identity of the target genes which

GAM417 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6049] Nucleotide sequences of the GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM417 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM417 are further described hereinbelow with reference to Table Table1.

[6050] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM417 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6051]

[6052] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 418 (GAM418) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6053] GAM418 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM418 was detected is described hereinabove with reference to Figs. 2-8.

[6054] GAM418 gene, herein designated GAM GENE, and GAM418 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6055] GAM418 gene, herein designated GAM GENE, encodes a GAM418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM418 precursor RNA is designated SEQ ID:6529, and is provided hereinbelow with reference to the sequence listing part.

[6056] GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6057] An enzyme complex designated DICER COMPLEX, dices the GAM418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM418 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM418 RNA is designated SEQ ID:6530, and is provided hereinbelow with reference to the sequence listing part.

[6058] GAM418 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM418 target RNA, herein designated GAM TARGET RNA. GAM418 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6059] GAM418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM418 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM418 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM418 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM418 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6060] The complementary binding of GAM418 RNA, herein designated GAM RNA, to target binding sites on GAM418 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM418 target RNA, herein desig-

nated GAM TARGET RNA, into GAM418 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6061] It is appreciated that GAM418 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM418 target genes. The mRNA of each one of this plurality of GAM418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM418 RNA, herein designated GAM RNA, and which when bound by GAM418 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM418 target proteins.

[6062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM418 gene, herein designated GAM GENE, on one or more GAM418 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6063] It is yet further appreciated that specific functions, and accordingly utilities, of GAM418 correlate with, and may be deduced from, the identity of the target genes which GAM418 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6064] Nucleotide sequences of the GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM418 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM418 are further described hereinbelow with reference to Table Table1.

[6065] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM418 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6066]

[6067] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 419 (GAM419) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6068] GAM419 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM419 was detected is described hereinabove with reference to Figs. 2-8.

[6069] GAM419 gene, herein designated GAM GENE, and GAM419 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6070] GAM419 gene, herein designated GAM GENE, encodes a GAM419 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM419 precursor RNA is designated SEQ ID:6547, and is provided hereinbelow with ref-

erence to the sequence listing part.

[6071] GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6072] An enzyme complex designated DICER COMPLEX, dices the GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM419 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM419 RNA is designated SEQ ID:6548, and is provided hereinbelow with reference to the sequence listing part.

[6073] GAM419 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM419 target RNA, herein designated GAM TARGET RNA.

GAM419 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6074] GAM419 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM419 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM419 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM419 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM419 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6075] The complementary binding of GAM419 RNA, herein designated GAM RNA, to target binding sites on GAM419 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM419 target RNA, herein designated GAM TARGET RNA, into GAM419 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6076] It is appreciated that GAM419 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM419 target genes. The mRNA of each one of this plurality of GAM419 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM419 RNA, herein designated GAM RNA, and which when bound by GAM419 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM419 target proteins.

[6077] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM419 gene, herein designated GAM GENE, on one or more GAM419 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6078] It is yet further appreciated that specific functions, and accordingly utilities, of GAM419 correlate with, and may be deduced from, the identity of the target genes which GAM419 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6079] Nucleotide sequences of the GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM419 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM419 are further described hereinbelow with reference to Table Table1.

[6080] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM419 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6081]

[6082] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 420 (GAM420) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6083] GAM420 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM420 was detected is described hereinabove with reference to Figs. 2-8.

[6084] GAM420 gene, herein designated GAM GENE, and GAM420 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6085] GAM420 gene, herein designated GAM GENE, encodes a GAM420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM420 precursor RNA is designated SEQ ID:6550, and is provided hereinbelow with reference to the sequence listing part.

[6086] GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6087] An enzyme complex designated DICER COMPLEX, dices the GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM420 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM420 RNA is designated SEQ ID:6551, and is provided hereinbelow with reference to the sequence listing part.

[6088] GAM420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM420 target RNA, herein designated GAM TARGET RNA. GAM420 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6089] GAM420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM420 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM420 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM420 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6090] The complementary binding of GAM420 RNA, herein designated GAM RNA, to target binding sites on GAM420 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM420 target RNA, herein designated GAM TARGET RNA, into GAM420 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6091] It is appreciated that GAM420 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM420 target genes. The mRNA of each one of this plurality of GAM420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM420 RNA, herein designated GAM RNA, and which when bound by GAM420 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM420 target proteins.

[6092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM420 gene, herein designated GAM GENE, on one or more GAM420 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[6093] It is yet further appreciated that specific functions, and accordingly utilities, of GAM420 correlate with, and may be deduced from, the identity of the target genes which GAM420 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6094] Nucleotide sequences of the GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM420 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM420 are further described hereinbelow with reference to Table Table1.

[6095] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM420 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6096]

[6097] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

421 (GAM421) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6098] GAM421 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM421 was detected is described hereinabove with reference to Figs. 2-8.

[6099] GAM421 gene, herein designated GAM GENE, and GAM421 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6100] GAM421 gene, herein designated GAM GENE, encodes a GAM421 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM421 precursor RNA is designated SEQ ID:6561, and is provided hereinbelow with reference to the sequence listing part.

[6101] GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6102] An enzyme complex designated DICER COMPLEX, dices the GAM421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM421 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of GAM421 RNA is designated SEQ ID:6562, and is provided hereinbelow with reference to the sequence listing part.

[6103] GAM421 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM421 target RNA, herein designated GAM TARGET RNA. GAM421 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6104] GAM421 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM421 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM421 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM421 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM421 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6105] The complementary binding of GAM421 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM421 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM421 target RNA, herein designated GAM TARGET RNA, into GAM421 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6106] It is appreciated that GAM421 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM421 target genes. The mRNA of each one of this plurality of GAM421 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM421 RNA, herein designated GAM RNA, and which when bound by GAM421 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM421 target proteins.

[6107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM421 gene, herein designated GAM GENE, on one or more GAM421 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6108] It is yet further appreciated that specific functions, and accordingly utilities, of GAM421 correlate with, and may be deduced from, the identity of the target genes which GAM421 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6109] Nucleotide sequences of the GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM421 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM421 are further described hereinbelow with reference to Table Table1.

[6110] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM421 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6111]

[6112] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 422 (GAM422) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6113] GAM422 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM422 was detected is described hereinabove with reference to Figs. 2-8.

[6114] GAM422 gene, herein designated GAM GENE, and GAM422 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6115] GAM422 gene, herein designated GAM GENE, encodes a GAM422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM422 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM422 precursor RNA is designated SEQ ID:6593, and is provided hereinbelow with reference to the sequence listing part.

[6116] GAM422 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6117] An enzyme complex designated DICER COMPLEX, dices the GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM422 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 60%) nucleotide sequence of GAM422 RNA is designated SEQ ID:6594, and is provided hereinbelow with reference to the sequence listing part.

[6118] GAM422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM422 target RNA, herein designated GAM TARGET RNA. GAM422 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6119] GAM422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM422 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM422 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM422 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6120] The complementary binding of GAM422 RNA, herein designated GAM RNA, to target binding sites on GAM422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM422 target RNA, herein designated GAM TARGET RNA, into GAM422 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6121] It is appreciated that GAM422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM422 target genes. The mRNA of each one of this plurality of GAM422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM422 RNA, herein designated GAM RNA, and which when bound by

GAM422 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM422 target proteins.

[6122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM422 gene, herein designated GAM GENE, on one or more GAM422 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6123] It is yet further appreciated that specific functions, and accordingly utilities, of GAM422 correlate with, and may be deduced from, the identity of the target genes which GAM422 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[6124] Nucleotide sequences of the GAM422 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM422 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM422 are further described hereinbelow with reference to Table Table1.

[6125] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM422 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6126]

[6127] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 423 (GAM423) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6128] GAM423 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM423 was detected is described hereinabove with reference to Figs. 2-8.

[6129] GAM423 gene, herein designated GAM GENE, and GAM423 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6130] GAM423 gene, herein designated GAM GENE, encodes a GAM423 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM423 precursor RNA is designated SEQ ID:6611, and is provided hereinbelow with reference to the sequence listing part.

[6131] GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6132] An enzyme complex designated DICER COMPLEX, dices the GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM423 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM423 RNA is designated SEQ ID:6612, and is provided hereinbelow with reference to the sequence listing part.

[6133] GAM423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM423 target RNA, herein designated GAM TARGET RNA. GAM423 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6134] GAM423 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM423 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM423 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM423 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM423 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6135] The complementary binding of GAM423 RNA, herein designated GAM RNA, to target binding sites on GAM423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM423 target RNA, herein designated GAM TARGET RNA, into GAM423 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6136] It is appreciated that GAM423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM423 target genes. The mRNA of each one of this plu-

rality of GAM423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM423 RNA, herein designated GAM RNA, and which when bound by GAM423 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM423 target proteins.

[6137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM423 gene, herein designated GAM GENE, on one or more GAM423 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6138] It is yet further appreciated that specific functions, and accordingly utilities, of GAM423 correlate with, and may be deduced from, the identity of the target genes which GAM423 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6139] Nucleotide sequences of the GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM423 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM423 are further described hereinbelow with reference to Table Table1.

[6140] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM423 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6141]

[6142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 424 (GAM424) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[6143] GAM424 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM424 was detected is described hereinabove with reference to Figs. 2-8.

[6144] GAM424 gene, herein designated GAM GENE, and GAM424 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6145] GAM424 gene, herein designated GAM GENE, encodes a GAM424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM424 precursor RNA is designated SEQ ID:6623, and is provided hereinbelow with reference to the sequence listing part.

[6146] GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6147] An enzyme complex designated DICER COMPLEX, dices the GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM424 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 20%) nucleotide sequence of GAM424 RNA is designated SEQ ID:6624, and is provided hereinbelow with reference to the sequence listing part.

[6148] GAM424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM424 target RNA, herein designated GAM TARGET RNA.
GAM424 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[6149] GAM424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM424 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM424 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM424 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6150] The complementary binding of GAM424 RNA, herein designated GAM RNA, to target binding sites on GAM424 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM424 target RNA, herein designated GAM TARGET RNA, into GAM424 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6151] It is appreciated that GAM424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM424 target genes. The mRNA of each one of this plurality of GAM424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM424 RNA, herein designated GAM RNA, and which when bound by GAM424 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM424 target proteins.

[6152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM424 gene, herein designated GAM GENE, on one or more GAM424 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM424 correlate with, and may be deduced from, the identity of the target genes which GAM424 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6154] Nucleotide sequences of the GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM424 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM424 are further described hereinbelow with reference to Table Table1.

[6155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM424 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6156]

[6157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 425 (GAM425) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6158] GAM425 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM425 was detected is described hereinabove with reference to Figs. 2-8.

[6159] GAM425 gene, herein designated GAM GENE, and GAM425 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6160] GAM425 gene, herein designated GAM GENE, encodes a GAM425 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM425 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM425 precursor RNA is designated SEQ ID:6673, and is provided hereinbelow with reference to the sequence listing part.

[6161] GAM425 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6162] An enzyme complex designated DICER COMPLEX, dices the GAM425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM425 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of

GAM425 RNA is designated SEQ ID:6674, and is provided hereinbelow with reference to the sequence listing part.

[6163] GAM425 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM425 target RNA, herein designated GAM TARGET RNA. GAM425 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6164] GAM425 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM425 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM425 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM425 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM425 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6165] The complementary binding of GAM425 RNA, herein designated GAM RNA, to target binding sites on GAM425 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM425 target RNA, herein designated GAM TARGET RNA, into GAM425 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6166] It is appreciated that GAM425 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM425 target genes. The mRNA of each one of this plurality of GAM425 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM425 RNA, herein designated GAM RNA, and which when bound by GAM425 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM425 target proteins.

[6167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM425 gene, herein designated GAM GENE, on one or more GAM425 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6168] It is yet further appreciated that specific functions, and accordingly utilities, of GAM425 correlate with, and may be deduced from, the identity of the target genes which GAM425 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6169] Nucleotide sequences of the GAM425 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM425 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM425 are further described hereinbelow with reference to Table Table1.

[6170] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM425 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6171]

[6172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 426 (GAM426) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6173] GAM426 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM426 was detected is described hereinabove

with reference to Figs. 2-8.

[6174] GAM426 gene, herein designated GAM GENE, and GAM426 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6175] GAM426 gene, herein designated GAM GENE, encodes a GAM426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM426 precursor RNA is designated SEQ ID:6679, and is provided hereinbelow with reference to the sequence listing part.

[6176] GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6177] An enzyme complex designated DICER COMPLEX, dices the GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM426 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of GAM426 RNA is designated SEQ ID:6680, and is provided hereinbelow with reference to the sequence listing part.

[6178] GAM426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM426 target RNA, herein designated GAM TARGET RNA. GAM426 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6179] GAM426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM426 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM426 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM426 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM426 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6180] The complementary binding of GAM426 RNA, herein designated GAM RNA, to target binding sites on GAM426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM426 target RNA, herein designated GAM TARGET RNA, into GAM426 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[6181] It is appreciated that GAM426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM426 target genes. The mRNA of each one of this plurality of GAM426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM426 RNA, herein designated GAM RNA, and which when bound by GAM426 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM426 target proteins.

[6182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM426 gene, herein designated GAM GENE, on one or more GAM426 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM426 correlate with, and may be deduced from, the identity of the target genes which GAM426 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6184] Nucleotide sequences of the GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM426 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM426 are further described hereinbelow with reference to Table Table1.

[6185] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM426 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6186]

[6187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 427 (GAM427) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6188] GAM427 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM427 was detected is described hereinabove with reference to Figs. 2-8.

[6189] GAM427 gene, herein designated GAM GENE, and GAM427 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6190] GAM427 gene, herein designated GAM GENE, encodes a GAM427 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM427 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM427 precursor RNA is designated SEQ ID:6693, and is provided hereinbelow with reference to the sequence listing part.

[6191] GAM427 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6192] An enzyme complex designated DICER COMPLEX, dices the GAM427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM427 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM427 RNA is designated SEQ ID:6694, and is provided hereinbelow with reference to the sequence listing part.

[6193] GAM427 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM427 target RNA, herein designated GAM TARGET RNA.

GAM427 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6194] GAM427 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM427 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM427 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM427 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM427 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6195] The complementary binding of GAM427 RNA, herein designated GAM RNA, to target binding sites on GAM427 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM427 target RNA, herein designated GAM TARGET RNA, into GAM427 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6196] It is appreciated that GAM427 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM427 target genes. The mRNA of each one of this plurality of GAM427 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM427 RNA, herein designated GAM RNA, and which when bound by GAM427 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM427 target proteins.

[6197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM427 gene, herein designated GAM GENE, on one or more GAM427 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM427 correlate with, and may be deduced from, the identity of the target genes which GAM427 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6199] Nucleotide sequences of the GAM427 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM427 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM427 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM427 are further described hereinbelow with reference to Table Table1.

[6200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM427 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6201]

[6202] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 428 (GAM428) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6203] GAM428 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM428 was detected is described hereinabove with reference to Figs. 2-8.

[6204] GAM428 gene, herein designated GAM GENE, and GAM428 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6205] GAM428 gene, herein designated GAM GENE, encodes a

GAM428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM428 precursor RNA is designated SEQ ID:6716, and is provided hereinbelow with reference to the sequence listing part.

[6206] GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6207] An enzyme complex designated DICER COMPLEX, dices the GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM428 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of GAM428 RNA is designated SEQ ID:6717, and is provided hereinbelow with reference to the sequence listing part.

[6208] GAM428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM428 target RNA, herein designated GAM TARGET RNA. GAM428 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6209] GAM428 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM428 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM428 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM428 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6210] The complementary binding of GAM428 RNA, herein designated GAM RNA, to target binding sites on GAM428 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM428 target RNA, herein designated GAM TARGET RNA, into GAM428 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6211] It is appreciated that GAM428 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM428 target genes. The mRNA of each one of this plurality of GAM428 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM428 RNA, herein designated GAM RNA, and which when bound by GAM428 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM428 target proteins.

[6212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM428 gene, herein designated GAM GENE, on one or more GAM428 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6213] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM428 correlate with, and may be deduced from, the identity of the target genes which GAM428 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6214] Nucleotide sequences of the GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM428 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM428 are further described hereinbelow with reference to Table Table1.

[6215] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM428 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6216]

[6217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 429 (GAM429) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[6218] GAM429 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM429 was detected is described hereinabove with reference to Figs. 2-8.

[6219] GAM429 gene, herein designated GAM GENE, and GAM429 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6220] GAM429 gene, herein designated GAM GENE, encodes a GAM429 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM429 precursor RNA is designated SEQ ID:6729, and is provided hereinbelow with reference to the sequence listing part.

[6221] GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6222] An enzyme complex designated DICER COMPLEX, dices the GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM429 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM429 RNA is designated SEQ ID:6730, and is provided hereinbelow with reference to the sequence listing part.

[6223] GAM429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM429 target RNA, herein designated GAM TARGET RNA.
GAM429 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6224] GAM429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM429 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM429 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM429 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6225] The complementary binding of GAM429 RNA, herein designated GAM RNA, to target binding sites on GAM429 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM429 target RNA, herein designated GAM TARGET RNA, into GAM429 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6226] It is appreciated that GAM429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM429 target genes. The mRNA of each one of this plurality of GAM429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM429 RNA, herein designated GAM RNA, and which when bound by GAM429 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM429 target proteins.

[6227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM429 gene, herein designated GAM GENE, on one or more GAM429 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6228] It is yet further appreciated that specific functions, and accordingly utilities, of GAM429 correlate with, and may be deduced from, the identity of the target genes which GAM429 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6229] Nucleotide sequences of the GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM429 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM429 are further described hereinbelow with reference to Table Table1.

[6230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM429 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6231]

[6232] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 430 (GAM430) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6233] GAM430 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM430 was detected is described hereinabove with reference to Figs. 2-8.

[6234] GAM430 gene, herein designated GAM GENE, and GAM430 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6235] GAM430 gene, herein designated GAM GENE, encodes a GAM430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM430 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM430 precursor RNA is designated SEQ ID:6752, and is provided hereinbelow with reference to the sequence listing part.

[6236] GAM430 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6237] An enzyme complex designated DICER COMPLEX, dices the GAM430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM430 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM430 RNA is designated SEQ ID:6753, and is provided

hereinbelow with reference to the sequence listing part.

[6238] GAM430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM430 target RNA, herein designated GAM TARGET RNA.
GAM430 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6239] GAM430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM430 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM430 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM430 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6240] The complementary binding of GAM430 RNA, herein designated GAM RNA, to target binding sites on GAM430 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM430 target RNA, herein designated GAM TARGET RNA, into GAM430 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6241] It is appreciated that GAM430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM430 target genes. The mRNA of each one of this plurality of GAM430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM430 RNA, herein designated GAM RNA, and which when bound by GAM430 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM430 tar-

get proteins.

[6242] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM430 gene, herein designated GAM GENE, on one or more GAM430 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6243] It is yet further appreciated that specific functions, and accordingly utilities, of GAM430 correlate with, and may be deduced from, the identity of the target genes which GAM430 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6244] Nucleotide sequences of the GAM430 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM430 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM430 are further described hereinbelow with reference to Table Table1.

[6245] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM430 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6246]

[6247] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 431 (GAM431) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6248] GAM431 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM431 was detected is described hereinabove with reference to Figs. 2-8.

[6249] GAM431 gene, herein designated GAM GENE, and GAM431 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6250] GAM431 gene, herein designated GAM GENE, encodes a GAM431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM431 precursor RNA is designated SEQ ID:6759, and is provided hereinbelow with reference to the sequence listing part.

[6251] GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6252] An enzyme complex designated DICER COMPLEX, dices

the GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM431 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of GAM431 RNA is designated SEQ ID:6760, and is provided hereinbelow with reference to the sequence listing part.

[6253] GAM431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM431 target RNA, herein designated GAM TARGET RNA. GAM431 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6254] GAM431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM431

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM431 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM431 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6255] The complementary binding of GAM431 RNA, herein designated GAM RNA, to target binding sites on GAM431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM431 target RNA, herein designated GAM TARGET RNA, into GAM431 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6256] It is appreciated that GAM431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM431 target genes. The mRNA of each one of this plurality of GAM431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM431 RNA, herein designated GAM RNA, and which when bound by GAM431 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM431 target proteins.

[6257] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM431 gene, herein designated GAM GENE, on one or more GAM431 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6258] It is yet further appreciated that specific functions, and accordingly utilities, of GAM431 correlate with, and may be deduced from, the identity of the target genes which GAM431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6259] Nucleotide sequences of the GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM431 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM431 are further described hereinbelow with reference to Table Table1.

[6260] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM431 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6261]

[6262] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 432 (GAM432) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6263] GAM432 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM432 was detected is described hereinabove with reference to Figs. 2-8.

[6264] GAM432 gene, herein designated GAM GENE, and GAM432 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6265] GAM432 gene, herein designated GAM GENE, encodes a GAM432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM432 precursor RNA is designated SEQ ID:6766, and is provided hereinbelow with reference to the sequence listing part.

[6266] GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM432 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6267] An enzyme complex designated DICER COMPLEX, dices the GAM432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM432 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 36%) nucleotide sequence of GAM432 RNA is designated SEQ ID:6767, and is provided hereinbelow with reference to the sequence listing part.

[6268] GAM432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM432 target RNA, herein designated GAM TARGET RNA. GAM432 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6269] GAM432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM432 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM432 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM432 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6270] The complementary binding of GAM432 RNA, herein designated GAM RNA, to target binding sites on GAM432 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM432 target RNA, herein designated GAM TARGET RNA, into GAM432 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6271] It is appreciated that GAM432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM432 target genes. The mRNA of each one of this plurality of GAM432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM432 RNA, herein designated GAM RNA, and which when bound by GAM432 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM432 target proteins.

[6272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM432 gene, herein designated GAM GENE, on one or

more GAM432 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM432 correlate with, and may be deduced from, the identity of the target genes which GAM432 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6274] Nucleotide sequences of the GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM432 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM432 are further de-

scribed hereinbelow with reference to Table Table1.

[6275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM432 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6276]

[6277] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 433 (GAM433) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6278] GAM433 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM433 was detected is described hereinabove with reference to Figs. 2-8.

[6279] GAM433 gene, herein designated GAM GENE, and GAM433 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6280] GAM433 gene, herein designated GAM GENE, encodes a GAM433 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM433 precursor RNA is designated SEQ ID:6788, and is provided hereinbelow with reference to the sequence listing part.

[6281] GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6282] An enzyme complex designated DICER COMPLEX, dices the GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM433 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM433 RNA is designated SEQ ID:6789, and is provided hereinbelow with reference to the sequence listing part.

[6283] GAM433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM433 target RNA, herein designated GAM TARGET RNA. GAM433 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6284] GAM433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM433 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM433 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM433 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6285] The complementary binding of GAM433 RNA, herein designated GAM RNA, to target binding sites on GAM433 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM433 target RNA, herein designated GAM TARGET RNA, into GAM433 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6286] It is appreciated that GAM433 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM433 target genes. The mRNA of each one of this plurality of GAM433 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM433 RNA, herein designated GAM RNA, and which when bound by GAM433 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM433 target proteins.

[6287] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM433 gene, herein designated GAM GENE, on one or more GAM433 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6288] It is yet further appreciated that specific functions, and accordingly utilities, of GAM433 correlate with, and may

be deduced from, the identity of the target genes which GAM433 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6289] Nucleotide sequences of the GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM433 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM433 are further described hereinbelow with reference to Table Table1.

[6290] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM433 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6291]

[6292] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 434 (GAM434) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6293] GAM434 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM434 was detected is described hereinabove with reference to Figs. 2-8.

[6294] GAM434 gene, herein designated GAM GENE, and GAM434 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6295] GAM434 gene, herein designated GAM GENE, encodes a GAM434 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM434 precursor RNA is designated SEQ ID:6806, and is provided hereinbelow with reference to the sequence listing part.

[6296] GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6297] An enzyme complex designated DICER COMPLEX, dices the GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM434 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM434 RNA is designated SEQ ID:6807, and is provided hereinbelow with reference to the sequence listing part.

[6298] GAM434 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM434 target RNA, herein designated GAM TARGET RNA. GAM434 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6299] GAM434 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM434 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM434 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM434 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM434 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6300] The complementary binding of GAM434 RNA, herein designated GAM RNA, to target binding sites on GAM434 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM434 target RNA, herein designated GAM TARGET RNA, into GAM434 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6301] It is appreciated that GAM434 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM434 target genes. The mRNA of each one of this plurality of GAM434 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM434 RNA, herein designated GAM RNA, and which when bound by GAM434 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM434 target proteins.

[6302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM434 gene, herein designated GAM GENE, on one or more GAM434 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6303] It is yet further appreciated that specific functions, and accordingly utilities, of GAM434 correlate with, and may be deduced from, the identity of the target genes which GAM434 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6304] Nucleotide sequences of the GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM434 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM434 are further described hereinbelow with reference to Table Table1.

[6305] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM434 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6306]

[6307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 435 (GAM435) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6308] GAM435 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM435 was detected is described hereinabove with reference to Figs. 2-8.

[6309] GAM435 gene, herein designated GAM GENE, and GAM435 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6310] GAM435 gene, herein designated GAM GENE, encodes a GAM435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM435 precursor RNA is desig-

nated SEQ ID:6817, and is provided hereinbelow with reference to the sequence listing part.

[6311] GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6312] An enzyme complex designated DICER COMPLEX, dices the GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM435 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM435 RNA is designated SEQ ID:6818, and is provided hereinbelow with reference to the sequence listing part.

[6313] GAM435 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM435 target RNA, herein designated GAM TARGET RNA. GAM435 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6314] GAM435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM435 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM435 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM435

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6315] The complementary binding of GAM435 RNA, herein designated GAM RNA, to target binding sites on GAM435 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM435 target RNA, herein designated GAM TARGET RNA, into GAM435 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6316] It is appreciated that GAM435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM435 target genes. The mRNA of each one of this plurality of GAM435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM435 RNA, herein designated GAM RNA, and which when bound by GAM435 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM435 target proteins.

[6317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM435 gene, herein designated GAM GENE, on one or more GAM435 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM435 correlate with, and may be deduced from, the identity of the target genes which GAM435 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6319] Nucleotide sequences of the GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM435 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM435 are further described hereinbelow with reference to Table Table1.

[6320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM435 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6321]

[6322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 436 (GAM436) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6323] GAM436 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM436 was detected is described hereinabove with reference to Figs. 2-8.

[6324] GAM436 gene, herein designated GAM GENE, and

GAM436 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6325] GAM436 gene, herein designated GAM GENE, encodes a GAM436 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM436 precursor RNA is designated SEQ ID:6826, and is provided hereinbelow with reference to the sequence listing part.

[6326] GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6327] An enzyme complex designated DICER COMPLEX, dices the GAM436 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM436 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM436 RNA is designated SEQ ID:6827, and is provided hereinbelow with reference to the sequence listing part.

[6328] GAM436 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM436 target RNA, herein designated GAM TARGET RNA. GAM436 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6329] GAM436 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM436 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM436 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM436 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM436 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6330] The complementary binding of GAM436 RNA, herein designated GAM RNA, to target binding sites on GAM436 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM436 target RNA, herein designated GAM TARGET RNA, into GAM436 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6331] It is appreciated that GAM436 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM436 target genes. The mRNA of each one of this plurality of GAM436 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM436 RNA, herein designated GAM RNA, and which when bound by GAM436 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM436 target proteins.

[6332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM436 gene, herein designated GAM GENE, on one or more GAM436 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM436 correlate with, and may be deduced from, the identity of the target genes which GAM436 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6334] Nucleotide sequences of the GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM436 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM436 are further described hereinbelow with reference to Table Table1.

[6335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM436 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6336]

[6337] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 437 (GAM437) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6338] GAM437 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM437 was detected is described hereinabove with reference to Figs. 2-8.

[6339] GAM437 gene, herein designated GAM GENE, and GAM437 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6340] GAM437 gene, herein designated GAM GENE, encodes a GAM437 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM437 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM437 precursor RNA is designated SEQ ID:6856, and is provided hereinbelow with reference to the sequence listing part.

[6341] GAM437 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6342] An enzyme complex designated DICER COMPLEX, dices the GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM437 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM437 RNA is designated SEQ ID:6857, and is provided hereinbelow with reference to the sequence listing part.

[6343] GAM437 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM437 target RNA, herein designated GAM TARGET RNA. GAM437 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6344] GAM437 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM437 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM437 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM437 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM437 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6345] The complementary binding of GAM437 RNA, herein designated GAM RNA, to target binding sites on GAM437 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM437 target RNA, herein designated GAM TARGET RNA, into GAM437 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6346] It is appreciated that GAM437 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM437 target genes. The mRNA of each one of this plurality of GAM437 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM437 RNA, herein designated GAM RNA, and which when bound by GAM437 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM437 target proteins.

[6347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM437 gene, herein designated GAM GENE, on one or more GAM437 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6348] It is yet further appreciated that specific functions, and accordingly utilities, of GAM437 correlate with, and may be deduced from, the identity of the target genes which GAM437 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6349] Nucleotide sequences of the GAM437 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM437 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM437 are further described hereinbelow with reference to Table Table1.

[6350] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM437 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6351]

[6352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 438 (GAM438) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6353] GAM438 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM438 was detected is described hereinabove with reference to Figs. 2-8.

[6354] GAM438 gene, herein designated GAM GENE, and GAM438 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6355] GAM438 gene, herein designated GAM GENE, encodes a GAM438 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM438 precursor RNA is designated SEQ ID:6869, and is provided hereinbelow with reference to the sequence listing part.

[6356] GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6357] An enzyme complex designated DICER COMPLEX, dices the GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM438 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM438 RNA is designated SEQ ID:6870, and is provided hereinbelow with reference to the sequence listing part.

[6358] GAM438 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM438 target RNA, herein designated GAM TARGET RNA. GAM438 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6359] GAM438 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM438 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM438 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM438 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM438 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6360] The complementary binding of GAM438 RNA, herein designated GAM RNA, to target binding sites on GAM438 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM438 target RNA, herein designated GAM TARGET RNA, into GAM438 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6361] It is appreciated that GAM438 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM438 target genes. The mRNA of each one of this plurality of GAM438 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM438 RNA,

herein designated GAM RNA, and which when bound by GAM438 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM438 target proteins.

[6362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM438 gene, herein designated GAM GENE, on one or more GAM438 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM438 correlate with, and may be deduced from, the identity of the target genes which

GAM438 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6364] Nucleotide sequences of the GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM438 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM438 are further described hereinbelow with reference to Table Table1.

[6365] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM438 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6366]

[6367] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 439 (GAM439) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6368] GAM439 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM439 was detected is described hereinabove with reference to Figs. 2-8.

[6369] GAM439 gene, herein designated GAM GENE, and GAM439 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6370] GAM439 gene, herein designated GAM GENE, encodes a GAM439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM439 precursor RNA is designated SEQ ID:6887, and is provided hereinbelow with reference to the sequence listing part.

[6371] GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6372] An enzyme complex designated DICER COMPLEX, dices the GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM439 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM439 RNA is designated SEQ ID:6888, and is provided hereinbelow with reference to the sequence listing part.

[6373] GAM439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM439 target RNA, herein designated GAM TARGET RNA.
GAM439 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6374] GAM439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM439 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM439 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM439 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6375] The complementary binding of GAM439 RNA, herein designated GAM RNA, to target binding sites on GAM439 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM439 target RNA, herein desig-

nated GAM TARGET RNA, into GAM439 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6376] It is appreciated that GAM439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM439 target genes. The mRNA of each one of this plurality of GAM439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM439 RNA, herein designated GAM RNA, and which when bound by GAM439 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM439 target proteins.

[6377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM439 gene, herein designated GAM GENE, on one or more GAM439 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6378] It is yet further appreciated that specific functions, and accordingly utilities, of GAM439 correlate with, and may be deduced from, the identity of the target genes which GAM439 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6379] Nucleotide sequences of the GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM439 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM439 are further described hereinbelow with reference to Table Table1.

[6380] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM439 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6381]

[6382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 440 (GAM440) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6383] GAM440 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM440 was detected is described hereinabove with reference to Figs. 2-8.

[6384] GAM440 gene, herein designated GAM GENE, and GAM440 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6385] GAM440 gene, herein designated GAM GENE, encodes a GAM440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM440 precursor RNA is designated SEQ ID:6903, and is provided hereinbelow with ref-

erence to the sequence listing part.

[6386] GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6387] An enzyme complex designated DICER COMPLEX, dices the GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM440 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM440 RNA is designated SEQ ID:6904, and is provided hereinbelow with reference to the sequence listing part.

[6388] GAM440 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM440 target RNA, herein designated GAM TARGET RNA.

GAM440 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6389] GAM440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM440 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM440 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM440 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6390] The complementary binding of GAM440 RNA, herein designated GAM RNA, to target binding sites on GAM440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM440 target RNA, herein designated GAM TARGET RNA, into GAM440 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6391] It is appreciated that GAM440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM440 target genes. The mRNA of each one of this plurality of GAM440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM440 RNA, herein designated GAM RNA, and which when bound by GAM440 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM440 target proteins.

[6392] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM440 gene, herein designated GAM GENE, on one or more GAM440 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM440 correlate with, and may be deduced from, the identity of the target genes which GAM440 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6394] Nucleotide sequences of the GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM440 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM440 are further described hereinbelow with reference to Table Table1.

[6395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM440 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6396]

[6397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 441 (GAM441) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6398] GAM441 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM441 was detected is described hereinabove with reference to Figs. 2-8.

[6399] GAM441 gene, herein designated GAM GENE, and GAM441 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6400] GAM441 gene, herein designated GAM GENE, encodes a GAM441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM441 precursor RNA is designated SEQ ID:6916, and is provided hereinbelow with reference to the sequence listing part.

[6401] GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6402] An enzyme complex designated DICER COMPLEX, dices the GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM441 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM441 RNA is designated SEQ ID:6917, and is provided hereinbelow with reference to the sequence listing part.

[6403] GAM441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM441 target RNA, herein designated GAM TARGET RNA. GAM441 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6404] GAM441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM441 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM441 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM441 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6405] The complementary binding of GAM441 RNA, herein designated GAM RNA, to target binding sites on GAM441 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM441 target RNA, herein designated GAM TARGET RNA, into GAM441 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6406] It is appreciated that GAM441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM441 target genes. The mRNA of each one of this plurality of GAM441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM441 RNA, herein designated GAM RNA, and which when bound by GAM441 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM441 target proteins.

[6407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM441 gene, herein designated GAM GENE, on one or more GAM441 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[6408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM441 correlate with, and may be deduced from, the identity of the target genes which GAM441 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6409] Nucleotide sequences of the GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM441 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM441 are further described hereinbelow with reference to Table Table1.

[6410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM441 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6411]

[6412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

442 (GAM442) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6413] GAM442 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM442 was detected is described hereinabove with reference to Figs. 2-8.

[6414] GAM442 gene, herein designated GAM GENE, and GAM442 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6415] GAM442 gene, herein designated GAM GENE, encodes a GAM442 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM442 precursor RNA is designated SEQ ID:6920, and is provided hereinbelow with reference to the sequence listing part.

[6416] GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6417] An enzyme complex designated DICER COMPLEX, dices the GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM442 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM442 RNA is designated SEQ ID:6921, and is provided hereinbelow with reference to the sequence listing part.

[6418] GAM442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM442 target RNA, herein designated GAM TARGET RNA. GAM442 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6419] GAM442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM442 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM442 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM442 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6420] The complementary binding of GAM442 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM442 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM442 target RNA, herein designated GAM TARGET RNA, into GAM442 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6421] It is appreciated that GAM442 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM442 target genes. The mRNA of each one of this plurality of GAM442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM442 RNA, herein designated GAM RNA, and which when bound by GAM442 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM442 target proteins.

[6422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM442 gene, herein designated GAM GENE, on one or more GAM442 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM442 correlate with, and may be deduced from, the identity of the target genes which GAM442 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6424] Nucleotide sequences of the GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM442 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM442 are further described hereinbelow with reference to Table Table1.

[6425] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM442 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6426]

[6427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 443 (GAM443) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6428] GAM443 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM443 was detected is described hereinabove with reference to Figs. 2-8.

[6429] GAM443 gene, herein designated GAM GENE, and GAM443 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6430] GAM443 gene, herein designated GAM GENE, encodes a GAM443 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM443 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM443 precursor RNA is designated SEQ ID:6933, and is provided hereinbelow with reference to the sequence listing part.

[6431] GAM443 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6432] An enzyme complex designated DICER COMPLEX, dices the GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM443 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 62%) nucleotide sequence of GAM443 RNA is designated SEQ ID:6934, and is provided hereinbelow with reference to the sequence listing part.

[6433] GAM443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM443 target RNA, herein designated GAM TARGET RNA. GAM443 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6434] GAM443 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM443 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM443 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM443 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6435] The complementary binding of GAM443 RNA, herein designated GAM RNA, to target binding sites on GAM443 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM443 target RNA, herein designated GAM TARGET RNA, into GAM443 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6436] It is appreciated that GAM443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM443 target genes. The mRNA of each one of this plurality of GAM443 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM443 RNA, herein designated GAM RNA, and which when bound by

GAM443 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM443 target proteins.

[6437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM443 gene, herein designated GAM GENE, on one or more GAM443 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM443 correlate with, and may be deduced from, the identity of the target genes which GAM443 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[6439] Nucleotide sequences of the GAM443 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM443 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM443 are further described hereinbelow with reference to Table Table1.

[6440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM443 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6441]

[6442] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 444 (GAM444) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6443] GAM444 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM444 was detected is described hereinabove with reference to Figs. 2-8.

[6444] GAM444 gene, herein designated GAM GENE, and GAM444 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6445] GAM444 gene, herein designated GAM GENE, encodes a GAM444 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM444 precursor RNA is designated SEQ ID:6946, and is provided hereinbelow with reference to the sequence listing part.

[6446] GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6447] An enzyme complex designated DICER COMPLEX, dices the GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM444 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM444 RNA is designated SEQ ID:6947, and is provided hereinbelow with reference to the sequence listing part.

[6448] GAM444 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM444 target RNA, herein designated GAM TARGET RNA. GAM444 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6449] GAM444 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM444 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM444 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM444 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM444 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6450] The complementary binding of GAM444 RNA, herein designated GAM RNA, to target binding sites on GAM444 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM444 target RNA, herein designated GAM TARGET RNA, into GAM444 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6451] It is appreciated that GAM444 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM444 target genes. The mRNA of each one of this plurality of GAM444 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM444 RNA, herein designated GAM RNA, and which when bound by GAM444 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM444 target proteins.

[6452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM444 gene, herein designated GAM GENE, on one or more GAM444 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6453] It is yet further appreciated that specific functions, and accordingly utilities, of GAM444 correlate with, and may be deduced from, the identity of the target genes which GAM444 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6454] Nucleotide sequences of the GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM444 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM444 are further described hereinbelow with reference to Table Table1.

[6455] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM444 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6456]

[6457] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 445 (GAM445) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6458] GAM445 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM445 was detected is described hereinabove with reference to Figs. 2-8.

[6459] GAM445 gene, herein designated GAM GENE, and GAM445 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6460] GAM445 gene, herein designated GAM GENE, encodes a GAM445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM445 precursor RNA is designated SEQ ID:6957, and is provided hereinbelow with reference to the sequence listing part.

[6461] GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6462] An enzyme complex designated DICER COMPLEX, dices the GAM445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM445 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM445 RNA is designated SEQ ID:6958, and is provided hereinbelow with reference to the sequence listing part.

[6463] GAM445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM445

target RNA, herein designated GAM TARGET RNA.

GAM445 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6464] GAM445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM445 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM445 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM445 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6465] The complementary binding of GAM445 RNA, herein designated GAM RNA, to target binding sites on GAM445 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM445 target RNA, herein designated GAM TARGET RNA, into GAM445 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6466] It is appreciated that GAM445 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM445 target genes. The mRNA of each one of this plurality of GAM445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM445 RNA, herein designated GAM RNA, and which when bound by GAM445 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM445 target proteins.

[6467] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM445 gene, herein designated GAM GENE, on one or more GAM445 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6468] It is yet further appreciated that specific functions, and accordingly utilities, of GAM445 correlate with, and may be deduced from, the identity of the target genes which GAM445 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6469] Nucleotide sequences of the GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM445 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM445 are further described hereinbelow with reference to Table Table1.

[6470] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM445 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6471]

[6472] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 446 (GAM446) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6473] GAM446 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM446 was detected is described hereinabove with reference to Figs. 2-8.

[6474] GAM446 gene, herein designated GAM GENE, and GAM446 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6475] GAM446 gene, herein designated GAM GENE, encodes a GAM446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM446 precursor RNA is designated SEQ ID:6982, and is provided hereinbelow with reference to the sequence listing part.

[6476] GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6477] An enzyme complex designated DICER COMPLEX, dices the GAM446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM446 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM446 RNA is designated SEQ ID:6983, and is provided hereinbelow with reference to the sequence listing part.

[6478] GAM446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM446 target RNA, herein designated GAM TARGET RNA. GAM446 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6479] GAM446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM446 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM446 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM446 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6480] The complementary binding of GAM446 RNA, herein designated GAM RNA, to target binding sites on GAM446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM446 target RNA, herein designated GAM TARGET RNA, into GAM446 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6481] It is appreciated that GAM446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM446 target genes. The mRNA of each one of this plu-

rality of GAM446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM446 RNA, herein designated GAM RNA, and which when bound by GAM446 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM446 target proteins.

[6482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM446 gene, herein designated GAM GENE, on one or more GAM446 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6483] It is yet further appreciated that specific functions, and accordingly utilities, of GAM446 correlate with, and may be deduced from, the identity of the target genes which GAM446 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6484] Nucleotide sequences of the GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM446 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM446 are further described hereinbelow with reference to Table Table1.

[6485] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM446 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6486]

[6487] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 447 (GAM447) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[6488] GAM447 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM447 was detected is described hereinabove with reference to Figs. 2-8.

[6489] GAM447 gene, herein designated GAM GENE, and GAM447 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6490] GAM447 gene, herein designated GAM GENE, encodes a GAM447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM447 precursor RNA is designated SEQ ID:7008, and is provided hereinbelow with reference to the sequence listing part.

[6491] GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6492] An enzyme complex designated DICER COMPLEX, dices the GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM447 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM447 RNA is designated SEQ ID:7009, and is provided hereinbelow with reference to the sequence listing part.

[6493] GAM447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM447 target RNA, herein designated GAM TARGET RNA.
GAM447 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[6494] GAM447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM447 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM447 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM447 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6495] The complementary binding of GAM447 RNA, herein designated GAM RNA, to target binding sites on GAM447 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM447 target RNA, herein designated GAM TARGET RNA, into GAM447 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6496] It is appreciated that GAM447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM447 target genes. The mRNA of each one of this plurality of GAM447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM447 RNA, herein designated GAM RNA, and which when bound by GAM447 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM447 target proteins.

[6497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM447 gene, herein designated GAM GENE, on one or more GAM447 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6498] It is yet further appreciated that specific functions, and accordingly utilities, of GAM447 correlate with, and may be deduced from, the identity of the target genes which GAM447 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6499] Nucleotide sequences of the GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM447 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM447 are further described hereinbelow with reference to Table Table1.

[6500] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM447 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6501]

[6502] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 448 (GAM448) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6503] GAM448 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM448 was detected is described hereinabove with reference to Figs. 2-8.

[6504] GAM448 gene, herein designated GAM GENE, and GAM448 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6505] GAM448 gene, herein designated GAM GENE, encodes a GAM448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM448 precursor RNA is designated SEQ ID:7057, and is provided hereinbelow with reference to the sequence listing part.

[6506] GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6507] An enzyme complex designated DICER COMPLEX, dices the GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM448 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of

GAM448 RNA is designated SEQ ID:7009, and is provided hereinbelow with reference to the sequence listing part.

[6508] GAM448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM448 target RNA, herein designated GAM TARGET RNA. GAM448 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6509] GAM448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM448 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM448 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM448 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6510] The complementary binding of GAM448 RNA, herein designated GAM RNA, to target binding sites on GAM448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM448 target RNA, herein designated GAM TARGET RNA, into GAM448 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6511] It is appreciated that GAM448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM448 target genes. The mRNA of each one of this plurality of GAM448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM448 RNA, herein designated GAM RNA, and which when bound by GAM448 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM448 target proteins.

[6512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM448 gene, herein designated GAM GENE, on one or more GAM448 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6513] It is yet further appreciated that specific functions, and accordingly utilities, of GAM448 correlate with, and may be deduced from, the identity of the target genes which GAM448 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6514] Nucleotide sequences of the GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM448 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM448 are further described hereinbelow with reference to Table Table1.

[6515] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM448 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6516]

[6517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 449 (GAM449) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6518] GAM449 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM449 was detected is described hereinabove

with reference to Figs. 2-8.

[6519] GAM449 gene, herein designated GAM GENE, and GAM449 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6520] GAM449 gene, herein designated GAM GENE, encodes a GAM449 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM449 precursor RNA is designated SEQ ID:7061, and is provided hereinbelow with reference to the sequence listing part.

[6521] GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6522] An enzyme complex designated DICER COMPLEX, dices the GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM449 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM449 RNA is designated SEQ ID:7062, and is provided hereinbelow with reference to the sequence listing part.

[6523] GAM449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM449 target RNA, herein designated GAM TARGET RNA. GAM449 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6524] GAM449 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM449 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM449 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM449 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM449 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6525] The complementary binding of GAM449 RNA, herein designated GAM RNA, to target binding sites on GAM449 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM449 target RNA, herein designated GAM TARGET RNA, into GAM449 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[6526] It is appreciated that GAM449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM449 target genes. The mRNA of each one of this plurality of GAM449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM449 RNA, herein designated GAM RNA, and which when bound by GAM449 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM449 target proteins.

[6527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM449 gene, herein designated GAM GENE, on one or more GAM449 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6528] It is yet further appreciated that specific functions, and accordingly utilities, of GAM449 correlate with, and may be deduced from, the identity of the target genes which GAM449 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6529] Nucleotide sequences of the GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM449 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM449 are further described hereinbelow with reference to Table Table1.

[6530] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM449 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6531]

[6532] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 450 (GAM450) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6533] GAM450 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM450 was detected is described hereinabove with reference to Figs. 2-8.

[6534] GAM450 gene, herein designated GAM GENE, and GAM450 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6535] GAM450 gene, herein designated GAM GENE, encodes a GAM450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM450 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM450 precursor RNA is designated SEQ ID:7075, and is provided hereinbelow with reference to the sequence listing part.

[6536] GAM450 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6537] An enzyme complex designated DICER COMPLEX, dices the GAM450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM450 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM450 RNA is designated SEQ ID:7076, and is provided hereinbelow with reference to the sequence listing part.

[6538] GAM450 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM450 target RNA, herein designated GAM TARGET RNA.

GAM450 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6539] GAM450 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM450 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM450 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM450 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6540] The complementary binding of GAM450 RNA, herein designated GAM RNA, to target binding sites on GAM450 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM450 target RNA, herein designated GAM TARGET RNA, into GAM450 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6541] It is appreciated that GAM450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM450 target genes. The mRNA of each one of this plurality of GAM450 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM450 RNA, herein designated GAM RNA, and which when bound by GAM450 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM450 target proteins.

[6542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM450 gene, herein designated GAM GENE, on one or more GAM450 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6543] It is yet further appreciated that specific functions, and accordingly utilities, of GAM450 correlate with, and may be deduced from, the identity of the target genes which GAM450 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6544] Nucleotide sequences of the GAM450 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM450 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM450 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM450 are further described hereinbelow with reference to Table Table1.

[6545] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM450 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6546]

[6547] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 451 (GAM451) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6548] GAM451 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM451 was detected is described hereinabove with reference to Figs. 2-8.

[6549] GAM451 gene, herein designated GAM GENE, and GAM451 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6550] GAM451 gene, herein designated GAM GENE, encodes a

GAM451 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM451 precursor RNA is designated SEQ ID:7091, and is provided hereinbelow with reference to the sequence listing part.

[6551] GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6552] An enzyme complex designated DICER COMPLEX, dices the GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM451 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM451 RNA is designated SEQ ID:7092, and is provided hereinbelow with reference to the sequence listing part.

[6553] GAM451 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM451 target RNA, herein designated GAM TARGET RNA. GAM451 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6554] GAM451 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM451 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM451 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM451 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM451 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6555] The complementary binding of GAM451 RNA, herein designated GAM RNA, to target binding sites on GAM451 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM451 target RNA, herein designated GAM TARGET RNA, into GAM451 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6556] It is appreciated that GAM451 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM451 target genes. The mRNA of each one of this plurality of GAM451 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM451 RNA, herein designated GAM RNA, and which when bound by GAM451 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM451 target proteins.

[6557] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM451 gene, herein designated GAM GENE, on one or more GAM451 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6558] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM451 correlate with, and may be deduced from, the identity of the target genes which GAM451 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6559] Nucleotide sequences of the GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM451 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM451 are further described hereinbelow with reference to Table Table1.

[6560] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM451 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6561]

[6562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 452 (GAM452) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[6563] GAM452 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM452 was detected is described hereinabove with reference to Figs. 2-8.

[6564] GAM452 gene, herein designated GAM GENE, and GAM452 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6565] GAM452 gene, herein designated GAM GENE, encodes a GAM452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM452 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM452 precursor RNA is designated SEQ ID:7099, and is provided hereinbelow with reference to the sequence listing part.

[6566] GAM452 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6567] An enzyme complex designated DICER COMPLEX, dices the GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM452 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 24%) nucleotide sequence of GAM452 RNA is designated SEQ ID:7100, and is provided hereinbelow with reference to the sequence listing part.

[6568] GAM452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM452 target RNA, herein designated GAM TARGET RNA. GAM452 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6569] GAM452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM452 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM452 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM452 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6570] The complementary binding of GAM452 RNA, herein designated GAM RNA, to target binding sites on GAM452 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM452 target RNA, herein designated GAM TARGET RNA, into GAM452 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6571] It is appreciated that GAM452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM452 target genes. The mRNA of each one of this plurality of GAM452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM452 RNA, herein designated GAM RNA, and which when bound by GAM452 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM452 target proteins.

[6572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM452 gene, herein designated GAM GENE, on one or more GAM452 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM452 correlate with, and may be deduced from, the identity of the target genes which GAM452 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6574] Nucleotide sequences of the GAM452 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM452 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM452 are further described hereinbelow with reference to Table Table1.

[6575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM452 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6576]

[6577] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 453 (GAM453) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6578] GAM453 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM453 was detected is described hereinabove with reference to Figs. 2-8.

[6579] GAM453 gene, herein designated GAM GENE, and GAM453 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6580] GAM453 gene, herein designated GAM GENE, encodes a GAM453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM453 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM453 precursor RNA is designated SEQ ID:7116, and is provided hereinbelow with reference to the sequence listing part.

[6581] GAM453 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6582] An enzyme complex designated DICER COMPLEX, dices the GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM453 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM453 RNA is designated SEQ ID:3102, and is provided

hereinbelow with reference to the sequence listing part.

[6583] GAM453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM453 target RNA, herein designated GAM TARGET RNA.
GAM453 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6584] GAM453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM453 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM453 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM453 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6585] The complementary binding of GAM453 RNA, herein designated GAM RNA, to target binding sites on GAM453 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM453 target RNA, herein designated GAM TARGET RNA, into GAM453 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6586] It is appreciated that GAM453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM453 target genes. The mRNA of each one of this plurality of GAM453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM453 RNA, herein designated GAM RNA, and which when bound by GAM453 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM453 tar-

get proteins.

[6587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM453 gene, herein designated GAM GENE, on one or more GAM453 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6588] It is yet further appreciated that specific functions, and accordingly utilities, of GAM453 correlate with, and may be deduced from, the identity of the target genes which GAM453 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6589] Nucleotide sequences of the GAM453 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM453 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM453 are further described hereinbelow with reference to Table Table1.

[6590] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM453 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6591]

[6592] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 454 (GAM454) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6593] GAM454 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM454 was detected is described hereinabove with reference to Figs. 2-8.

[6594] GAM454 gene, herein designated GAM GENE, and GAM454 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6595] GAM454 gene, herein designated GAM GENE, encodes a GAM454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM454 precursor RNA is designated SEQ ID:7127, and is provided hereinbelow with reference to the sequence listing part.

[6596] GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6597] An enzyme complex designated DICER COMPLEX, dices

the GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM454 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM454 RNA is designated SEQ ID:7128, and is provided hereinbelow with reference to the sequence listing part.

[6598] GAM454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM454 target RNA, herein designated GAM TARGET RNA. GAM454 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6599] GAM454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM454

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM454 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM454 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6600] The complementary binding of GAM454 RNA, herein designated GAM RNA, to target binding sites on GAM454 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM454 target RNA, herein designated GAM TARGET RNA, into GAM454 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6601] It is appreciated that GAM454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM454 target genes. The mRNA of each one of this plurality of GAM454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM454 RNA, herein designated GAM RNA, and which when bound by GAM454 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM454 target proteins.

[6602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM454 gene, herein designated GAM GENE, on one or more GAM454 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6603] It is yet further appreciated that specific functions, and accordingly utilities, of GAM454 correlate with, and may be deduced from, the identity of the target genes which GAM454 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6604] Nucleotide sequences of the GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM454 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM454 are further described hereinbelow with reference to Table Table1.

[6605] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM454 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6606]

[6607] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 455 (GAM455) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6608] GAM455 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM455 was detected is described hereinabove with reference to Figs. 2-8.

[6609] GAM455 gene, herein designated GAM GENE, and GAM455 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6610] GAM455 gene, herein designated GAM GENE, encodes a GAM455 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM455 precursor RNA is designated SEQ ID:7145, and is provided hereinbelow with reference to the sequence listing part.

[6611] GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM455 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6612] An enzyme complex designated DICER COMPLEX, dices the GAM455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM455 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM455 RNA is designated SEQ ID:7146, and is provided hereinbelow with reference to the sequence listing part.

[6613] GAM455 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM455 target RNA, herein designated GAM TARGET RNA. GAM455 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6614] GAM455 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM455 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM455 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM455 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM455 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6615] The complementary binding of GAM455 RNA, herein designated GAM RNA, to target binding sites on GAM455 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM455 target RNA, herein designated GAM TARGET RNA, into GAM455 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6616] It is appreciated that GAM455 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM455 target genes. The mRNA of each one of this plurality of GAM455 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM455 RNA, herein designated GAM RNA, and which when bound by GAM455 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM455 target proteins.

[6617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM455 gene, herein designated GAM GENE, on one or

more GAM455 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM455 correlate with, and may be deduced from, the identity of the target genes which GAM455 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6619] Nucleotide sequences of the GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM455 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM455 are further de-

scribed hereinbelow with reference to Table Table1.

[6620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM455 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6621]

[6622] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 456 (GAM456) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6623] GAM456 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM456 was detected is described hereinabove with reference to Figs. 2-8.

[6624] GAM456 gene, herein designated GAM GENE, and GAM456 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6625] GAM456 gene, herein designated GAM GENE, encodes a GAM456 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM456 precursor RNA is designated SEQ ID:7191, and is provided hereinbelow with reference to the sequence listing part.

[6626] GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6627] An enzyme complex designated DICER COMPLEX, dices the GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM456 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM456 RNA is designated SEQ ID:7192, and is provided hereinbelow with reference to the sequence listing part.

[6628] GAM456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM456 target RNA, herein designated GAM TARGET RNA. GAM456 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6629] GAM456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM456 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM456 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM456 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6630] The complementary binding of GAM456 RNA, herein designated GAM RNA, to target binding sites on GAM456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM456 target RNA, herein designated GAM TARGET RNA, into GAM456 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6631] It is appreciated that GAM456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM456 target genes. The mRNA of each one of this plurality of GAM456 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM456 RNA, herein designated GAM RNA, and which when bound by GAM456 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM456 target proteins.

[6632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM456 gene, herein designated GAM GENE, on one or more GAM456 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM456 correlate with, and may

be deduced from, the identity of the target genes which GAM456 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6634] Nucleotide sequences of the GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM456 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM456 are further described hereinbelow with reference to Table Table1.

[6635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM456 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6636]

[6637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 457 (GAM457) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6638] GAM457 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM457 was detected is described hereinabove with reference to Figs. 2-8.

[6639] GAM457 gene, herein designated GAM GENE, and GAM457 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6640] GAM457 gene, herein designated GAM GENE, encodes a GAM457 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM457 precursor RNA is designated SEQ ID:7205, and is provided hereinbelow with reference to the sequence listing part.

[6641] GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6642] An enzyme complex designated DICER COMPLEX, dices the GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM457 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 26%) nucleotide sequence of GAM457 RNA is designated SEQ ID:7206, and is provided hereinbelow with reference to the sequence listing part.

[6643] GAM457 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM457 target RNA, herein designated GAM TARGET RNA. GAM457 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6644] GAM457 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM457 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM457 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM457 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM457 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6645] The complementary binding of GAM457 RNA, herein designated GAM RNA, to target binding sites on GAM457 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM457 target RNA, herein designated GAM TARGET RNA, into GAM457 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6646] It is appreciated that GAM457 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM457 target genes. The mRNA of each one of this plurality of GAM457 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM457 RNA, herein designated GAM RNA, and which when bound by GAM457 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM457 target proteins.

[6647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM457 gene, herein designated GAM GENE, on one or more GAM457 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM457 correlate with, and may be deduced from, the identity of the target genes which GAM457 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6649] Nucleotide sequences of the GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM457 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM457 are further described hereinbelow with reference to Table Table1.

[6650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM457 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6651]

[6652] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 458 (GAM458) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6653] GAM458 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM458 was detected is described hereinabove with reference to Figs. 2-8.

[6654] GAM458 gene, herein designated GAM GENE, and GAM458 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6655] GAM458 gene, herein designated GAM GENE, encodes a GAM458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM458 precursor RNA is desig-

nated SEQ ID:7226, and is provided hereinbelow with reference to the sequence listing part.

[6656] GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6657] An enzyme complex designated DICER COMPLEX, dices the GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM458 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM458 RNA is designated SEQ ID:7227, and is provided hereinbelow with reference to the sequence listing part.

[6658] GAM458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM458 target RNA, herein designated GAM TARGET RNA. GAM458 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6659] GAM458 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM458 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM458 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM458

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6660] The complementary binding of GAM458 RNA, herein designated GAM RNA, to target binding sites on GAM458 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM458 target RNA, herein designated GAM TARGET RNA, into GAM458 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6661] It is appreciated that GAM458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM458 target genes. The mRNA of each one of this plurality of GAM458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM458 RNA, herein designated GAM RNA, and which when bound by GAM458 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM458 target proteins.

[6662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM458 gene, herein designated GAM GENE, on one or more GAM458 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6663] It is yet further appreciated that specific functions, and accordingly utilities, of GAM458 correlate with, and may be deduced from, the identity of the target genes which GAM458 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6664] Nucleotide sequences of the GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM458 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM458 are further described hereinbelow with reference to Table Table1.

[6665] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM458 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6666]

[6667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 459 (GAM459) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6668] GAM459 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM459 was detected is described hereinabove with reference to Figs. 2-8.

[6669] GAM459 gene, herein designated GAM GENE, and

GAM459 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6670] GAM459 gene, herein designated GAM GENE, encodes a GAM459 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM459 precursor RNA is designated SEQ ID:7262, and is provided hereinbelow with reference to the sequence listing part.

[6671] GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6672] An enzyme complex designated DICER COMPLEX, dices the GAM459 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM459 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM459 RNA is designated SEQ ID:7263, and is provided hereinbelow with reference to the sequence listing part.

[6673] GAM459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM459 target RNA, herein designated GAM TARGET RNA. GAM459 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6674] GAM459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM459 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM459 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM459 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6675] The complementary binding of GAM459 RNA, herein designated GAM RNA, to target binding sites on GAM459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM459 target RNA, herein designated GAM TARGET RNA, into GAM459 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6676] It is appreciated that GAM459 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM459 target genes. The mRNA of each one of this plurality of GAM459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM459 RNA, herein designated GAM RNA, and which when bound by GAM459 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM459 target proteins.

[6677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM459 gene, herein designated GAM GENE, on one or more GAM459 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM459 correlate with, and may be deduced from, the identity of the target genes which GAM459 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6679] Nucleotide sequences of the GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM459 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM459 are further described hereinbelow with reference to Table Table1.

[6680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM459 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6681]

[6682] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 460 (GAM460) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6683] GAM460 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM460 was detected is described hereinabove with reference to Figs. 2-8.

[6684] GAM460 gene, herein designated GAM GENE, and GAM460 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6685] GAM460 gene, herein designated GAM GENE, encodes a GAM460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM460 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM460 precursor RNA is designated SEQ ID:7273, and is provided hereinbelow with reference to the sequence listing part.

[6686] GAM460 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6687] An enzyme complex designated DICER COMPLEX, dices the GAM460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM460 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM460 RNA is designated SEQ ID:7274, and is provided hereinbelow with reference to the sequence listing part.

[6688] GAM460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM460 target RNA, herein designated GAM TARGET RNA. GAM460 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6689] GAM460 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM460 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM460 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM460 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6690] The complementary binding of GAM460 RNA, herein designated GAM RNA, to target binding sites on GAM460 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM460 target RNA, herein designated GAM TARGET RNA, into GAM460 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6691] It is appreciated that GAM460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM460 target genes. The mRNA of each one of this plurality of GAM460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM460 RNA, herein designated GAM RNA, and which when bound by GAM460 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM460 target proteins.

[6692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM460 gene, herein designated GAM GENE, on one or more GAM460 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6693] It is yet further appreciated that specific functions, and accordingly utilities, of GAM460 correlate with, and may be deduced from, the identity of the target genes which GAM460 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6694] Nucleotide sequences of the GAM460 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM460 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM460 are further described hereinbelow with reference to Table Table1.

[6695] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM460 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6696]

[6697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 461 (GAM461) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6698] GAM461 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM461 was detected is described hereinabove with reference to Figs. 2-8.

[6699] GAM461 gene, herein designated GAM GENE, and GAM461 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6700] GAM461 gene, herein designated GAM GENE, encodes a GAM461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM461 precursor RNA is designated SEQ ID:7296, and is provided hereinbelow with reference to the sequence listing part.

[6701] GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6702] An enzyme complex designated DICER COMPLEX, dices the GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM461 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM461 RNA is designated SEQ ID:5801, and is provided hereinbelow with reference to the sequence listing part.

[6703] GAM461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM461 target RNA, herein designated GAM TARGET RNA. GAM461 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6704] GAM461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM461 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM461 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM461 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6705] The complementary binding of GAM461 RNA, herein designated GAM RNA, to target binding sites on GAM461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM461 target RNA, herein designated GAM TARGET RNA, into GAM461 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6706] It is appreciated that GAM461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM461 target genes. The mRNA of each one of this plurality of GAM461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM461 RNA,

herein designated GAM RNA, and which when bound by GAM461 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM461 target proteins.

[6707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM461 gene, herein designated GAM GENE, on one or more GAM461 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM461 correlate with, and may be deduced from, the identity of the target genes which

GAM461 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6709] Nucleotide sequences of the GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM461 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM461 are further described hereinbelow with reference to Table Table1.

[6710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM461 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6711]

[6712] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 462 (GAM462) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6713] GAM462 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM462 was detected is described hereinabove with reference to Figs. 2-8.

[6714] GAM462 gene, herein designated GAM GENE, and GAM462 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6715] GAM462 gene, herein designated GAM GENE, encodes a GAM462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM462 precursor RNA is designated SEQ ID:7301, and is provided hereinbelow with reference to the sequence listing part.

[6716] GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6717] An enzyme complex designated DICER COMPLEX, dices the GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM462 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM462 RNA is designated SEQ ID:7302, and is provided hereinbelow with reference to the sequence listing part.

[6718] GAM462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM462 target RNA, herein designated GAM TARGET RNA.
GAM462 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6719] GAM462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM462 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM462 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM462 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6720] The complementary binding of GAM462 RNA, herein designated GAM RNA, to target binding sites on GAM462 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM462 target RNA, herein desig-

nated GAM TARGET RNA, into GAM462 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6721] It is appreciated that GAM462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM462 target genes. The mRNA of each one of this plurality of GAM462 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM462 RNA, herein designated GAM RNA, and which when bound by GAM462 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM462 target proteins.

[6722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM462 gene, herein designated GAM GENE, on one or more GAM462 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6723] It is yet further appreciated that specific functions, and accordingly utilities, of GAM462 correlate with, and may be deduced from, the identity of the target genes which GAM462 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6724] Nucleotide sequences of the GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM462 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM462 are further described hereinbelow with reference to Table Table1.

[6725] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM462 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6726]

[6727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 463 (GAM463) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6728] GAM463 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM463 was detected is described hereinabove with reference to Figs. 2-8.

[6729] GAM463 gene, herein designated GAM GENE, and GAM463 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6730] GAM463 gene, herein designated GAM GENE, encodes a GAM463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM463 precursor RNA is designated SEQ ID:7309, and is provided hereinbelow with ref-

erence to the sequence listing part.

[6731] GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6732] An enzyme complex designated DICER COMPLEX, dices the GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM463 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM463 RNA is designated SEQ ID:7310, and is provided hereinbelow with reference to the sequence listing part.

[6733] GAM463 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM463 target RNA, herein designated GAM TARGET RNA.

GAM463 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6734] GAM463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM463 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM463 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM463 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6735] The complementary binding of GAM463 RNA, herein designated GAM RNA, to target binding sites on GAM463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM463 target RNA, herein designated GAM TARGET RNA, into GAM463 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6736] It is appreciated that GAM463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM463 target genes. The mRNA of each one of this plurality of GAM463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM463 RNA, herein designated GAM RNA, and which when bound by GAM463 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM463 target proteins.

[6737] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM463 gene, herein designated GAM GENE, on one or more GAM463 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM463 correlate with, and may be deduced from, the identity of the target genes which GAM463 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6739] Nucleotide sequences of the GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM463 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM463 are further described hereinbelow with reference to Table Table1.

[6740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM463 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6741]

[6742] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 464 (GAM464) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6743] GAM464 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM464 was detected is described hereinabove with reference to Figs. 2-8.

[6744] GAM464 gene, herein designated GAM GENE, and GAM464 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6745] GAM464 gene, herein designated GAM GENE, encodes a GAM464 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM464 precursor RNA is designated SEQ ID:7323, and is provided hereinbelow with reference to the sequence listing part.

[6746] GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6747] An enzyme complex designated DICER COMPLEX, dices the GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM464 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM464 RNA is designated SEQ ID:7324, and is provided hereinbelow with reference to the sequence listing part.

[6748] GAM464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM464 target RNA, herein designated GAM TARGET RNA. GAM464 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6749] GAM464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM464 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM464 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM464 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM464 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6750] The complementary binding of GAM464 RNA, herein designated GAM RNA, to target binding sites on GAM464 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM464 target RNA, herein designated GAM TARGET RNA, into GAM464 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6751] It is appreciated that GAM464 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM464 target genes. The mRNA of each one of this plurality of GAM464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM464 RNA, herein designated GAM RNA, and which when bound by GAM464 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM464 target proteins.

[6752] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM464 gene, herein designated GAM GENE, on one or more GAM464 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[6753] It is yet further appreciated that specific functions, and accordingly utilities, of GAM464 correlate with, and may be deduced from, the identity of the target genes which GAM464 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6754] Nucleotide sequences of the GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM464 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM464 are further described hereinbelow with reference to Table Table1.

[6755] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM464 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6756]

[6757] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

465 (GAM465) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6758] GAM465 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM465 was detected is described hereinabove with reference to Figs. 2-8.

[6759] GAM465 gene, herein designated GAM GENE, and GAM465 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6760] GAM465 gene, herein designated GAM GENE, encodes a GAM465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM465 precursor RNA is designated SEQ ID:7338, and is provided hereinbelow with reference to the sequence listing part.

[6761] GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6762] An enzyme complex designated DICER COMPLEX, dices the GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM465 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 35%) nucleotide sequence of GAM465 RNA is designated SEQ ID:7339, and is provided hereinbelow with reference to the sequence listing part.

[6763] GAM465 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM465 target RNA, herein designated GAM TARGET RNA. GAM465 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6764] GAM465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM465 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM465 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM465 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM465 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6765] The complementary binding of GAM465 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM465 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM465 target RNA, herein designated GAM TARGET RNA, into GAM465 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6766] It is appreciated that GAM465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM465 target genes. The mRNA of each one of this plurality of GAM465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM465 RNA, herein designated GAM RNA, and which when bound by GAM465 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM465 target proteins.

[6767] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM465 gene, herein designated GAM GENE, on one or more GAM465 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6768] It is yet further appreciated that specific functions, and accordingly utilities, of GAM465 correlate with, and may be deduced from, the identity of the target genes which GAM465 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6769] Nucleotide sequences of the GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM465 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM465 are further described hereinbelow with reference to Table Table1.

[6770] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM465 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6771]

[6772] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 466 (GAM466) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6773] GAM466 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM466 was detected is described hereinabove with reference to Figs. 2-8.

[6774] GAM466 gene, herein designated GAM GENE, and GAM466 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6775] GAM466 gene, herein designated GAM GENE, encodes a GAM466 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM466 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM466 precursor RNA is designated SEQ ID:7348, and is provided hereinbelow with reference to the sequence listing part.

[6776] GAM466 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6777] An enzyme complex designated DICER COMPLEX, dices the GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM466 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 40%) nucleotide sequence of GAM466 RNA is designated SEQ ID:7349, and is provided hereinbelow with reference to the sequence listing part.

[6778] GAM466 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM466 target RNA, herein designated GAM TARGET RNA. GAM466 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6779] GAM466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM466 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM466 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM466 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6780] The complementary binding of GAM466 RNA, herein designated GAM RNA, to target binding sites on GAM466 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM466 target RNA, herein designated GAM TARGET RNA, into GAM466 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6781] It is appreciated that GAM466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM466 target genes. The mRNA of each one of this plurality of GAM466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM466 RNA, herein designated GAM RNA, and which when bound by

GAM466 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM466 target proteins.

[6782] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM466 gene, herein designated GAM GENE, on one or more GAM466 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6783] It is yet further appreciated that specific functions, and accordingly utilities, of GAM466 correlate with, and may be deduced from, the identity of the target genes which GAM466 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[6784] Nucleotide sequences of the GAM466 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM466 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM466 are further described hereinbelow with reference to Table Table1.

[6785] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM466 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6786]

[6787] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 467 (GAM467) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6788] GAM467 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM467 was detected is described hereinabove with reference to Figs. 2-8.

[6789] GAM467 gene, herein designated GAM GENE, and GAM467 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6790] GAM467 gene, herein designated GAM GENE, encodes a GAM467 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM467 precursor RNA is designated SEQ ID:7361, and is provided hereinbelow with reference to the sequence listing part.

[6791] GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6792] An enzyme complex designated DICER COMPLEX, dices the GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM467 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM467 RNA is designated SEQ ID:7362, and is provided hereinbelow with reference to the sequence listing part.

[6793] GAM467 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM467 target RNA, herein designated GAM TARGET RNA. GAM467 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6794] GAM467 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM467 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM467 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM467 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM467 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6795] The complementary binding of GAM467 RNA, herein designated GAM RNA, to target binding sites on GAM467 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM467 target RNA, herein designated GAM TARGET RNA, into GAM467 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6796] It is appreciated that GAM467 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM467 target genes. The mRNA of each one of this plurality of GAM467 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM467 RNA, herein designated GAM RNA, and which when bound by GAM467 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM467 target proteins.

[6797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM467 gene, herein designated GAM GENE, on one or more GAM467 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6798] It is yet further appreciated that specific functions, and accordingly utilities, of GAM467 correlate with, and may be deduced from, the identity of the target genes which GAM467 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6799] Nucleotide sequences of the GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM467 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM467 are further described hereinbelow with reference to Table Table1.

[6800] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM467 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6801]

[6802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 468 (GAM468) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6803] GAM468 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM468 was detected is described hereinabove with reference to Figs. 2-8.

[6804] GAM468 gene, herein designated GAM GENE, and GAM468 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6805] GAM468 gene, herein designated GAM GENE, encodes a GAM468 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM468 precursor RNA is designated SEQ ID:7380, and is provided hereinbelow with reference to the sequence listing part.

[6806] GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6807] An enzyme complex designated DICER COMPLEX, dices the GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM468 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM468 RNA is designated SEQ ID:7381, and is provided hereinbelow with reference to the sequence listing part.

[6808] GAM468 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM468

target RNA, herein designated GAM TARGET RNA.

GAM468 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6809] GAM468 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM468 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM468 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM468 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM468 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6810] The complementary binding of GAM468 RNA, herein designated GAM RNA, to target binding sites on GAM468 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM468 target RNA, herein designated GAM TARGET RNA, into GAM468 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6811] It is appreciated that GAM468 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM468 target genes. The mRNA of each one of this plurality of GAM468 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM468 RNA, herein designated GAM RNA, and which when bound by GAM468 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM468 target proteins.

[6812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM468 gene, herein designated GAM GENE, on one or more GAM468 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6813] It is yet further appreciated that specific functions, and accordingly utilities, of GAM468 correlate with, and may be deduced from, the identity of the target genes which GAM468 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6814] Nucleotide sequences of the GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM468 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM468 are further described hereinbelow with reference to Table Table1.

[6815] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM468 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6816]

[6817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 469 (GAM469) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6818] GAM469 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM469 was detected is described hereinabove with reference to Figs. 2-8.

[6819] GAM469 gene, herein designated GAM GENE, and GAM469 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6820] GAM469 gene, herein designated GAM GENE, encodes a GAM469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM469 precursor RNA is designated SEQ ID:7395, and is provided hereinbelow with reference to the sequence listing part.

[6821] GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6822] An enzyme complex designated DICER COMPLEX, dices the GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM469 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of GAM469 RNA is designated SEQ ID:7396, and is provided hereinbelow with reference to the sequence listing part.

[6823] GAM469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM469 target RNA, herein designated GAM TARGET RNA. GAM469 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6824] GAM469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM469 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM469 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM469 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6825] The complementary binding of GAM469 RNA, herein designated GAM RNA, to target binding sites on GAM469 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM469 target RNA, herein designated GAM TARGET RNA, into GAM469 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6826] It is appreciated that GAM469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM469 target genes. The mRNA of each one of this plu-

rality of GAM469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM469 RNA, herein designated GAM RNA, and which when bound by GAM469 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM469 target proteins.

[6827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM469 gene, herein designated GAM GENE, on one or more GAM469 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM469 correlate with, and may be deduced from, the identity of the target genes which GAM469 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6829] Nucleotide sequences of the GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM469 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM469 are further described hereinbelow with reference to Table Table1.

[6830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM469 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6831]

[6832] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 470 (GAM470) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[6833] GAM470 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM470 was detected is described hereinabove with reference to Figs. 2-8.

[6834] GAM470 gene, herein designated GAM GENE, and GAM470 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6835] GAM470 gene, herein designated GAM GENE, encodes a GAM470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM470 precursor RNA is designated SEQ ID:7429, and is provided hereinbelow with reference to the sequence listing part.

[6836] GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6837] An enzyme complex designated DICER COMPLEX, dices the GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM470 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 39%) nucleotide sequence of GAM470 RNA is designated SEQ ID:7430, and is provided hereinbelow with reference to the sequence listing part.

[6838] GAM470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM470 target RNA, herein designated GAM TARGET RNA.
GAM470 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[6839] GAM470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM470 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM470 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM470 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6840] The complementary binding of GAM470 RNA, herein designated GAM RNA, to target binding sites on GAM470 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM470 target RNA, herein designated GAM TARGET RNA, into GAM470 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6841] It is appreciated that GAM470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM470 target genes. The mRNA of each one of this plurality of GAM470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM470 RNA, herein designated GAM RNA, and which when bound by GAM470 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM470 target proteins.

[6842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM470 gene, herein designated GAM GENE, on one or more GAM470 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6843] It is yet further appreciated that specific functions, and accordingly utilities, of GAM470 correlate with, and may be deduced from, the identity of the target genes which GAM470 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6844] Nucleotide sequences of the GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM470 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM470 are further described hereinbelow with reference to Table Table1.

[6845] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM470 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6846]

[6847] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 471 (GAM471) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6848] GAM471 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM471 was detected is described hereinabove with reference to Figs. 2-8.

[6849] GAM471 gene, herein designated GAM GENE, and GAM471 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6850] GAM471 gene, herein designated GAM GENE, encodes a GAM471 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM471 precursor RNA is designated SEQ ID:7457, and is provided hereinbelow with reference to the sequence listing part.

[6851] GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6852] An enzyme complex designated DICER COMPLEX, dices the GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM471 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 33%) nucleotide sequence of

GAM471 RNA is designated SEQ ID:7458, and is provided hereinbelow with reference to the sequence listing part.

[6853] GAM471 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM471 target RNA, herein designated GAM TARGET RNA. GAM471 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6854] GAM471 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM471 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM471 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM471 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM471 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6855] The complementary binding of GAM471 RNA, herein designated GAM RNA, to target binding sites on GAM471 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM471 target RNA, herein designated GAM TARGET RNA, into GAM471 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6856] It is appreciated that GAM471 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM471 target genes. The mRNA of each one of this plurality of GAM471 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM471 RNA, herein designated GAM RNA, and which when bound by GAM471 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM471 target proteins.

[6857] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM471 gene, herein designated GAM GENE, on one or more GAM471 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6858] It is yet further appreciated that specific functions, and accordingly utilities, of GAM471 correlate with, and may be deduced from, the identity of the target genes which GAM471 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6859] Nucleotide sequences of the GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM471 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM471 are further described hereinbelow with reference to Table Table1.

[6860] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM471 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6861]

[6862] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 472 (GAM472) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6863] GAM472 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM472 was detected is described hereinabove

with reference to Figs. 2-8.

[6864] GAM472 gene, herein designated GAM GENE, and GAM472 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6865] GAM472 gene, herein designated GAM GENE, encodes a GAM472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM472 precursor RNA is designated SEQ ID:7463, and is provided hereinbelow with reference to the sequence listing part.

[6866] GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6867] An enzyme complex designated DICER COMPLEX, dices the GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM472 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM472 RNA is designated SEQ ID:7464, and is provided hereinbelow with reference to the sequence listing part.

[6868] GAM472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM472 target RNA, herein designated GAM TARGET RNA. GAM472 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6869] GAM472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM472 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM472 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM472 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM472 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6870] The complementary binding of GAM472 RNA, herein designated GAM RNA, to target binding sites on GAM472 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM472 target RNA, herein designated GAM TARGET RNA, into GAM472 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[6871] It is appreciated that GAM472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM472 target genes. The mRNA of each one of this plurality of GAM472 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM472 RNA, herein designated GAM RNA, and which when bound by GAM472 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM472 target proteins.

[6872] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM472 gene, herein designated GAM GENE, on one or more GAM472 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6873] It is yet further appreciated that specific functions, and accordingly utilities, of GAM472 correlate with, and may be deduced from, the identity of the target genes which GAM472 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6874] Nucleotide sequences of the GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM472 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM472 are further described hereinbelow with reference to Table Table1.

[6875] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM472 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6876]

[6877] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 473 (GAM473) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6878] GAM473 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM473 was detected is described hereinabove with reference to Figs. 2-8.

[6879] GAM473 gene, herein designated GAM GENE, and GAM473 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6880] GAM473 gene, herein designated GAM GENE, encodes a GAM473 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM473 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM473 precursor RNA is designated SEQ ID:7481, and is provided hereinbelow with reference to the sequence listing part.

[6881] GAM473 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6882] An enzyme complex designated DICER COMPLEX, dices the GAM473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM473 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 18%) nucleotide sequence of GAM473 RNA is designated SEQ ID:7482, and is provided hereinbelow with reference to the sequence listing part.

[6883] GAM473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM473 target RNA, herein designated GAM TARGET RNA.

GAM473 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6884] GAM473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM473 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM473 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM473 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6885] The complementary binding of GAM473 RNA, herein designated GAM RNA, to target binding sites on GAM473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM473 target RNA, herein designated GAM TARGET RNA, into GAM473 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6886] It is appreciated that GAM473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM473 target genes. The mRNA of each one of this plurality of GAM473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM473 RNA, herein designated GAM RNA, and which when bound by GAM473 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM473 target proteins.

[6887] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM473 gene, herein designated GAM GENE, on one or more GAM473 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6888] It is yet further appreciated that specific functions, and accordingly utilities, of GAM473 correlate with, and may be deduced from, the identity of the target genes which GAM473 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6889] Nucleotide sequences of the GAM473 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM473 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM473 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM473 are further described hereinbelow with reference to Table Table1.

[6890] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM473 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6891]

[6892] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 474 (GAM474) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6893] GAM474 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM474 was detected is described hereinabove with reference to Figs. 2-8.

[6894] GAM474 gene, herein designated GAM GENE, and GAM474 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6895] GAM474 gene, herein designated GAM GENE, encodes a

GAM474 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM474 precursor RNA is designated SEQ ID:7493, and is provided hereinbelow with reference to the sequence listing part.

[6896] GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6897] An enzyme complex designated DICER COMPLEX, dices the GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM474 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of GAM474 RNA is designated SEQ ID:7494, and is provided hereinbelow with reference to the sequence listing part.

[6898] GAM474 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM474 target RNA, herein designated GAM TARGET RNA. GAM474 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6899] GAM474 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM474 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM474 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM474 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM474 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6900] The complementary binding of GAM474 RNA, herein designated GAM RNA, to target binding sites on GAM474 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM474 target RNA, herein designated GAM TARGET RNA, into GAM474 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6901] It is appreciated that GAM474 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM474 target genes. The mRNA of each one of this plurality of GAM474 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM474 RNA, herein designated GAM RNA, and which when bound by GAM474 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM474 target proteins.

[6902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM474 gene, herein designated GAM GENE, on one or more GAM474 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6903] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM474 correlate with, and may be deduced from, the identity of the target genes which GAM474 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6904] Nucleotide sequences of the GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM474 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM474 are further described hereinbelow with reference to Table Table1.

[6905] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM474 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6906]

[6907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 475 (GAM475) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[6908] GAM475 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM475 was detected is described hereinabove with reference to Figs. 2-8.

[6909] GAM475 gene, herein designated GAM GENE, and GAM475 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6910] GAM475 gene, herein designated GAM GENE, encodes a GAM475 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM475 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM475 precursor RNA is designated SEQ ID:7511, and is provided hereinbelow with reference to the sequence listing part.

[6911] GAM475 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6912] An enzyme complex designated DICER COMPLEX, dices the GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM475 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 27%) nucleotide sequence of GAM475 RNA is designated SEQ ID:7512, and is provided hereinbelow with reference to the sequence listing part.

[6913] GAM475 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM475 target RNA, herein designated GAM TARGET RNA. GAM475 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6914] GAM475 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM475 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM475 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM475 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM475 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6915] The complementary binding of GAM475 RNA, herein designated GAM RNA, to target binding sites on GAM475 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM475 target RNA, herein designated GAM TARGET RNA, into GAM475 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6916] It is appreciated that GAM475 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM475 target genes. The mRNA of each one of this plurality of GAM475 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM475 RNA, herein designated GAM RNA, and which when bound by GAM475 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM475 target proteins.

[6917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM475 gene, herein designated GAM GENE, on one or more GAM475 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM475 correlate with, and may be deduced from, the identity of the target genes which GAM475 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6919] Nucleotide sequences of the GAM475 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM475 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM475 are further described hereinbelow with reference to Table Table1.

[6920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM475 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6921]

[6922] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 476 (GAM476) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6923] GAM476 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM476 was detected is described hereinabove with reference to Figs. 2-8.

[6924] GAM476 gene, herein designated GAM GENE, and GAM476 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6925] GAM476 gene, herein designated GAM GENE, encodes a GAM476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM476 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM476 precursor RNA is designated SEQ ID:7541, and is provided hereinbelow with reference to the sequence listing part.

[6926] GAM476 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6927] An enzyme complex designated DICER COMPLEX, dices the GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM476 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of GAM476 RNA is designated SEQ ID:7542, and is provided

hereinbelow with reference to the sequence listing part.

[6928] GAM476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM476 target RNA, herein designated GAM TARGET RNA.

GAM476 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6929] GAM476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM476 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM476 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM476 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6930] The complementary binding of GAM476 RNA, herein designated GAM RNA, to target binding sites on GAM476 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM476 target RNA, herein designated GAM TARGET RNA, into GAM476 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6931] It is appreciated that GAM476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM476 target genes. The mRNA of each one of this plurality of GAM476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM476 RNA, herein designated GAM RNA, and which when bound by GAM476 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM476 tar-

get proteins.

[6932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM476 gene, herein designated GAM GENE, on one or more GAM476 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6933] It is yet further appreciated that specific functions, and accordingly utilities, of GAM476 correlate with, and may be deduced from, the identity of the target genes which GAM476 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6934] Nucleotide sequences of the GAM476 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM476 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM476 are further described hereinbelow with reference to Table Table1.

[6935] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM476 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6936]

[6937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 477 (GAM477) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6938] GAM477 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM477 was detected is described hereinabove with reference to Figs. 2-8.

[6939] GAM477 gene, herein designated GAM GENE, and GAM477 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6940] GAM477 gene, herein designated GAM GENE, encodes a GAM477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM477 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM477 precursor RNA is designated SEQ ID:7561, and is provided hereinbelow with reference to the sequence listing part.

[6941] GAM477 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6942] An enzyme complex designated DICER COMPLEX, dices

the GAM477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM477 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM477 RNA is designated SEQ ID:7562, and is provided hereinbelow with reference to the sequence listing part.

[6943] GAM477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM477 target RNA, herein designated GAM TARGET RNA. GAM477 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6944] GAM477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM477

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM477 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM477 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6945] The complementary binding of GAM477 RNA, herein designated GAM RNA, to target binding sites on GAM477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM477 target RNA, herein designated GAM TARGET RNA, into GAM477 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6946] It is appreciated that GAM477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM477 target genes. The mRNA of each one of this plurality of GAM477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM477 RNA, herein designated GAM RNA, and which when bound by GAM477 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM477 target proteins.

[6947] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM477 gene, herein designated GAM GENE, on one or more GAM477 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6948] It is yet further appreciated that specific functions, and accordingly utilities, of GAM477 correlate with, and may be deduced from, the identity of the target genes which GAM477 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6949] Nucleotide sequences of the GAM477 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM477 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM477 are further described hereinbelow with reference to Table Table1.

[6950] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM477 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6951]

[6952] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 478 (GAM478) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6953] GAM478 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM478 was detected is described hereinabove with reference to Figs. 2-8.

[6954] GAM478 gene, herein designated GAM GENE, and GAM478 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6955] GAM478 gene, herein designated GAM GENE, encodes a GAM478 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM478 precursor RNA is designated SEQ ID:7578, and is provided hereinbelow with reference to the sequence listing part.

[6956] GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM478 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6957] An enzyme complex designated DICER COMPLEX, dices the GAM478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM478 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM478 RNA is designated SEQ ID:7579, and is provided hereinbelow with reference to the sequence listing part.

[6958] GAM478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM478 target RNA, herein designated GAM TARGET RNA. GAM478 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6959] GAM478 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM478 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM478 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM478 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6960] The complementary binding of GAM478 RNA, herein designated GAM RNA, to target binding sites on GAM478 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM478 target RNA, herein designated GAM TARGET RNA, into GAM478 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6961] It is appreciated that GAM478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM478 target genes. The mRNA of each one of this plurality of GAM478 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM478 RNA, herein designated GAM RNA, and which when bound by GAM478 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM478 target proteins.

[6962] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM478 gene, herein designated GAM GENE, on one or

more GAM478 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6963] It is yet further appreciated that specific functions, and accordingly utilities, of GAM478 correlate with, and may be deduced from, the identity of the target genes which GAM478 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6964] Nucleotide sequences of the GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM478 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM478 are further de-

scribed hereinbelow with reference to Table Table1.

[6965] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM478 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6966]

[6967] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 479 (GAM479) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6968] GAM479 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM479 was detected is described hereinabove with reference to Figs. 2-8.

[6969] GAM479 gene, herein designated GAM GENE, and GAM479 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6970] GAM479 gene, herein designated GAM GENE, encodes a GAM479 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM479 precursor RNA is designated SEQ ID:7602, and is provided hereinbelow with reference to the sequence listing part.

[6971] GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6972] An enzyme complex designated DICER COMPLEX, dices the GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM479 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM479 RNA is designated SEQ ID:7603, and is provided hereinbelow with reference to the sequence listing part.

[6973] GAM479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM479 target RNA, herein designated GAM TARGET RNA. GAM479 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6974] GAM479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM479 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM479 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM479 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6975] The complementary binding of GAM479 RNA, herein designated GAM RNA, to target binding sites on GAM479 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM479 target RNA, herein designated GAM TARGET RNA, into GAM479 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6976] It is appreciated that GAM479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM479 target genes. The mRNA of each one of this plurality of GAM479 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM479 RNA, herein designated GAM RNA, and which when bound by GAM479 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM479 target proteins.

[6977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM479 gene, herein designated GAM GENE, on one or more GAM479 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6978] It is yet further appreciated that specific functions, and accordingly utilities, of GAM479 correlate with, and may

be deduced from, the identity of the target genes which GAM479 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6979] Nucleotide sequences of the GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM479 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM479 are further described hereinbelow with reference to Table Table1.

[6980] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM479 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6981]

[6982] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 480 (GAM480) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6983] GAM480 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM480 was detected is described hereinabove with reference to Figs. 2-8.

[6984] GAM480 gene, herein designated GAM GENE, and GAM480 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6985] GAM480 gene, herein designated GAM GENE, encodes a GAM480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM480 precursor RNA is designated SEQ ID:7622, and is provided hereinbelow with reference to the sequence listing part.

[6986] GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6987] An enzyme complex designated DICER COMPLEX, dices the GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM480 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of GAM480 RNA is designated SEQ ID:7623, and is provided hereinbelow with reference to the sequence listing part.

[6988] GAM480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM480 target RNA, herein designated GAM TARGET RNA. GAM480 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6989] GAM480 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM480 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM480 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM480 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6990] The complementary binding of GAM480 RNA, herein designated GAM RNA, to target binding sites on GAM480 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM480 target RNA, herein designated GAM TARGET RNA, into GAM480 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6991] It is appreciated that GAM480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM480 target genes. The mRNA of each one of this plurality of GAM480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM480 RNA, herein designated GAM RNA, and which when bound by GAM480 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM480 target proteins.

[6992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM480 gene, herein designated GAM GENE, on one or more GAM480 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6993] It is yet further appreciated that specific functions, and accordingly utilities, of GAM480 correlate with, and may be deduced from, the identity of the target genes which GAM480 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6994] Nucleotide sequences of the GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM480 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM480 are further described hereinbelow with reference to Table Table1.

[6995] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM480 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6996]

[6997] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 481 (GAM481) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6998] GAM481 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM481 was detected is described hereinabove with reference to Figs. 2-8.

[6999] GAM481 gene, herein designated GAM GENE, and GAM481 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7000] GAM481 gene, herein designated GAM GENE, encodes a GAM481 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM481 precursor RNA is desig-

nated SEQ ID:7628, and is provided hereinbelow with reference to the sequence listing part.

[7001] GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7002] An enzyme complex designated DICER COMPLEX, dices the GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM481 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM481 RNA is designated SEQ ID:7629, and is provided hereinbelow with reference to the sequence listing part.

[7003] GAM481 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM481 target RNA, herein designated GAM TARGET RNA. GAM481 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7004] GAM481 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM481 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM481 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM481 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM481

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7005] The complementary binding of GAM481 RNA, herein designated GAM RNA, to target binding sites on GAM481 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM481 target RNA, herein designated GAM TARGET RNA, into GAM481 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7006] It is appreciated that GAM481 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM481 target genes. The mRNA of each one of this plurality of GAM481 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM481 RNA, herein designated GAM RNA, and which when bound by GAM481 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM481 target proteins.

[7007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM481 gene, herein designated GAM GENE, on one or more GAM481 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7008] It is yet further appreciated that specific functions, and accordingly utilities, of GAM481 correlate with, and may be deduced from, the identity of the target genes which GAM481 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7009] Nucleotide sequences of the GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM481 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM481 are further described hereinbelow with reference to Table Table1.

[7010] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM481 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7011]

[7012] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 482 (GAM482) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7013] GAM482 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM482 was detected is described hereinabove with reference to Figs. 2-8.

[7014] GAM482 gene, herein designated GAM GENE, and

GAM482 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7015] GAM482 gene, herein designated GAM GENE, encodes a GAM482 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM482 precursor RNA is designated SEQ ID:7634, and is provided hereinbelow with reference to the sequence listing part.

[7016] GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7017] An enzyme complex designated DICER COMPLEX, dices the GAM482 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM482 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM482 RNA is designated SEQ ID:7635, and is provided hereinbelow with reference to the sequence listing part.

[7018] GAM482 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM482 target RNA, herein designated GAM TARGET RNA. GAM482 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7019] GAM482 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM482 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM482 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM482 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM482 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7020] The complementary binding of GAM482 RNA, herein designated GAM RNA, to target binding sites on GAM482 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM482 target RNA, herein designated GAM TARGET RNA, into GAM482 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7021] It is appreciated that GAM482 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM482 target genes. The mRNA of each one of this plurality of GAM482 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM482 RNA, herein designated GAM RNA, and which when bound by GAM482 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM482 target proteins.

[7022] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM482 gene, herein designated GAM GENE, on one or more GAM482 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7023] It is yet further appreciated that specific functions, and accordingly utilities, of GAM482 correlate with, and may be deduced from, the identity of the target genes which GAM482 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7024] Nucleotide sequences of the GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM482 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM482 are further described hereinbelow with reference to Table Table1.

[7025] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM482 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7026]

[7027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 483 (GAM483) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7028] GAM483 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM483 was detected is described hereinabove with reference to Figs. 2-8.

[7029] GAM483 gene, herein designated GAM GENE, and GAM483 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7030] GAM483 gene, herein designated GAM GENE, encodes a GAM483 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM483 precursor RNA is designated SEQ ID:7637, and is provided hereinbelow with reference to the sequence listing part.

[7031] GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7032] An enzyme complex designated DICER COMPLEX, dices the GAM483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM483 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM483 RNA is designated SEQ ID:7638, and is provided hereinbelow with reference to the sequence listing part.

[7033] GAM483 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM483 target RNA, herein designated GAM TARGET RNA. GAM483 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7034] GAM483 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM483 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM483 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM483 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM483 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7035] The complementary binding of GAM483 RNA, herein designated GAM RNA, to target binding sites on GAM483 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM483 target RNA, herein designated GAM TARGET RNA, into GAM483 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7036] It is appreciated that GAM483 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM483 target genes. The mRNA of each one of this plurality of GAM483 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM483 RNA, herein designated GAM RNA, and which when bound by GAM483 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM483 target proteins.

[7037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM483 gene, herein designated GAM GENE, on one or more GAM483 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM483 correlate with, and may be deduced from, the identity of the target genes which GAM483 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7039] Nucleotide sequences of the GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM483 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM483 are further described hereinbelow with reference to Table Table1.

[7040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM483 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7041]

[7042] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 484 (GAM484) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7043] GAM484 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM484 was detected is described hereinabove with reference to Figs. 2-8.

[7044] GAM484 gene, herein designated GAM GENE, and GAM484 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7045] GAM484 gene, herein designated GAM GENE, encodes a GAM484 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM484 precursor RNA is designated SEQ ID:7649, and is provided hereinbelow with reference to the sequence listing part.

[7046] GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7047] An enzyme complex designated DICER COMPLEX, dices the GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM484 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM484 RNA is designated SEQ ID:7650, and is provided hereinbelow with reference to the sequence listing part.

[7048] GAM484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM484 target RNA, herein designated GAM TARGET RNA. GAM484 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7049] GAM484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM484 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM484 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM484 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7050] The complementary binding of GAM484 RNA, herein designated GAM RNA, to target binding sites on GAM484 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM484 target RNA, herein designated GAM TARGET RNA, into GAM484 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7051] It is appreciated that GAM484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM484 target genes. The mRNA of each one of this plurality of GAM484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM484 RNA,

herein designated GAM RNA, and which when bound by GAM484 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM484 target proteins.

[7052] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM484 gene, herein designated GAM GENE, on one or more GAM484 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7053] It is yet further appreciated that specific functions, and accordingly utilities, of GAM484 correlate with, and may be deduced from, the identity of the target genes which

GAM484 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7054] Nucleotide sequences of the GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM484 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM484 are further described hereinbelow with reference to Table Table1.

[7055] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM484 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7056]

[7057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 485 (GAM485) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7058] GAM485 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM485 was detected is described hereinabove with reference to Figs. 2-8.

[7059] GAM485 gene, herein designated GAM GENE, and GAM485 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7060] GAM485 gene, herein designated GAM GENE, encodes a GAM485 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM485 precursor RNA is designated SEQ ID:7667, and is provided hereinbelow with reference to the sequence listing part.

[7061] GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7062] An enzyme complex designated DICER COMPLEX, dices the GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM485 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM485 RNA is designated SEQ ID:7668, and is provided hereinbelow with reference to the sequence listing part.

[7063] GAM485 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM485 target RNA, herein designated GAM TARGET RNA.
GAM485 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7064] GAM485 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM485 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM485 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM485 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM485 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7065] The complementary binding of GAM485 RNA, herein designated GAM RNA, to target binding sites on GAM485 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM485 target RNA, herein desig-

nated GAM TARGET RNA, into GAM485 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7066] It is appreciated that GAM485 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM485 target genes. The mRNA of each one of this plurality of GAM485 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM485 RNA, herein designated GAM RNA, and which when bound by GAM485 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM485 target proteins.

[7067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM485 gene, herein designated GAM GENE, on one or more GAM485 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM485 correlate with, and may be deduced from, the identity of the target genes which GAM485 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7069] Nucleotide sequences of the GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM485 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM485 are further described hereinbelow with reference to Table Table1.

[7070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM485 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7071]

[7072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 486 (GAM486) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7073] GAM486 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM486 was detected is described hereinabove with reference to Figs. 2-8.

[7074] GAM486 gene, herein designated GAM GENE, and GAM486 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7075] GAM486 gene, herein designated GAM GENE, encodes a GAM486 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM486 precursor RNA is designated SEQ ID:7677, and is provided hereinbelow with ref-

erence to the sequence listing part.

[7076] GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7077] An enzyme complex designated DICER COMPLEX, dices the GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM486 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM486 RNA is designated SEQ ID:7678, and is provided hereinbelow with reference to the sequence listing part.

[7078] GAM486 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM486 target RNA, herein designated GAM TARGET RNA.

GAM486 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7079] GAM486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM486 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM486 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM486 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7080] The complementary binding of GAM486 RNA, herein designated GAM RNA, to target binding sites on GAM486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM486 target RNA, herein designated GAM TARGET RNA, into GAM486 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7081] It is appreciated that GAM486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM486 target genes. The mRNA of each one of this plurality of GAM486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM486 RNA, herein designated GAM RNA, and which when bound by GAM486 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM486 target proteins.

[7082] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM486 gene, herein designated GAM GENE, on one or more GAM486 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM486 correlate with, and may be deduced from, the identity of the target genes which GAM486 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7084] Nucleotide sequences of the GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM486 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM486 are further described hereinbelow with reference to Table Table1.

[7085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM486 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7086]

[7087] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 487 (GAM487) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7088] GAM487 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM487 was detected is described hereinabove with reference to Figs. 2-8.

[7089] GAM487 gene, herein designated GAM GENE, and GAM487 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[7090] GAM487 gene, herein designated GAM GENE, encodes a GAM487 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM487 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM487 precursor RNA is designated SEQ ID:7689, and is provided hereinbelow with reference to the sequence listing part.

[7091] GAM487 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7092] An enzyme complex designated DICER COMPLEX, dices the GAM487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM487 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM487 RNA is designated SEQ ID:7690, and is provided hereinbelow with reference to the sequence listing part.

[7093] GAM487 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM487 target RNA, herein designated GAM TARGET RNA. GAM487 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7094] GAM487 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM487 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM487 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM487 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM487 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7095] The complementary binding of GAM487 RNA, herein designated GAM RNA, to target binding sites on GAM487 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM487 target RNA, herein designated GAM TARGET RNA, into GAM487 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7096] It is appreciated that GAM487 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM487 target genes. The mRNA of each one of this plurality of GAM487 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM487 RNA, herein designated GAM RNA, and which when bound by GAM487 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM487 target proteins.

[7097] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM487 gene, herein designated GAM GENE, on one or more GAM487 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7098] It is yet further appreciated that specific functions, and accordingly utilities, of GAM487 correlate with, and may be deduced from, the identity of the target genes which GAM487 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7099] Nucleotide sequences of the GAM487 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM487 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM487 are further described hereinbelow with reference to Table Table1.

[7100] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM487 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7101]

[7102] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

488 (GAM488) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7103] GAM488 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM488 was detected is described hereinabove with reference to Figs. 2-8.

[7104] GAM488 gene, herein designated GAM GENE, and GAM488 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7105] GAM488 gene, herein designated GAM GENE, encodes a GAM488 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM488 precursor RNA is designated SEQ ID:7704, and is provided hereinbelow with reference to the sequence listing part.

[7106] GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7107] An enzyme complex designated DICER COMPLEX, dices the GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM488 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 23%) nucleotide sequence of GAM488 RNA is designated SEQ ID:7705, and is provided hereinbelow with reference to the sequence listing part.

[7108] GAM488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM488 target RNA, herein designated GAM TARGET RNA. GAM488 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7109] GAM488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM488 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM488 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM488 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM488 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7110] The complementary binding of GAM488 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM488 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM488 target RNA, herein designated GAM TARGET RNA, into GAM488 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7111] It is appreciated that GAM488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM488 target genes. The mRNA of each one of this plurality of GAM488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM488 RNA, herein designated GAM RNA, and which when bound by GAM488 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM488 target proteins.

[7112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM488 gene, herein designated GAM GENE, on one or more GAM488 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7113] It is yet further appreciated that specific functions, and accordingly utilities, of GAM488 correlate with, and may be deduced from, the identity of the target genes which GAM488 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7114] Nucleotide sequences of the GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM488 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM488 are further described hereinbelow with reference to Table Table1.

[7115] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM488 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7116]

[7117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 489 (GAM489) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7118] GAM489 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM489 was detected is described hereinabove with reference to Figs. 2-8.

[7119] GAM489 gene, herein designated GAM GENE, and GAM489 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7120] GAM489 gene, herein designated GAM GENE, encodes a GAM489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM489 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM489 precursor RNA is designated SEQ ID:7719, and is provided hereinbelow with reference to the sequence listing part.

[7121] GAM489 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7122] An enzyme complex designated DICER COMPLEX, dices the GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM489 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 79%) nucleotide sequence of GAM489 RNA is designated SEQ ID:7720, and is provided hereinbelow with reference to the sequence listing part.

[7123] GAM489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM489 target RNA, herein designated GAM TARGET RNA. GAM489 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7124] GAM489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM489 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM489 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM489 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7125] The complementary binding of GAM489 RNA, herein designated GAM RNA, to target binding sites on GAM489 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM489 target RNA, herein designated GAM TARGET RNA, into GAM489 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7126] It is appreciated that GAM489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM489 target genes. The mRNA of each one of this plurality of GAM489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM489 RNA, herein designated GAM RNA, and which when bound by

GAM489 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM489 target proteins.

[7127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM489 gene, herein designated GAM GENE, on one or more GAM489 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7128] It is yet further appreciated that specific functions, and accordingly utilities, of GAM489 correlate with, and may be deduced from, the identity of the target genes which GAM489 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[7129] Nucleotide sequences of the GAM489 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM489 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM489 are further described hereinbelow with reference to Table Table1.

[7130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM489 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7131]

[7132] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 490 (GAM490) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7133] GAM490 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM490 was detected is described hereinabove with reference to Figs. 2-8.

[7134] GAM490 gene, herein designated GAM GENE, and GAM490 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7135] GAM490 gene, herein designated GAM GENE, encodes a GAM490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM490 precursor RNA is designated SEQ ID:7736, and is provided hereinbelow with reference to the sequence listing part.

[7136] GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7137] An enzyme complex designated DICER COMPLEX, dices the GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM490 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM490 RNA is designated SEQ ID:7737, and is provided hereinbelow with reference to the sequence listing part.

[7138] GAM490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM490 target RNA, herein designated GAM TARGET RNA. GAM490 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7139] GAM490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM490 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM490 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM490 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM490 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7140] The complementary binding of GAM490 RNA, herein designated GAM RNA, to target binding sites on GAM490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM490 target RNA, herein designated GAM TARGET RNA, into GAM490 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7141] It is appreciated that GAM490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM490 target genes. The mRNA of each one of this plurality of GAM490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM490 RNA, herein designated GAM RNA, and which when bound by GAM490 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM490 target proteins.

[7142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM490 gene, herein designated GAM GENE, on one or more GAM490 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7143] It is yet further appreciated that specific functions, and accordingly utilities, of GAM490 correlate with, and may be deduced from, the identity of the target genes which GAM490 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7144] Nucleotide sequences of the GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM490 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM490 are further described hereinbelow with reference to Table Table1.

[7145] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM490 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7146]

[7147] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 491 (GAM491) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7148] GAM491 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM491 was detected is described hereinabove with reference to Figs. 2-8.

[7149] GAM491 gene, herein designated GAM GENE, and GAM491 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7150] GAM491 gene, herein designated GAM GENE, encodes a GAM491 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM491 precursor RNA is designated SEQ ID:7753, and is provided hereinbelow with reference to the sequence listing part.

[7151] GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7152] An enzyme complex designated DICER COMPLEX, dices

the GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM491 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM491 RNA is designated SEQ ID:7754, and is provided hereinbelow with reference to the sequence listing part.

[7153] GAM491 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM491 target RNA, herein designated GAM TARGET RNA. GAM491 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7154] GAM491 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM491 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM491

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM491 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM491 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7155] The complementary binding of GAM491 RNA, herein designated GAM RNA, to target binding sites on GAM491 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM491 target RNA, herein designated GAM TARGET RNA, into GAM491 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7156] It is appreciated that GAM491 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM491 target genes. The mRNA of each one of this plurality of GAM491 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM491 RNA, herein designated GAM RNA, and which when bound by GAM491 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM491 target proteins.

[7157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM491 gene, herein designated GAM GENE, on one or more GAM491 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7158] It is yet further appreciated that specific functions, and accordingly utilities, of GAM491 correlate with, and may be deduced from, the identity of the target genes which GAM491 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7159] Nucleotide sequences of the GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM491 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM491 are further described hereinbelow with reference to Table Table1.

[7160] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM491 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7161]

[7162] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 492 (GAM492) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7163] GAM492 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM492 was detected is described hereinabove with reference to Figs. 2-8.

[7164] GAM492 gene, herein designated GAM GENE, and GAM492 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7165] GAM492 gene, herein designated GAM GENE, encodes a GAM492 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM492 precursor RNA is designated SEQ ID:7778, and is provided hereinbelow with reference to the sequence listing part.

[7166] GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM492 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7167] An enzyme complex designated DICER COMPLEX, dices the GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM492 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM492 RNA is designated SEQ ID:7779, and is provided hereinbelow with reference to the sequence listing part.

[7168] GAM492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM492 target RNA, herein designated GAM TARGET RNA. GAM492 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7169] GAM492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM492 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM492 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM492 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[7170] The complementary binding of GAM492 RNA, herein designated GAM RNA, to target binding sites on GAM492 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM492 target RNA, herein designated GAM TARGET RNA, into GAM492 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7171] It is appreciated that GAM492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM492 target genes. The mRNA of each one of this plurality of GAM492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM492 RNA, herein designated GAM RNA, and which when bound by GAM492 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM492 target proteins.

[7172] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM492 gene, herein designated GAM GENE, on one or

more GAM492 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7173] It is yet further appreciated that specific functions, and accordingly utilities, of GAM492 correlate with, and may be deduced from, the identity of the target genes which GAM492 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7174] Nucleotide sequences of the GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM492 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM492 are further de-

scribed hereinbelow with reference to Table Table1.

[7175] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM492 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7176]

[7177] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 493 (GAM493) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7178] GAM493 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM493 was detected is described hereinabove with reference to Figs. 2-8.

[7179] GAM493 gene, herein designated GAM GENE, and GAM493 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7180] GAM493 gene, herein designated GAM GENE, encodes a GAM493 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM493 precursor RNA is designated SEQ ID:7803, and is provided hereinbelow with reference to the sequence listing part.

[7181] GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7182] An enzyme complex designated DICER COMPLEX, dices the GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM493 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 22%) nucleotide sequence of GAM493 RNA is designated SEQ ID:7804, and is provided hereinbelow with reference to the sequence listing part.

[7183] GAM493 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM493 target RNA, herein designated GAM TARGET RNA. GAM493 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7184] GAM493 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM493 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM493 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM493 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM493 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7185] The complementary binding of GAM493 RNA, herein designated GAM RNA, to target binding sites on GAM493 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM493 target RNA, herein designated GAM TARGET RNA, into GAM493 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7186] It is appreciated that GAM493 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM493 target genes. The mRNA of each one of this plurality of GAM493 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM493 RNA, herein designated GAM RNA, and which when bound by GAM493 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM493 target proteins.

[7187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM493 gene, herein designated GAM GENE, on one or more GAM493 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7188] It is yet further appreciated that specific functions, and accordingly utilities, of GAM493 correlate with, and may

be deduced from, the identity of the target genes which GAM493 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7189] Nucleotide sequences of the GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM493 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM493 are further described hereinbelow with reference to Table Table1.

[7190] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM493 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7191]

[7192] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 494 (GAM494) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7193] GAM494 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM494 was detected is described hereinabove with reference to Figs. 2-8.

[7194] GAM494 gene, herein designated GAM GENE, and GAM494 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7195] GAM494 gene, herein designated GAM GENE, encodes a GAM494 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM494 precursor RNA is designated SEQ ID:7821, and is provided hereinbelow with reference to the sequence listing part.

[7196] GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7197] An enzyme complex designated DICER COMPLEX, dices the GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM494 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM494 RNA is designated SEQ ID:7822, and is provided hereinbelow with reference to the sequence listing part.

[7198] GAM494 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM494 target RNA, herein designated GAM TARGET RNA. GAM494 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7199] GAM494 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM494 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM494 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM494 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM494 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7200] The complementary binding of GAM494 RNA, herein designated GAM RNA, to target binding sites on GAM494 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM494 target RNA, herein designated GAM TARGET RNA, into GAM494 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7201] It is appreciated that GAM494 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM494 target genes. The mRNA of each one of this plurality of GAM494 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM494 RNA, herein designated GAM RNA, and which when bound by GAM494 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM494 target proteins.

[7202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM494 gene, herein designated GAM GENE, on one or more GAM494 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7203] It is yet further appreciated that specific functions, and accordingly utilities, of GAM494 correlate with, and may be deduced from, the identity of the target genes which GAM494 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7204] Nucleotide sequences of the GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM494 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM494 are further described hereinbelow with reference to Table Table1.

[7205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM494 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7206]

[7207] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 495 (GAM495) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7208] GAM495 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM495 was detected is described hereinabove with reference to Figs. 2-8.

[7209] GAM495 gene, herein designated GAM GENE, and GAM495 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7210] GAM495 gene, herein designated GAM GENE, encodes a GAM495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM495 precursor RNA is desig-

nated SEQ ID:7835, and is provided hereinbelow with reference to the sequence listing part.

[7211] GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7212] An enzyme complex designated DICER COMPLEX, dices the GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM495 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM495 RNA is designated SEQ ID:7836, and is provided hereinbelow with reference to the sequence listing part.

[7213] GAM495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM495 target RNA, herein designated GAM TARGET RNA. GAM495 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7214] GAM495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM495 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM495 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM495

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7215] The complementary binding of GAM495 RNA, herein designated GAM RNA, to target binding sites on GAM495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM495 target RNA, herein designated GAM TARGET RNA, into GAM495 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7216] It is appreciated that GAM495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM495 target genes. The mRNA of each one of this plurality of GAM495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM495 RNA, herein designated GAM RNA, and which when bound by GAM495 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM495 target proteins.

[7217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM495 gene, herein designated GAM GENE, on one or more GAM495 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7218] It is yet further appreciated that specific functions, and accordingly utilities, of GAM495 correlate with, and may be deduced from, the identity of the target genes which GAM495 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7219] Nucleotide sequences of the GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM495 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM495 are further described hereinbelow with reference to Table Table1.

[7220] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM495 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7221]

[7222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 496 (GAM496) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7223] GAM496 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM496 was detected is described hereinabove with reference to Figs. 2-8.

[7224] GAM496 gene, herein designated GAM GENE, and

GAM496 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7225] GAM496 gene, herein designated GAM GENE, encodes a GAM496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM496 precursor RNA is designated SEQ ID:7839, and is provided hereinbelow with reference to the sequence listing part.

[7226] GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7227] An enzyme complex designated DICER COMPLEX, dices the GAM496 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM496 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM496 RNA is designated SEQ ID:7840, and is provided hereinbelow with reference to the sequence listing part.

[7228] GAM496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM496 target RNA, herein designated GAM TARGET RNA. GAM496 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7229] GAM496 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM496 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM496 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM496 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7230] The complementary binding of GAM496 RNA, herein designated GAM RNA, to target binding sites on GAM496 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM496 target RNA, herein designated GAM TARGET RNA, into GAM496 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7231] It is appreciated that GAM496 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM496 target genes. The mRNA of each one of this plurality of GAM496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM496 RNA, herein designated GAM RNA, and which when bound by GAM496 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM496 target proteins.

[7232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM496 gene, herein designated GAM GENE, on one or more GAM496 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM496 correlate with, and may be deduced from, the identity of the target genes which GAM496 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7234] Nucleotide sequences of the GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM496 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM496 are further described hereinbelow with reference to Table Table1.

[7235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM496 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7236]

[7237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 497 (GAM497) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7238] GAM497 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM497 was detected is described hereinabove with reference to Figs. 2-8.

[7239] GAM497 gene, herein designated GAM GENE, and GAM497 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7240] GAM497 gene, herein designated GAM GENE, encodes a GAM497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM497 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM497 precursor RNA is designated SEQ ID:7858, and is provided hereinbelow with reference to the sequence listing part.

[7241] GAM497 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7242] An enzyme complex designated DICER COMPLEX, dices the GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM497 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM497 RNA is designated SEQ ID:7859, and is provided hereinbelow with reference to the sequence listing part.

[7243] GAM497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM497 target RNA, herein designated GAM TARGET RNA. GAM497 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7244] GAM497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM497 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM497 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM497 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7245] The complementary binding of GAM497 RNA, herein designated GAM RNA, to target binding sites on GAM497 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM497 target RNA, herein designated GAM TARGET RNA, into GAM497 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7246] It is appreciated that GAM497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM497 target genes. The mRNA of each one of this plurality of GAM497 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM497 RNA, herein designated GAM RNA, and which when bound by GAM497 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM497 target proteins.

[7247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM497 gene, herein designated GAM GENE, on one or more GAM497 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM497 correlate with, and may be deduced from, the identity of the target genes which GAM497 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7249] Nucleotide sequences of the GAM497 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM497 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM497 are further described hereinbelow with reference to Table Table1.

[7250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM497 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7251]

[7252] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 498 (GAM498) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7253] GAM498 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM498 was detected is described hereinabove with reference to Figs. 2-8.

[7254] GAM498 gene, herein designated GAM GENE, and GAM498 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7255] GAM498 gene, herein designated GAM GENE, encodes a GAM498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM498 precursor RNA is designated SEQ ID:7876, and is provided hereinbelow with reference to the sequence listing part.

[7256] GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7257] An enzyme complex designated DICER COMPLEX, dices the GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM498 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM498 RNA is designated SEQ ID:7877, and is provided hereinbelow with reference to the sequence listing part.

[7258] GAM498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM498 target RNA, herein designated GAM TARGET RNA. GAM498 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7259] GAM498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM498 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM498 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM498 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7260] The complementary binding of GAM498 RNA, herein designated GAM RNA, to target binding sites on GAM498 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM498 target RNA, herein designated GAM TARGET RNA, into GAM498 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7261] It is appreciated that GAM498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM498 target genes. The mRNA of each one of this plurality of GAM498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM498 RNA,

herein designated GAM RNA, and which when bound by GAM498 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM498 target proteins.

[7262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM498 gene, herein designated GAM GENE, on one or more GAM498 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM498 correlate with, and may be deduced from, the identity of the target genes which

GAM498 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7264] Nucleotide sequences of the GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM498 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM498 are further described hereinbelow with reference to Table Table1.

[7265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM498 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7266]

[7267] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 499 (GAM499) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7268] GAM499 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM499 was detected is described hereinabove with reference to Figs. 2-8.

[7269] GAM499 gene, herein designated GAM GENE, and GAM499 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7270] GAM499 gene, herein designated GAM GENE, encodes a GAM499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM499 precursor RNA is designated SEQ ID:7890, and is provided hereinbelow with reference to the sequence listing part.

[7271] GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7272] An enzyme complex designated DICER COMPLEX, dices the GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM499 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of GAM499 RNA is designated SEQ ID:7891, and is provided hereinbelow with reference to the sequence listing part.

[7273] GAM499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM499 target RNA, herein designated GAM TARGET RNA.
GAM499 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7274] GAM499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM499 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM499 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM499 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7275] The complementary binding of GAM499 RNA, herein designated GAM RNA, to target binding sites on GAM499 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM499 target RNA, herein desig-

nated GAM TARGET RNA, into GAM499 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7276] It is appreciated that GAM499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM499 target genes. The mRNA of each one of this plurality of GAM499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM499 RNA, herein designated GAM RNA, and which when bound by GAM499 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM499 target proteins.

[7277] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM499 gene, herein designated GAM GENE, on one or more GAM499 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7278] It is yet further appreciated that specific functions, and accordingly utilities, of GAM499 correlate with, and may be deduced from, the identity of the target genes which GAM499 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7279] Nucleotide sequences of the GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM499 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM499 are further described hereinbelow with reference to Table Table1.

[7280] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM499 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7281]

[7282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 500 (GAM500) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7283] GAM500 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM500 was detected is described hereinabove with reference to Figs. 2-8.

[7284] GAM500 gene, herein designated GAM GENE, and GAM500 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7285] GAM500 gene, herein designated GAM GENE, encodes a GAM500 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM500 precursor RNA is designated SEQ ID:7896, and is provided hereinbelow with ref-

erence to the sequence listing part.

[7286] GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7287] An enzyme complex designated DICER COMPLEX, dices the GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM500 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM500 RNA is designated SEQ ID:7897, and is provided hereinbelow with reference to the sequence listing part.

[7288] GAM500 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM500 target RNA, herein designated GAM TARGET RNA.

GAM500 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7289] GAM500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM500 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM500 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM500 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7290] The complementary binding of GAM500 RNA, herein designated GAM RNA, to target binding sites on GAM500 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM500 target RNA, herein designated GAM TARGET RNA, into GAM500 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7291] It is appreciated that GAM500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM500 target genes. The mRNA of each one of this plurality of GAM500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM500 RNA, herein designated GAM RNA, and which when bound by GAM500 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM500 target proteins.

[7292] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM500 gene, herein designated GAM GENE, on one or more GAM500 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM500 correlate with, and may be deduced from, the identity of the target genes which GAM500 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7294] Nucleotide sequences of the GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM500 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM500 are further described hereinbelow with reference to Table Table1.

[7295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM500 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7296]

[7297] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 501 (GAM501) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7298] GAM501 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM501 was detected is described hereinabove with reference to Figs. 2-8.

[7299] GAM501 gene, herein designated GAM GENE, and GAM501 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[7300] GAM501 gene, herein designated GAM GENE, encodes a GAM501 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM501 precursor RNA is designated SEQ ID:7909, and is provided hereinbelow with reference to the sequence listing part.

[7301] GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7302] An enzyme complex designated DICER COMPLEX, dices the GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM501 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 23%) nucleotide sequence of GAM501 RNA is designated SEQ ID:7910, and is provided hereinbelow with reference to the sequence listing part.

[7303] GAM501 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM501 target RNA, herein designated GAM TARGET RNA. GAM501 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7304] GAM501 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM501 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM501 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM501 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM501 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7305] The complementary binding of GAM501 RNA, herein designated GAM RNA, to target binding sites on GAM501 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM501 target RNA, herein designated GAM TARGET RNA, into GAM501 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7306] It is appreciated that GAM501 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM501 target genes. The mRNA of each one of this plurality of GAM501 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM501 RNA, herein designated GAM RNA, and which when bound by GAM501 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM501 target proteins.

[7307] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM501 gene, herein designated GAM GENE, on one or more GAM501 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7308] It is yet further appreciated that specific functions, and accordingly utilities, of GAM501 correlate with, and may be deduced from, the identity of the target genes which GAM501 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7309] Nucleotide sequences of the GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM501 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM501 are further described hereinbelow with reference to Table Table1.

[7310] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM501 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7311]

[7312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

502 (GAM502) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7313] GAM502 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM502 was detected is described hereinabove with reference to Figs. 2-8.

[7314] GAM502 gene, herein designated GAM GENE, and GAM502 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7315] GAM502 gene, herein designated GAM GENE, encodes a GAM502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM502 precursor RNA is designated SEQ ID:7918, and is provided hereinbelow with reference to the sequence listing part.

[7316] GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7317] An enzyme complex designated DICER COMPLEX, dices the GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM502 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM502 RNA is designated SEQ ID:7919, and is provided hereinbelow with reference to the sequence listing part.

[7318] GAM502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM502 target RNA, herein designated GAM TARGET RNA. GAM502 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7319] GAM502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM502 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM502 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM502 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7320] The complementary binding of GAM502 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM502 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM502 target RNA, herein designated GAM TARGET RNA, into GAM502 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7321] It is appreciated that GAM502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM502 target genes. The mRNA of each one of this plurality of GAM502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM502 RNA, herein designated GAM RNA, and which when bound by GAM502 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM502 target proteins.

[7322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM502 gene, herein designated GAM GENE, on one or more GAM502 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM502 correlate with, and may be deduced from, the identity of the target genes which GAM502 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7324] Nucleotide sequences of the GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM502 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM502 are further described hereinbelow with reference to Table Table1.

[7325] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM502 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7326]

[7327] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 503 (GAM503) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7328] GAM503 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM503 was detected is described hereinabove with reference to Figs. 2-8.

[7329] GAM503 gene, herein designated GAM GENE, and GAM503 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7330] GAM503 gene, herein designated GAM GENE, encodes a GAM503 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM503 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM503 precursor RNA is designated SEQ ID:7924, and is provided hereinbelow with reference to the sequence listing part.

[7331] GAM503 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7332] An enzyme complex designated DICER COMPLEX, dices the GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM503 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 82%) nucleotide sequence of GAM503 RNA is designated SEQ ID:7925, and is provided hereinbelow with reference to the sequence listing part.

[7333] GAM503 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM503 target RNA, herein designated GAM TARGET RNA. GAM503 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7334] GAM503 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM503 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM503 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM503 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM503 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7335] The complementary binding of GAM503 RNA, herein designated GAM RNA, to target binding sites on GAM503 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM503 target RNA, herein designated GAM TARGET RNA, into GAM503 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7336] It is appreciated that GAM503 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM503 target genes. The mRNA of each one of this plurality of GAM503 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM503 RNA, herein designated GAM RNA, and which when bound by

GAM503 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM503 target proteins.

[7337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM503 gene, herein designated GAM GENE, on one or more GAM503 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7338] It is yet further appreciated that specific functions, and accordingly utilities, of GAM503 correlate with, and may be deduced from, the identity of the target genes which GAM503 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[7339] Nucleotide sequences of the GAM503 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM503 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM503 are further described hereinbelow with reference to Table Table1.

[7340] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM503 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7341]

[7342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 504 (GAM504) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7343] GAM504 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM504 was detected is described hereinabove with reference to Figs. 2-8.

[7344] GAM504 gene, herein designated GAM GENE, and GAM504 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7345] GAM504 gene, herein designated GAM GENE, encodes a GAM504 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM504 precursor RNA is designated SEQ ID:7952, and is provided hereinbelow with reference to the sequence listing part.

[7346] GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7347] An enzyme complex designated DICER COMPLEX, dices the GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM504 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM504 RNA is designated SEQ ID:7953, and is provided hereinbelow with reference to the sequence listing part.

[7348] GAM504 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM504 target RNA, herein designated GAM TARGET RNA. GAM504 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7349] GAM504 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM504 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM504 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM504 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM504 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7350] The complementary binding of GAM504 RNA, herein designated GAM RNA, to target binding sites on GAM504 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM504 target RNA, herein designated GAM TARGET RNA, into GAM504 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7351] It is appreciated that GAM504 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM504 target genes. The mRNA of each one of this plurality of GAM504 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM504 RNA, herein designated GAM RNA, and which when bound by GAM504 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM504 target proteins.

[7352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM504 gene, herein designated GAM GENE, on one or more GAM504 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM504 correlate with, and may be deduced from, the identity of the target genes which GAM504 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7354] Nucleotide sequences of the GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM504 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM504 are further described hereinbelow with reference to Table Table1.

[7355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM504 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7356]

[7357] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 505 (GAM505) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7358] GAM505 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM505 was detected is described hereinabove with reference to Figs. 2-8.

[7359] GAM505 gene, herein designated GAM GENE, and GAM505 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7360] GAM505 gene, herein designated GAM GENE, encodes a GAM505 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM505 precursor RNA is designated SEQ ID:7992, and is provided hereinbelow with reference to the sequence listing part.

[7361] GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7362] An enzyme complex designated DICER COMPLEX, dices the GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM505 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM505 RNA is designated SEQ ID:7993, and is provided hereinbelow with reference to the sequence listing part.

[7363] GAM505 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM505

target RNA, herein designated GAM TARGET RNA.

GAM505 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7364] GAM505 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM505 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM505 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM505 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM505 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7365] The complementary binding of GAM505 RNA, herein designated GAM RNA, to target binding sites on GAM505 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM505 target RNA, herein designated GAM TARGET RNA, into GAM505 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7366] It is appreciated that GAM505 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM505 target genes. The mRNA of each one of this plurality of GAM505 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM505 RNA, herein designated GAM RNA, and which when bound by GAM505 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM505 target proteins.

[7367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM505 gene, herein designated GAM GENE, on one or more GAM505 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7368] It is yet further appreciated that specific functions, and accordingly utilities, of GAM505 correlate with, and may be deduced from, the identity of the target genes which GAM505 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7369] Nucleotide sequences of the GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM505 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM505 are further described hereinbelow with reference to Table Table1.

[7370] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM505 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7371]

[7372] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 506 (GAM506) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7373] GAM506 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM506 was detected is described hereinabove with reference to Figs. 2-8.

[7374] GAM506 gene, herein designated GAM GENE, and GAM506 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7375] GAM506 gene, herein designated GAM GENE, encodes a GAM506 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM506 precursor RNA is designated SEQ ID:8026, and is provided hereinbelow with reference to the sequence listing part.

[7376] GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7377] An enzyme complex designated DICER COMPLEX, dices the GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM506 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 23%) nucleotide sequence of GAM506 RNA is designated SEQ ID:8027, and is provided hereinbelow with reference to the sequence listing part.

[7378] GAM506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM506 target RNA, herein designated GAM TARGET RNA. GAM506 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7379] GAM506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM506 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM506 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM506 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7380] The complementary binding of GAM506 RNA, herein designated GAM RNA, to target binding sites on GAM506 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM506 target RNA, herein designated GAM TARGET RNA, into GAM506 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7381] It is appreciated that GAM506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM506 target genes. The mRNA of each one of this plu-

rality of GAM506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM506 RNA, herein designated GAM RNA, and which when bound by GAM506 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM506 target proteins.

[7382] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM506 gene, herein designated GAM GENE, on one or more GAM506 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7383] It is yet further appreciated that specific functions, and accordingly utilities, of GAM506 correlate with, and may be deduced from, the identity of the target genes which GAM506 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7384] Nucleotide sequences of the GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM506 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM506 are further described hereinbelow with reference to Table Table1.

[7385] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM506 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7386]

[7387] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 507 (GAM507) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[7388] GAM507 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM507 was detected is described hereinabove with reference to Figs. 2-8.

[7389] GAM507 gene, herein designated GAM GENE, and GAM507 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7390] GAM507 gene, herein designated GAM GENE, encodes a GAM507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM507 precursor RNA is designated SEQ ID:8051, and is provided hereinbelow with reference to the sequence listing part.

[7391] GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7392] An enzyme complex designated DICER COMPLEX, dices the GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM507 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM507 RNA is designated SEQ ID:8052, and is provided hereinbelow with reference to the sequence listing part.

[7393] GAM507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM507 target RNA, herein designated GAM TARGET RNA.
GAM507 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[7394] GAM507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM507 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM507 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM507 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7395] The complementary binding of GAM507 RNA, herein designated GAM RNA, to target binding sites on GAM507 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM507 target RNA, herein designated GAM TARGET RNA, into GAM507 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7396] It is appreciated that GAM507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM507 target genes. The mRNA of each one of this plurality of GAM507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM507 RNA, herein designated GAM RNA, and which when bound by GAM507 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM507 target proteins.

[7397] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM507 gene, herein designated GAM GENE, on one or more GAM507 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7398] It is yet further appreciated that specific functions, and accordingly utilities, of GAM507 correlate with, and may be deduced from, the identity of the target genes which GAM507 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7399] Nucleotide sequences of the GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM507 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM507 are further described hereinbelow with reference to Table Table1.

[7400] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM507 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7401]

[7402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 508 (GAM508) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7403] GAM508 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM508 was detected is described hereinabove with reference to Figs. 2-8.

[7404] GAM508 gene, herein designated GAM GENE, and GAM508 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7405] GAM508 gene, herein designated GAM GENE, encodes a GAM508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM508 precursor RNA is designated SEQ ID:8071, and is provided hereinbelow with reference to the sequence listing part.

[7406] GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7407] An enzyme complex designated DICER COMPLEX, dices the GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM508 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of

GAM508 RNA is designated SEQ ID:8072, and is provided hereinbelow with reference to the sequence listing part.

[7408] GAM508 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM508 target RNA, herein designated GAM TARGET RNA. GAM508 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7409] GAM508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM508 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM508 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM508 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7410] The complementary binding of GAM508 RNA, herein designated GAM RNA, to target binding sites on GAM508 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM508 target RNA, herein designated GAM TARGET RNA, into GAM508 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7411] It is appreciated that GAM508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM508 target genes. The mRNA of each one of this plurality of GAM508 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM508 RNA, herein designated GAM RNA, and which when bound by GAM508 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM508 target proteins.

[7412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM508 gene, herein designated GAM GENE, on one or more GAM508 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM508 correlate with, and may be deduced from, the identity of the target genes which GAM508 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7414] Nucleotide sequences of the GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM508 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM508 are further described hereinbelow with reference to Table Table1.

[7415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM508 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7416]

[7417] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 509 (GAM509) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7418] GAM509 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM509 was detected is described hereinabove

with reference to Figs. 2-8.

[7419] GAM509 gene, herein designated GAM GENE, and GAM509 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7420] GAM509 gene, herein designated GAM GENE, encodes a GAM509 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM509 precursor RNA is designated SEQ ID:8091, and is provided hereinbelow with reference to the sequence listing part.

[7421] GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7422] An enzyme complex designated DICER COMPLEX, dices the GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM509 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM509 RNA is designated SEQ ID:8092, and is provided hereinbelow with reference to the sequence listing part.

[7423] GAM509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM509 target RNA, herein designated GAM TARGET RNA. GAM509 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7424] GAM509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM509 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM509 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM509 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM509 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7425] The complementary binding of GAM509 RNA, herein designated GAM RNA, to target binding sites on GAM509 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM509 target RNA, herein designated GAM TARGET RNA, into GAM509 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[7426] It is appreciated that GAM509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM509 target genes. The mRNA of each one of this plurality of GAM509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM509 RNA, herein designated GAM RNA, and which when bound by GAM509 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM509 target proteins.

[7427] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM509 gene, herein designated GAM GENE, on one or more GAM509 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7428] It is yet further appreciated that specific functions, and accordingly utilities, of GAM509 correlate with, and may be deduced from, the identity of the target genes which GAM509 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7429] Nucleotide sequences of the GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM509 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM509 are further described hereinbelow with reference to Table Table1.

[7430] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM509 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7431]

[7432] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 510 (GAM510) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7433] GAM510 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM510 was detected is described hereinabove with reference to Figs. 2-8.

[7434] GAM510 gene, herein designated GAM GENE, and GAM510 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7435] GAM510 gene, herein designated GAM GENE, encodes a GAM510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM510 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM510 precursor RNA is designated SEQ ID:8109, and is provided hereinbelow with reference to the sequence listing part.

[7436] GAM510 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7437] An enzyme complex designated DICER COMPLEX, dices the GAM510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM510 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 33%) nucleotide sequence of GAM510 RNA is designated SEQ ID:8110, and is provided hereinbelow with reference to the sequence listing part.

[7438] GAM510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM510 target RNA, herein designated GAM TARGET RNA.

GAM510 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7439] GAM510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM510 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM510 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM510 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7440] The complementary binding of GAM510 RNA, herein designated GAM RNA, to target binding sites on GAM510 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM510 target RNA, herein designated GAM TARGET RNA, into GAM510 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7441] It is appreciated that GAM510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM510 target genes. The mRNA of each one of this plurality of GAM510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM510 RNA, herein designated GAM RNA, and which when bound by GAM510 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM510 target proteins.

[7442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM510 gene, herein designated GAM GENE, on one or more GAM510 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7443] It is yet further appreciated that specific functions, and accordingly utilities, of GAM510 correlate with, and may be deduced from, the identity of the target genes which GAM510 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7444] Nucleotide sequences of the GAM510 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM510 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM510 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM510 are further described hereinbelow with reference to Table Table1.

[7445] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM510 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7446]

[7447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 511 (GAM511) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7448] GAM511 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM511 was detected is described hereinabove with reference to Figs. 2-8.

[7449] GAM511 gene, herein designated GAM GENE, and GAM511 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7450] GAM511 gene, herein designated GAM GENE, encodes a

GAM511 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM511 precursor RNA is designated SEQ ID:8136, and is provided hereinbelow with reference to the sequence listing part.

[7451] GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7452] An enzyme complex designated DICER COMPLEX, dices the GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM511 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM511 RNA is designated SEQ ID:8137, and is provided hereinbelow with reference to the sequence listing part.

[7453] GAM511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM511 target RNA, herein designated GAM TARGET RNA. GAM511 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7454] GAM511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM511 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM511 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM511 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM511 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7455] The complementary binding of GAM511 RNA, herein designated GAM RNA, to target binding sites on GAM511 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM511 target RNA, herein designated GAM TARGET RNA, into GAM511 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7456] It is appreciated that GAM511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM511 target genes. The mRNA of each one of this plurality of GAM511 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM511 RNA, herein designated GAM RNA, and which when bound by GAM511 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM511 target proteins.

[7457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM511 gene, herein designated GAM GENE, on one or more GAM511 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7458] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM511 correlate with, and may be deduced from, the identity of the target genes which GAM511 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7459] Nucleotide sequences of the GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM511 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM511 are further described hereinbelow with reference to Table Table1.

[7460] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM511 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7461]

[7462] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 512 (GAM512) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7463] GAM512 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM512 was detected is described hereinabove with reference to Figs. 2-8.

[7464] GAM512 gene, herein designated GAM GENE, and GAM512 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7465] GAM512 gene, herein designated GAM GENE, encodes a GAM512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM512 precursor RNA is designated SEQ ID:8149, and is provided hereinbelow with reference to the sequence listing part.

[7466] GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7467] An enzyme complex designated DICER COMPLEX, dices the GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM512 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of GAM512 RNA is designated SEQ ID:8150, and is provided hereinbelow with reference to the sequence listing part.

[7468] GAM512 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM512 target RNA, herein designated GAM TARGET RNA. GAM512 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7469] GAM512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM512 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM512 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM512 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7470] The complementary binding of GAM512 RNA, herein designated GAM RNA, to target binding sites on GAM512 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM512 target RNA, herein designated GAM TARGET RNA, into GAM512 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7471] It is appreciated that GAM512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM512 target genes. The mRNA of each one of this plurality of GAM512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM512 RNA, herein designated GAM RNA, and which when bound by GAM512 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM512 target proteins.

[7472] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM512 gene, herein designated GAM GENE, on one or more GAM512 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7473] It is yet further appreciated that specific functions, and accordingly utilities, of GAM512 correlate with, and may be deduced from, the identity of the target genes which GAM512 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7474] Nucleotide sequences of the GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM512 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM512 are further described hereinbelow with reference to Table Table1.

[7475] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM512 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7476]

[7477] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 513 (GAM513) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7478] GAM513 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM513 was detected is described hereinabove with reference to Figs. 2-8.

[7479] GAM513 gene, herein designated GAM GENE, and GAM513 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7480] GAM513 gene, herein designated GAM GENE, encodes a GAM513 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM513 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM513 precursor RNA is designated SEQ ID:8162, and is provided hereinbelow with reference to the sequence listing part.

[7481] GAM513 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7482] An enzyme complex designated DICER COMPLEX, dices the GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM513 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM513 RNA is designated SEQ ID:8163, and is provided

hereinbelow with reference to the sequence listing part.

[7483] GAM513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM513 target RNA, herein designated GAM TARGET RNA. GAM513 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7484] GAM513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM513 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM513 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM513 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7485] The complementary binding of GAM513 RNA, herein designated GAM RNA, to target binding sites on GAM513 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM513 target RNA, herein designated GAM TARGET RNA, into GAM513 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7486] It is appreciated that GAM513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM513 target genes. The mRNA of each one of this plurality of GAM513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM513 RNA, herein designated GAM RNA, and which when bound by GAM513 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM513 tar-

get proteins.

[7487] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM513 gene, herein designated GAM GENE, on one or more GAM513 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7488] It is yet further appreciated that specific functions, and accordingly utilities, of GAM513 correlate with, and may be deduced from, the identity of the target genes which GAM513 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7489] Nucleotide sequences of the GAM513 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM513 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM513 are further described hereinbelow with reference to Table Table1.

[7490] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM513 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7491]

[7492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 514 (GAM514) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7493] GAM514 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM514 was detected is described hereinabove with reference to Figs. 2-8.

[7494] GAM514 gene, herein designated GAM GENE, and GAM514 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7495] GAM514 gene, herein designated GAM GENE, encodes a GAM514 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM514 precursor RNA is designated SEQ ID:8187, and is provided hereinbelow with reference to the sequence listing part.

[7496] GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7497] An enzyme complex designated DICER COMPLEX, dices

the GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM514 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM514 RNA is designated SEQ ID:8188, and is provided hereinbelow with reference to the sequence listing part.

[7498] GAM514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM514 target RNA, herein designated GAM TARGET RNA. GAM514 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7499] GAM514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM514

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM514 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM514 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7500] The complementary binding of GAM514 RNA, herein designated GAM RNA, to target binding sites on GAM514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM514 target RNA, herein designated GAM TARGET RNA, into GAM514 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7501] It is appreciated that GAM514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM514 target genes. The mRNA of each one of this plurality of GAM514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM514 RNA, herein designated GAM RNA, and which when bound by GAM514 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM514 target proteins.

[7502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM514 gene, herein designated GAM GENE, on one or more GAM514 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7503] It is yet further appreciated that specific functions, and accordingly utilities, of GAM514 correlate with, and may be deduced from, the identity of the target genes which GAM514 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7504] Nucleotide sequences of the GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM514 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM514 are further described hereinbelow with reference to Table Table1.

[7505] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM514 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7506]

[7507] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 515 (GAM515) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7508] GAM515 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM515 was detected is described hereinabove with reference to Figs. 2-8.

[7509] GAM515 gene, herein designated GAM GENE, and GAM515 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7510] GAM515 gene, herein designated GAM GENE, encodes a GAM515 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM515 precursor RNA is designated SEQ ID:8210, and is provided hereinbelow with reference to the sequence listing part.

[7511] GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM515 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7512] An enzyme complex designated DICER COMPLEX, dices the GAM515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM515 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of GAM515 RNA is designated SEQ ID:8211, and is provided hereinbelow with reference to the sequence listing part.

[7513] GAM515 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM515 target RNA, herein designated GAM TARGET RNA. GAM515 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7514] GAM515 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM515 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM515 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM515 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM515 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[7515] The complementary binding of GAM515 RNA, herein designated GAM RNA, to target binding sites on GAM515 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM515 target RNA, herein designated GAM TARGET RNA, into GAM515 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7516] It is appreciated that GAM515 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM515 target genes. The mRNA of each one of this plurality of GAM515 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM515 RNA, herein designated GAM RNA, and which when bound by GAM515 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM515 target proteins.

[7517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM515 gene, herein designated GAM GENE, on one or

more GAM515 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7518] It is yet further appreciated that specific functions, and accordingly utilities, of GAM515 correlate with, and may be deduced from, the identity of the target genes which GAM515 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7519] Nucleotide sequences of the GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM515 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM515 are further de-

scribed hereinbelow with reference to Table Table1.

[7520] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM515 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7521]

[7522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 516 (GAM516) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7523] GAM516 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM516 was detected is described hereinabove with reference to Figs. 2-8.

[7524] GAM516 gene, herein designated GAM GENE, and GAM516 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7525] GAM516 gene, herein designated GAM GENE, encodes a GAM516 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM516 precursor RNA is designated SEQ ID:8218, and is provided hereinbelow with reference to the sequence listing part.

[7526] GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7527] An enzyme complex designated DICER COMPLEX, dices the GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM516 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM516 RNA is designated SEQ ID:8219, and is provided hereinbelow with reference to the sequence listing part.

[7528] GAM516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM516 target RNA, herein designated GAM TARGET RNA. GAM516 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7529] GAM516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM516 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM516 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM516 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7530] The complementary binding of GAM516 RNA, herein designated GAM RNA, to target binding sites on GAM516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM516 target RNA, herein designated GAM TARGET RNA, into GAM516 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7531] It is appreciated that GAM516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM516 target genes. The mRNA of each one of this plurality of GAM516 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM516 RNA, herein designated GAM RNA, and which when bound by GAM516 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM516 target proteins.

[7532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM516 gene, herein designated GAM GENE, on one or more GAM516 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM516 correlate with, and may

be deduced from, the identity of the target genes which GAM516 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7534] Nucleotide sequences of the GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM516 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM516 are further described hereinbelow with reference to Table Table1.

[7535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM516 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7536]

[7537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 517 (GAM517) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7538] GAM517 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM517 was detected is described hereinabove with reference to Figs. 2-8.

[7539] GAM517 gene, herein designated GAM GENE, and GAM517 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7540] GAM517 gene, herein designated GAM GENE, encodes a GAM517 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM517 precursor RNA is designated SEQ ID:8236, and is provided hereinbelow with reference to the sequence listing part.

[7541] GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7542] An enzyme complex designated DICER COMPLEX, dices the GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM517 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of GAM517 RNA is designated SEQ ID:8237, and is provided hereinbelow with reference to the sequence listing part.

[7543] GAM517 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM517 target RNA, herein designated GAM TARGET RNA. GAM517 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7544] GAM517 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM517 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM517 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM517 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM517 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7545] The complementary binding of GAM517 RNA, herein designated GAM RNA, to target binding sites on GAM517 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM517 target RNA, herein designated GAM TARGET RNA, into GAM517 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7546] It is appreciated that GAM517 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM517 target genes. The mRNA of each one of this plurality of GAM517 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM517 RNA, herein designated GAM RNA, and which when bound by GAM517 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM517 target proteins.

[7547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM517 gene, herein designated GAM GENE, on one or more GAM517 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM517 correlate with, and may be deduced from, the identity of the target genes which GAM517 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7549] Nucleotide sequences of the GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM517 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM517 are further described hereinbelow with reference to Table Table1.

[7550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM517 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7551]

[7552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 518 (GAM518) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7553] GAM518 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM518 was detected is described hereinabove with reference to Figs. 2-8.

[7554] GAM518 gene, herein designated GAM GENE, and GAM518 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7555] GAM518 gene, herein designated GAM GENE, encodes a GAM518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM518 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM518 precursor RNA is desig-

nated SEQ ID:8254, and is provided hereinbelow with reference to the sequence listing part.

[7556] GAM518 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7557] An enzyme complex designated DICER COMPLEX, dices the GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM518 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of GAM518 RNA is designated SEQ ID:8255, and is provided hereinbelow with reference to the sequence listing part.

[7558] GAM518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM518 target RNA, herein designated GAM TARGET RNA. GAM518 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7559] GAM518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM518 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM518 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM518

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7560] The complementary binding of GAM518 RNA, herein designated GAM RNA, to target binding sites on GAM518 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM518 target RNA, herein designated GAM TARGET RNA, into GAM518 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7561] It is appreciated that GAM518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM518 target genes. The mRNA of each one of this plurality of GAM518 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM518 RNA, herein designated GAM RNA, and which when bound by GAM518 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM518 target proteins.

[7562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM518 gene, herein designated GAM GENE, on one or more GAM518 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7563] It is yet further appreciated that specific functions, and accordingly utilities, of GAM518 correlate with, and may be deduced from, the identity of the target genes which GAM518 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7564] Nucleotide sequences of the GAM518 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM518 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM518 are further described hereinbelow with reference to Table Table1.

[7565] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM518 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7566]

[7567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 519 (GAM519) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7568] GAM519 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM519 was detected is described hereinabove with reference to Figs. 2-8.

[7569] GAM519 gene, herein designated GAM GENE, and

GAM519 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7570] GAM519 gene, herein designated GAM GENE, encodes a GAM519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM519 precursor RNA is designated SEQ ID:8272, and is provided hereinbelow with reference to the sequence listing part.

[7571] GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7572] An enzyme complex designated DICER COMPLEX, dices the GAM519 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM519 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of GAM519 RNA is designated SEQ ID:8273, and is provided hereinbelow with reference to the sequence listing part.

[7573] GAM519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM519 target RNA, herein designated GAM TARGET RNA. GAM519 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7574] GAM519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM519 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM519 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM519 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7575] The complementary binding of GAM519 RNA, herein designated GAM RNA, to target binding sites on GAM519 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM519 target RNA, herein designated GAM TARGET RNA, into GAM519 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7576] It is appreciated that GAM519 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM519 target genes. The mRNA of each one of this plurality of GAM519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM519 RNA, herein designated GAM RNA, and which when bound by GAM519 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM519 target proteins.

[7577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM519 gene, herein designated GAM GENE, on one or more GAM519 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM519 correlate with, and may be deduced from, the identity of the target genes which GAM519 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7579] Nucleotide sequences of the GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM519 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM519 are further described hereinbelow with reference to Table Table1.

[7580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM519 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7581]

[7582] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 520 (GAM520) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7583] GAM520 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM520 was detected is described hereinabove with reference to Figs. 2-8.

[7584] GAM520 gene, herein designated GAM GENE, and GAM520 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7585] GAM520 gene, herein designated GAM GENE, encodes a GAM520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM520 precursor RNA is designated SEQ ID:8283, and is provided hereinbelow with reference to the sequence listing part.

[7586] GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7587] An enzyme complex designated DICER COMPLEX, dices the GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM520 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 29%) nucleotide sequence of GAM520 RNA is designated SEQ ID:8284, and is provided hereinbelow with reference to the sequence listing part.

[7588] GAM520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM520 target RNA, herein designated GAM TARGET RNA. GAM520 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7589] GAM520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM520 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM520 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM520 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7590] The complementary binding of GAM520 RNA, herein designated GAM RNA, to target binding sites on GAM520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM520 target RNA, herein designated GAM TARGET RNA, into GAM520 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7591] It is appreciated that GAM520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM520 target genes. The mRNA of each one of this plurality of GAM520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM520 RNA, herein designated GAM RNA, and which when bound by GAM520 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM520 target proteins.

[7592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM520 gene, herein designated GAM GENE, on one or more GAM520 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7593] It is yet further appreciated that specific functions, and accordingly utilities, of GAM520 correlate with, and may be deduced from, the identity of the target genes which GAM520 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7594] Nucleotide sequences of the GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM520 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM520 are further described hereinbelow with reference to Table Table1.

[7595] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM520 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7596]

[7597] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 521 (GAM521) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7598] GAM521 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM521 was detected is described hereinabove with reference to Figs. 2-8.

[7599] GAM521 gene, herein designated GAM GENE, and GAM521 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7600] GAM521 gene, herein designated GAM GENE, encodes a GAM521 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM521 precursor RNA is designated SEQ ID:8300, and is provided hereinbelow with reference to the sequence listing part.

[7601] GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7602] An enzyme complex designated DICER COMPLEX, dices the GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM521 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM521 RNA is designated SEQ ID:8301, and is provided hereinbelow with reference to the sequence listing part.

[7603] GAM521 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM521 target RNA, herein designated GAM TARGET RNA. GAM521 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7604] GAM521 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM521 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM521 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM521 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM521 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7605] The complementary binding of GAM521 RNA, herein designated GAM RNA, to target binding sites on GAM521 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM521 target RNA, herein designated GAM TARGET RNA, into GAM521 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7606] It is appreciated that GAM521 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM521 target genes. The mRNA of each one of this plurality of GAM521 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM521 RNA,

herein designated GAM RNA, and which when bound by GAM521 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM521 target proteins.

[7607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM521 gene, herein designated GAM GENE, on one or more GAM521 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7608] It is yet further appreciated that specific functions, and accordingly utilities, of GAM521 correlate with, and may be deduced from, the identity of the target genes which

GAM521 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7609] Nucleotide sequences of the GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM521 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM521 are further described hereinbelow with reference to Table Table1.

[7610] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM521 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7611]

[7612] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 522 (GAM522) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7613] GAM522 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM522 was detected is described hereinabove with reference to Figs. 2-8.

[7614] GAM522 gene, herein designated GAM GENE, and GAM522 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7615] GAM522 gene, herein designated GAM GENE, encodes a GAM522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM522 precursor RNA is designated SEQ ID:8319, and is provided hereinbelow with reference to the sequence listing part.

[7616] GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7617] An enzyme complex designated DICER COMPLEX, dices the GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM522 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of GAM522 RNA is designated SEQ ID:8320, and is provided hereinbelow with reference to the sequence listing part.

[7618] GAM522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM522 target RNA, herein designated GAM TARGET RNA.
GAM522 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7619] GAM522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM522 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM522 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM522 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7620] The complementary binding of GAM522 RNA, herein designated GAM RNA, to target binding sites on GAM522 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM522 target RNA, herein desig-

nated GAM TARGET RNA, into GAM522 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7621] It is appreciated that GAM522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM522 target genes. The mRNA of each one of this plurality of GAM522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM522 RNA, herein designated GAM RNA, and which when bound by GAM522 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM522 target proteins.

[7622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM522 gene, herein designated GAM GENE, on one or more GAM522 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7623] It is yet further appreciated that specific functions, and accordingly utilities, of GAM522 correlate with, and may be deduced from, the identity of the target genes which GAM522 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7624] Nucleotide sequences of the GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM522 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM522 are further described hereinbelow with reference to Table Table1.

[7625] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM522 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7626]

[7627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 523 (GAM523) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7628] GAM523 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM523 was detected is described hereinabove with reference to Figs. 2-8.

[7629] GAM523 gene, herein designated GAM GENE, and GAM523 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7630] GAM523 gene, herein designated GAM GENE, encodes a GAM523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM523 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM523 precursor RNA is designated SEQ ID:8335, and is provided hereinbelow with ref-

erence to the sequence listing part.

[7631] GAM523 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7632] An enzyme complex designated DICER COMPLEX, dices the GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM523 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of GAM523 RNA is designated SEQ ID:8336, and is provided hereinbelow with reference to the sequence listing part.

[7633] GAM523 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM523 target RNA, herein designated GAM TARGET RNA.

GAM523 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7634] GAM523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM523 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM523 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM523 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7635] The complementary binding of GAM523 RNA, herein designated GAM RNA, to target binding sites on GAM523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM523 target RNA, herein designated GAM TARGET RNA, into GAM523 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7636] It is appreciated that GAM523 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM523 target genes. The mRNA of each one of this plurality of GAM523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM523 RNA, herein designated GAM RNA, and which when bound by GAM523 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM523 target proteins.

[7637] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM523 gene, herein designated GAM GENE, on one or more GAM523 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM523 correlate with, and may be deduced from, the identity of the target genes which GAM523 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7639] Nucleotide sequences of the GAM523 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM523 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM523 are further described hereinbelow with reference to Table Table1.

[7640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM523 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7641]

[7642] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 524 (GAM524) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7643] GAM524 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM524 was detected is described hereinabove with reference to Figs. 2-8.

[7644] GAM524 gene, herein designated GAM GENE, and GAM524 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[7645] GAM524 gene, herein designated GAM GENE, encodes a GAM524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM524 precursor RNA is designated SEQ ID:8344, and is provided hereinbelow with reference to the sequence listing part.

[7646] GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7647] An enzyme complex designated DICER COMPLEX, dices the GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM524 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of GAM524 RNA is designated SEQ ID:8345, and is provided hereinbelow with reference to the sequence listing part.

[7648] GAM524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM524 target RNA, herein designated GAM TARGET RNA. GAM524 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7649] GAM524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM524 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM524 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM524 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7650] The complementary binding of GAM524 RNA, herein designated GAM RNA, to target binding sites on GAM524 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM524 target RNA, herein designated GAM TARGET RNA, into GAM524 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7651] It is appreciated that GAM524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM524 target genes. The mRNA of each one of this plurality of GAM524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM524 RNA, herein designated GAM RNA, and which when bound by GAM524 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM524 target proteins.

[7652] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM524 gene, herein designated GAM GENE, on one or more GAM524 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7653] It is yet further appreciated that specific functions, and accordingly utilities, of GAM524 correlate with, and may be deduced from, the identity of the target genes which GAM524 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7654] Nucleotide sequences of the GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM524 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM524 are further described hereinbelow with reference to Table Table1.

[7655] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM524 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7656]

[7657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

525 (GAM525) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7658] GAM525 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM525 was detected is described hereinabove with reference to Figs. 2-8.

[7659] GAM525 gene, herein designated GAM GENE, and GAM525 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7660] GAM525 gene, herein designated GAM GENE, encodes a GAM525 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM525 precursor RNA is designated SEQ ID:8355, and is provided hereinbelow with reference to the sequence listing part.

[7661] GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7662] An enzyme complex designated DICER COMPLEX, dices the GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM525 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM525 RNA is designated SEQ ID:8356, and is provided hereinbelow with reference to the sequence listing part.

[7663] GAM525 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM525 target RNA, herein designated GAM TARGET RNA. GAM525 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7664] GAM525 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM525 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM525 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM525 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM525 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7665] The complementary binding of GAM525 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM525 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM525 target RNA, herein designated GAM TARGET RNA, into GAM525 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7666] It is appreciated that GAM525 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM525 target genes. The mRNA of each one of this plurality of GAM525 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM525 RNA, herein designated GAM RNA, and which when bound by GAM525 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM525 target proteins.

[7667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM525 gene, herein designated GAM GENE, on one or more GAM525 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM525 correlate with, and may be deduced from, the identity of the target genes which GAM525 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7669] Nucleotide sequences of the GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM525 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM525 are further described hereinbelow with reference to Table Table1.

[7670] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM525 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7671]

[7672] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 526 (GAM526) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7673] GAM526 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM526 was detected is described hereinabove with reference to Figs. 2-8.

[7674] GAM526 gene, herein designated GAM GENE, and GAM526 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7675] GAM526 gene, herein designated GAM GENE, encodes a GAM526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM526 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM526 precursor RNA is designated SEQ ID:8374, and is provided hereinbelow with reference to the sequence listing part.

[7676] GAM526 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7677] An enzyme complex designated DICER COMPLEX, dices the GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM526 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 61%) nucleotide sequence of GAM526 RNA is designated SEQ ID:6904, and is provided hereinbelow with reference to the sequence listing part.

[7678] GAM526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM526 target RNA, herein designated GAM TARGET RNA. GAM526 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7679] GAM526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM526 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM526 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM526 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7680] The complementary binding of GAM526 RNA, herein designated GAM RNA, to target binding sites on GAM526 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM526 target RNA, herein designated GAM TARGET RNA, into GAM526 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7681] It is appreciated that GAM526 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM526 target genes. The mRNA of each one of this plurality of GAM526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM526 RNA, herein designated GAM RNA, and which when bound by

GAM526 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM526 target proteins.

[7682] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM526 gene, herein designated GAM GENE, on one or more GAM526 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7683] It is yet further appreciated that specific functions, and accordingly utilities, of GAM526 correlate with, and may be deduced from, the identity of the target genes which GAM526 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[7684] Nucleotide sequences of the GAM526 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM526 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM526 are further described hereinbelow with reference to Table Table1.

[7685] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM526 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7686]

[7687] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 527 (GAM527) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7688] GAM527 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM527 was detected is described hereinabove with reference to Figs. 2-8.

[7689] GAM527 gene, herein designated GAM GENE, and GAM527 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7690] GAM527 gene, herein designated GAM GENE, encodes a GAM527 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM527 precursor RNA is designated SEQ ID:8390, and is provided hereinbelow with reference to the sequence listing part.

[7691] GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7692] An enzyme complex designated DICER COMPLEX, dices the GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM527 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 28%) nucleotide sequence of GAM527 RNA is designated SEQ ID:8391, and is provided hereinbelow with reference to the sequence listing part.

[7693] GAM527 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM527 target RNA, herein designated GAM TARGET RNA. GAM527 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7694] GAM527 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM527 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM527 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM527 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM527 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7695] The complementary binding of GAM527 RNA, herein designated GAM RNA, to target binding sites on GAM527 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM527 target RNA, herein designated GAM TARGET RNA, into GAM527 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7696] It is appreciated that GAM527 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM527 target genes. The mRNA of each one of this plurality of GAM527 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM527 RNA, herein designated GAM RNA, and which when bound by GAM527 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM527 target proteins.

[7697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM527 gene, herein designated GAM GENE, on one or more GAM527 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7698] It is yet further appreciated that specific functions, and accordingly utilities, of GAM527 correlate with, and may be deduced from, the identity of the target genes which GAM527 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7699] Nucleotide sequences of the GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM527 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM527 are further described hereinbelow with reference to Table Table1.

[7700] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM527 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7701]

[7702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 528 (GAM528) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7703] GAM528 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM528 was detected is described hereinabove with reference to Figs. 2-8.

[7704] GAM528 gene, herein designated GAM GENE, and GAM528 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7705] GAM528 gene, herein designated GAM GENE, encodes a GAM528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM528 precursor RNA is designated SEQ ID:8394, and is provided hereinbelow with reference to the sequence listing part.

[7706] GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7707] An enzyme complex designated DICER COMPLEX, dices the GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM528 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of GAM528 RNA is designated SEQ ID:8395, and is provided hereinbelow with reference to the sequence listing part.

[7708] GAM528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM528

target RNA, herein designated GAM TARGET RNA.

GAM528 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7709] GAM528 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM528 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM528 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM528 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7710] The complementary binding of GAM528 RNA, herein designated GAM RNA, to target binding sites on GAM528 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM528 target RNA, herein designated GAM TARGET RNA, into GAM528 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7711] It is appreciated that GAM528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM528 target genes. The mRNA of each one of this plurality of GAM528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM528 RNA, herein designated GAM RNA, and which when bound by GAM528 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM528 target proteins.

[7712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM528 gene, herein designated GAM GENE, on one or more GAM528 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM528 correlate with, and may be deduced from, the identity of the target genes which GAM528 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7714] Nucleotide sequences of the GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM528 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM528 are further described hereinbelow with reference to Table Table1.

[7715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM528 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7716]

[7717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 529 (GAM529) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7718] GAM529 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM529 was detected is described hereinabove with reference to Figs. 2-8.

[7719] GAM529 gene, herein designated GAM GENE, and GAM529 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7720] GAM529 gene, herein designated GAM GENE, encodes a GAM529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM529 precursor RNA is designated SEQ ID:8403, and is provided hereinbelow with reference to the sequence listing part.

[7721] GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7722] An enzyme complex designated DICER COMPLEX, dices the GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM529 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of GAM529 RNA is designated SEQ ID:8404, and is provided hereinbelow with reference to the sequence listing part.

[7723] GAM529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM529 target RNA, herein designated GAM TARGET RNA. GAM529 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7724] GAM529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM529 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM529 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM529 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7725] The complementary binding of GAM529 RNA, herein designated GAM RNA, to target binding sites on GAM529 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM529 target RNA, herein designated GAM TARGET RNA, into GAM529 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7726] It is appreciated that GAM529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM529 target genes. The mRNA of each one of this plu-

rality of GAM529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM529 RNA, herein designated GAM RNA, and which when bound by GAM529 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM529 target proteins.

[7727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM529 gene, herein designated GAM GENE, on one or more GAM529 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7728] It is yet further appreciated that specific functions, and accordingly utilities, of GAM529 correlate with, and may be deduced from, the identity of the target genes which GAM529 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7729] Nucleotide sequences of the GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM529 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM529 are further described hereinbelow with reference to Table Table1.

[7730] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM529 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7731]

[7732] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 530 (GAM530) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[7733] GAM530 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM530 was detected is described hereinabove with reference to Figs. 2-8.

[7734] GAM530 gene, herein designated GAM GENE, and GAM530 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7735] GAM530 gene, herein designated GAM GENE, encodes a GAM530 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM530 precursor RNA is designated SEQ ID:8432, and is provided hereinbelow with reference to the sequence listing part.

[7736] GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7737] An enzyme complex designated DICER COMPLEX, dices the GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM530 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of GAM530 RNA is designated SEQ ID:8433, and is provided hereinbelow with reference to the sequence listing part.

[7738] GAM530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM530 target RNA, herein designated GAM TARGET RNA.
GAM530 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[7739] GAM530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM530 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM530 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM530 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM530 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7740] The complementary binding of GAM530 RNA, herein designated GAM RNA, to target binding sites on GAM530 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM530 target RNA, herein designated GAM TARGET RNA, into GAM530 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7741] It is appreciated that GAM530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM530 target genes. The mRNA of each one of this plurality of GAM530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM530 RNA, herein designated GAM RNA, and which when bound by GAM530 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM530 target proteins.

[7742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM530 gene, herein designated GAM GENE, on one or more GAM530 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7743] It is yet further appreciated that specific functions, and accordingly utilities, of GAM530 correlate with, and may be deduced from, the identity of the target genes which GAM530 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7744] Nucleotide sequences of the GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM530 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM530 are further described hereinbelow with reference to Table Table1.

[7745] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM530 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7746]

[7747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 531 (GAM531) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7748] GAM531 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM531 was detected is described hereinabove with reference to Figs. 2-8.

[7749] GAM531 gene, herein designated GAM GENE, and GAM531 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7750] GAM531 gene, herein designated GAM GENE, encodes a GAM531 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM531 precursor RNA is designated SEQ ID:8440, and is provided hereinbelow with reference to the sequence listing part.

[7751] GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7752] An enzyme complex designated DICER COMPLEX, dices the GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM531 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of

GAM531 RNA is designated SEQ ID:8441, and is provided hereinbelow with reference to the sequence listing part.

[7753] GAM531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM531 target RNA, herein designated GAM TARGET RNA. GAM531 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7754] GAM531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM531 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM531 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM531 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7755] The complementary binding of GAM531 RNA, herein designated GAM RNA, to target binding sites on GAM531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM531 target RNA, herein designated GAM TARGET RNA, into GAM531 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7756] It is appreciated that GAM531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM531 target genes. The mRNA of each one of this plurality of GAM531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM531 RNA, herein designated GAM RNA, and which when bound by GAM531 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM531 target proteins.

[7757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM531 gene, herein designated GAM GENE, on one or more GAM531 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM531 correlate with, and may be deduced from, the identity of the target genes which GAM531 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7759] Nucleotide sequences of the GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM531 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM531 are further described hereinbelow with reference to Table Table1.

[7760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM531 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7761]

[7762] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 532 (GAM532) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7763] GAM532 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM532 was detected is described hereinabove

with reference to Figs. 2-8.

[7764] GAM532 gene, herein designated GAM GENE, and GAM532 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7765] GAM532 gene, herein designated GAM GENE, encodes a GAM532 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM532 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM532 precursor RNA is designated SEQ ID:8449, and is provided hereinbelow with reference to the sequence listing part.

[7766] GAM532 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7767] An enzyme complex designated DICER COMPLEX, dices the GAM532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM532 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of GAM532 RNA is designated SEQ ID:8441, and is provided hereinbelow with reference to the sequence listing part.

[7768] GAM532 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM532 target RNA, herein designated GAM TARGET RNA. GAM532 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7769] GAM532 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM532 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM532 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM532 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM532 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7770] The complementary binding of GAM532 RNA, herein designated GAM RNA, to target binding sites on GAM532 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM532 target RNA, herein designated GAM TARGET RNA, into GAM532 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[7771] It is appreciated that GAM532 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM532 target genes. The mRNA of each one of this plurality of GAM532 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM532 RNA, herein designated GAM RNA, and which when bound by GAM532 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM532 target proteins.

[7772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM532 gene, herein designated GAM GENE, on one or more GAM532 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7773] It is yet further appreciated that specific functions, and accordingly utilities, of GAM532 correlate with, and may be deduced from, the identity of the target genes which GAM532 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7774] Nucleotide sequences of the GAM532 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM532 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM532 are further described hereinbelow with reference to Table Table1.

[7775] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM532 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7776]

[7777] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 533 (GAM533) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7778] GAM533 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM533 was detected is described hereinabove with reference to Figs. 2-8.

[7779] GAM533 gene, herein designated GAM GENE, and GAM533 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7780] GAM533 gene, herein designated GAM GENE, encodes a GAM533 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM533 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM533 precursor RNA is designated SEQ ID:8469, and is provided hereinbelow with reference to the sequence listing part.

[7781] GAM533 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7782] An enzyme complex designated DICER COMPLEX, dices the GAM533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM533 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of GAM533 RNA is designated SEQ ID:8470, and is provided hereinbelow with reference to the sequence listing part.

[7783] GAM533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM533 target RNA, herein designated GAM TARGET RNA.

GAM533 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7784] GAM533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM533 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM533 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM533 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7785] The complementary binding of GAM533 RNA, herein designated GAM RNA, to target binding sites on GAM533 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM533 target RNA, herein designated GAM TARGET RNA, into GAM533 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7786] It is appreciated that GAM533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM533 target genes. The mRNA of each one of this plurality of GAM533 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM533 RNA, herein designated GAM RNA, and which when bound by GAM533 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM533 target proteins.

[7787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM533 gene, herein designated GAM GENE, on one or more GAM533 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7788] It is yet further appreciated that specific functions, and accordingly utilities, of GAM533 correlate with, and may be deduced from, the identity of the target genes which GAM533 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7789] Nucleotide sequences of the GAM533 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM533 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM533 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM533 are further described hereinbelow with reference to Table Table1.

[7790] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM533 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7791]

[7792] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 534 (GAM534) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7793] GAM534 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM534 was detected is described hereinabove with reference to Figs. 2-8.

[7794] GAM534 gene, herein designated GAM GENE, and GAM534 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7795] GAM534 gene, herein designated GAM GENE, encodes a

GAM534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM534 precursor RNA is designated SEQ ID:8493, and is provided hereinbelow with reference to the sequence listing part.

[7796] GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7797] An enzyme complex designated DICER COMPLEX, dices the GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM534 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM534 RNA is designated SEQ ID:8494, and is provided hereinbelow with reference to the sequence listing part.

[7798] GAM534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM534 target RNA, herein designated GAM TARGET RNA. GAM534 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7799] GAM534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM534 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM534 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM534 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7800] The complementary binding of GAM534 RNA, herein designated GAM RNA, to target binding sites on GAM534 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM534 target RNA, herein designated GAM TARGET RNA, into GAM534 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7801] It is appreciated that GAM534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM534 target genes. The mRNA of each one of this plurality of GAM534 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM534 RNA, herein designated GAM RNA, and which when bound by GAM534 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM534 target proteins.

[7802] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM534 gene, herein designated GAM GENE, on one or more GAM534 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7803] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM534 correlate with, and may be deduced from, the identity of the target genes which GAM534 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7804] Nucleotide sequences of the GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM534 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM534 are further described hereinbelow with reference to Table Table1.

[7805] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM534 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7806]

[7807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 535 (GAM535) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7808] GAM535 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM535 was detected is described hereinabove with reference to Figs. 2-8.

[7809] GAM535 gene, herein designated GAM GENE, and GAM535 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7810] GAM535 gene, herein designated GAM GENE, encodes a GAM535 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM535 precursor RNA is designated SEQ ID:8508, and is provided hereinbelow with reference to the sequence listing part.

[7811] GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7812] An enzyme complex designated DICER COMPLEX, dices the GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM535 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of GAM535 RNA is designated SEQ ID:8509, and is provided hereinbelow with reference to the sequence listing part.

[7813] GAM535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM535 target RNA, herein designated GAM TARGET RNA. GAM535 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7814] GAM535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM535 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM535 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM535 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7815] The complementary binding of GAM535 RNA, herein designated GAM RNA, to target binding sites on GAM535 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM535 target RNA, herein designated GAM TARGET RNA, into GAM535 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7816] It is appreciated that GAM535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM535 target genes. The mRNA of each one of this plurality of GAM535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM535 RNA, herein designated GAM RNA, and which when bound by GAM535 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM535 target proteins.

[7817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM535 gene, herein designated GAM GENE, on one or more GAM535 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7818] It is yet further appreciated that specific functions, and accordingly utilities, of GAM535 correlate with, and may be deduced from, the identity of the target genes which GAM535 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7819] Nucleotide sequences of the GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM535 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM535 are further described hereinbelow with reference to Table Table1.

[7820] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM535 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7821]

[7822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 536 (GAM536) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7823] GAM536 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM536 was detected is described hereinabove with reference to Figs. 2-8.

[7824] GAM536 gene, herein designated GAM GENE, and GAM536 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7825] GAM536 gene, herein designated GAM GENE, encodes a GAM536 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM536 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM536 precursor RNA is designated SEQ ID:8519, and is provided hereinbelow with reference to the sequence listing part.

[7826] GAM536 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7827] An enzyme complex designated DICER COMPLEX, dices the GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM536 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of GAM536 RNA is designated SEQ ID:8520, and is provided

hereinbelow with reference to the sequence listing part.

[7828] GAM536 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM536 target RNA, herein designated GAM TARGET RNA.

GAM536 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7829] GAM536 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM536 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM536 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM536 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM536 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7830] The complementary binding of GAM536 RNA, herein designated GAM RNA, to target binding sites on GAM536 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM536 target RNA, herein designated GAM TARGET RNA, into GAM536 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7831] It is appreciated that GAM536 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM536 target genes. The mRNA of each one of this plurality of GAM536 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM536 RNA, herein designated GAM RNA, and which when bound by GAM536 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM536 tar-

get proteins.

[7832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM536 gene, herein designated GAM GENE, on one or more GAM536 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM536 correlate with, and may be deduced from, the identity of the target genes which GAM536 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7834] Nucleotide sequences of the GAM536 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM536 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM536 are further described hereinbelow with reference to Table Table1.

[7835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM536 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7836]

[7837] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 537 (GAM537) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7838] GAM537 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM537 was detected is described hereinabove with reference to Figs. 2-8.

[7839] GAM537 gene, herein designated GAM GENE, and GAM537 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7840] GAM537 gene, herein designated GAM GENE, encodes a GAM537 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM537 precursor RNA is designated SEQ ID:8528, and is provided hereinbelow with reference to the sequence listing part.

[7841] GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7842] An enzyme complex designated DICER COMPLEX, dices

the GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM537 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 39%) nucleotide sequence of GAM537 RNA is designated SEQ ID:8529, and is provided hereinbelow with reference to the sequence listing part.

[7843] GAM537 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM537 target RNA, herein designated GAM TARGET RNA. GAM537 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7844] GAM537 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM537 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM537

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM537 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM537 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7845] The complementary binding of GAM537 RNA, herein designated GAM RNA, to target binding sites on GAM537 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM537 target RNA, herein designated GAM TARGET RNA, into GAM537 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7846] It is appreciated that GAM537 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM537 target genes. The mRNA of each one of this plurality of GAM537 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM537 RNA, herein designated GAM RNA, and which when bound by GAM537 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM537 target proteins.

[7847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM537 gene, herein designated GAM GENE, on one or more GAM537 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7848] It is yet further appreciated that specific functions, and accordingly utilities, of GAM537 correlate with, and may be deduced from, the identity of the target genes which GAM537 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7849] Nucleotide sequences of the GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM537 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM537 are further described hereinbelow with reference to Table Table1.

[7850] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM537 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7851]

[7852] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 538 (GAM538) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7853] GAM538 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM538 was detected is described hereinabove with reference to Figs. 2-8.

[7854] GAM538 gene, herein designated GAM GENE, and GAM538 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7855] GAM538 gene, herein designated GAM GENE, encodes a GAM538 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM538 precursor RNA is designated SEQ ID:8549, and is provided hereinbelow with reference to the sequence listing part.

[7856] GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM538 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7857] An enzyme complex designated DICER COMPLEX, dices the GAM538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM538 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 28%) nucleotide sequence of GAM538 RNA is designated SEQ ID:8550, and is provided hereinbelow with reference to the sequence listing part.

[7858] GAM538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM538 target RNA, herein designated GAM TARGET RNA. GAM538 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7859] GAM538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM538 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM538 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM538 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[7860] The complementary binding of GAM538 RNA, herein designated GAM RNA, to target binding sites on GAM538 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM538 target RNA, herein designated GAM TARGET RNA, into GAM538 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7861] It is appreciated that GAM538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM538 target genes. The mRNA of each one of this plurality of GAM538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM538 RNA, herein designated GAM RNA, and which when bound by GAM538 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM538 target proteins.

[7862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM538 gene, herein designated GAM GENE, on one or

more GAM538 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7863] It is yet further appreciated that specific functions, and accordingly utilities, of GAM538 correlate with, and may be deduced from, the identity of the target genes which GAM538 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7864] Nucleotide sequences of the GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM538 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM538 are further de-

scribed hereinbelow with reference to Table Table1.

[7865] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM538 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7866]

[7867] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 539 (GAM539) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7868] GAM539 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM539 was detected is described hereinabove with reference to Figs. 2-8.

[7869] GAM539 gene, herein designated GAM GENE, and GAM539 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7870] GAM539 gene, herein designated GAM GENE, encodes a GAM539 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM539 precursor RNA is designated SEQ ID:8564, and is provided hereinbelow with reference to the sequence listing part.

[7871] GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7872] An enzyme complex designated DICER COMPLEX, dices the GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM539 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of GAM539 RNA is designated SEQ ID:8565, and is provided hereinbelow with reference to the sequence listing part.

[7873] GAM539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM539 target RNA, herein designated GAM TARGET RNA. GAM539 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7874] GAM539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM539 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM539 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM539 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM539 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7875] The complementary binding of GAM539 RNA, herein designated GAM RNA, to target binding sites on GAM539 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM539 target RNA, herein designated GAM TARGET RNA, into GAM539 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7876] It is appreciated that GAM539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM539 target genes. The mRNA of each one of this plurality of GAM539 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM539 RNA, herein designated GAM RNA, and which when bound by GAM539 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM539 target proteins.

[7877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM539 gene, herein designated GAM GENE, on one or more GAM539 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM539 correlate with, and may

be deduced from, the identity of the target genes which GAM539 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7879] Nucleotide sequences of the GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM539 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM539 are further described hereinbelow with reference to Table Table1.

[7880] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM539 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7881]

[7882] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 540 (GAM540) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7883] GAM540 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM540 was detected is described hereinabove with reference to Figs. 2-8.

[7884] GAM540 gene, herein designated GAM GENE, and GAM540 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7885] GAM540 gene, herein designated GAM GENE, encodes a GAM540 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM540 precursor RNA is designated SEQ ID:8567, and is provided hereinbelow with reference to the sequence listing part.

[7886] GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7887] An enzyme complex designated DICER COMPLEX, dices the GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM540 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of GAM540 RNA is designated SEQ ID:8568, and is provided hereinbelow with reference to the sequence listing part.

[7888] GAM540 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM540 target RNA, herein designated GAM TARGET RNA. GAM540 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7889] GAM540 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM540 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM540 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM540 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM540 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7890] The complementary binding of GAM540 RNA, herein designated GAM RNA, to target binding sites on GAM540 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM540 target RNA, herein designated GAM TARGET RNA, into GAM540 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7891] It is appreciated that GAM540 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM540 target genes. The mRNA of each one of this plurality of GAM540 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM540 RNA, herein designated GAM RNA, and which when bound by GAM540 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM540 target proteins.

[7892] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM540 gene, herein designated GAM GENE, on one or more GAM540 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7893] It is yet further appreciated that specific functions, and accordingly utilities, of GAM540 correlate with, and may be deduced from, the identity of the target genes which GAM540 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7894] Nucleotide sequences of the GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM540 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM540 are further described hereinbelow with reference to Table Table1.

[7895] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM540 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7896]

[7897] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 541 (GAM541) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7898] GAM541 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM541 was detected is described hereinabove with reference to Figs. 2-8.

[7899] GAM541 gene, herein designated GAM GENE, and GAM541 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7900] GAM541 gene, herein designated GAM GENE, encodes a GAM541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM541 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM541 precursor RNA is desig-

nated SEQ ID:8573, and is provided hereinbelow with reference to the sequence listing part.

[7901] GAM541 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7902] An enzyme complex designated DICER COMPLEX, dices the GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM541 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 30%) nucleotide sequence of GAM541 RNA is designated SEQ ID:8574, and is provided hereinbelow with reference to the sequence listing part.

[7903] GAM541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM541 target RNA, herein designated GAM TARGET RNA. GAM541 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7904] GAM541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM541 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM541 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM541

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7905] The complementary binding of GAM541 RNA, herein designated GAM RNA, to target binding sites on GAM541 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM541 target RNA, herein designated GAM TARGET RNA, into GAM541 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7906] It is appreciated that GAM541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM541 target genes. The mRNA of each one of this plurality of GAM541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM541 RNA, herein designated GAM RNA, and which when bound by GAM541 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM541 target proteins.

[7907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM541 gene, herein designated GAM GENE, on one or more GAM541 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7908] It is yet further appreciated that specific functions, and accordingly utilities, of GAM541 correlate with, and may be deduced from, the identity of the target genes which GAM541 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7909] Nucleotide sequences of the GAM541 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM541 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM541 are further described hereinbelow with reference to Table Table1.

[7910] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM541 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7911]

[7912] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 542 (GAM542) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7913] GAM542 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM542 was detected is described hereinabove with reference to Figs. 2-8.

[7914] GAM542 gene, herein designated GAM GENE, and

GAM542 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7915] GAM542 gene, herein designated GAM GENE, encodes a GAM542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM542 precursor RNA is designated SEQ ID:8579, and is provided hereinbelow with reference to the sequence listing part.

[7916] GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7917] An enzyme complex designated DICER COMPLEX, dices the GAM542 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM542 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of GAM542 RNA is designated SEQ ID:8580, and is provided hereinbelow with reference to the sequence listing part.

[7918] GAM542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM542 target RNA, herein designated GAM TARGET RNA. GAM542 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7919] GAM542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM542 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM542 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM542 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7920] The complementary binding of GAM542 RNA, herein designated GAM RNA, to target binding sites on GAM542 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM542 target RNA, herein designated GAM TARGET RNA, into GAM542 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7921] It is appreciated that GAM542 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM542 target genes. The mRNA of each one of this plurality of GAM542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM542 RNA, herein designated GAM RNA, and which when bound by GAM542 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM542 target proteins.

[7922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM542 gene, herein designated GAM GENE, on one or more GAM542 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7923] It is yet further appreciated that specific functions, and accordingly utilities, of GAM542 correlate with, and may be deduced from, the identity of the target genes which GAM542 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7924] Nucleotide sequences of the GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM542 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM542 are further described hereinbelow with reference to Table Table1.

[7925] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM542 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7926]

[7927] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 543 (GAM543) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7928] GAM543 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM543 was detected is described hereinabove with reference to Figs. 2-8.

[7929] GAM543 gene, herein designated GAM GENE, and GAM543 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7930] GAM543 gene, herein designated GAM GENE, encodes a GAM543 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM543 precursor RNA is designated SEQ ID:8608, and is provided hereinbelow with reference to the sequence listing part.

[7931] GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7932] An enzyme complex designated DICER COMPLEX, dices the GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM543 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM543 RNA is designated SEQ ID:8609, and is provided hereinbelow with reference to the sequence listing part.

[7933] GAM543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM543 target RNA, herein designated GAM TARGET RNA. GAM543 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7934] GAM543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM543 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM543 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM543 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7935] The complementary binding of GAM543 RNA, herein designated GAM RNA, to target binding sites on GAM543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM543 target RNA, herein designated GAM TARGET RNA, into GAM543 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7936] It is appreciated that GAM543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM543 target genes. The mRNA of each one of this plurality of GAM543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM543 RNA, herein designated GAM RNA, and which when bound by GAM543 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM543 target proteins.

[7937] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM543 gene, herein designated GAM GENE, on one or more GAM543 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7938] It is yet further appreciated that specific functions, and accordingly utilities, of GAM543 correlate with, and may be deduced from, the identity of the target genes which GAM543 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7939] Nucleotide sequences of the GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM543 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM543 are further described hereinbelow with reference to Table Table1.

[7940] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM543 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7941]

[7942] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 544 (GAM544) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7943] GAM544 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM544 was detected is described hereinabove with reference to Figs. 2-8.

[7944] GAM544 gene, herein designated GAM GENE, and GAM544 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7945] GAM544 gene, herein designated GAM GENE, encodes a GAM544 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM544 precursor RNA is designated SEQ ID:8621, and is provided hereinbelow with reference to the sequence listing part.

[7946] GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7947] An enzyme complex designated DICER COMPLEX, dices the GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM544 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM544 RNA is designated SEQ ID:8622, and is provided hereinbelow with reference to the sequence listing part.

[7948] GAM544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM544 target RNA, herein designated GAM TARGET RNA. GAM544 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7949] GAM544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM544 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM544 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM544 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM544 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7950] The complementary binding of GAM544 RNA, herein designated GAM RNA, to target binding sites on GAM544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM544 target RNA, herein designated GAM TARGET RNA, into GAM544 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7951] It is appreciated that GAM544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM544 target genes. The mRNA of each one of this plurality of GAM544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM544 RNA,

herein designated GAM RNA, and which when bound by GAM544 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM544 target proteins.

[7952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM544 gene, herein designated GAM GENE, on one or more GAM544 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7953] It is yet further appreciated that specific functions, and accordingly utilities, of GAM544 correlate with, and may be deduced from, the identity of the target genes which

GAM544 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7954] Nucleotide sequences of the GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM544 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM544 are further described hereinbelow with reference to Table Table1.

[7955] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM544 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7956]

[7957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 545 (GAM545) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7958] GAM545 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM545 was detected is described hereinabove with reference to Figs. 2-8.

[7959] GAM545 gene, herein designated GAM GENE, and GAM545 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7960] GAM545 gene, herein designated GAM GENE, encodes a GAM545 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM545 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM545 precursor RNA is designated SEQ ID:8652, and is provided hereinbelow with reference to the sequence listing part.

[7961] GAM545 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7962] An enzyme complex designated DICER COMPLEX, dices the GAM545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM545 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM545 RNA is designated SEQ ID:8622, and is provided hereinbelow with reference to the sequence listing part.

[7963] GAM545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM545 target RNA, herein designated GAM TARGET RNA.
GAM545 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7964] GAM545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM545 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM545 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM545 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7965] The complementary binding of GAM545 RNA, herein designated GAM RNA, to target binding sites on GAM545 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM545 target RNA, herein desig-

nated GAM TARGET RNA, into GAM545 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7966] It is appreciated that GAM545 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM545 target genes. The mRNA of each one of this plurality of GAM545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM545 RNA, herein designated GAM RNA, and which when bound by GAM545 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM545 target proteins.

[7967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM545 gene, herein designated GAM GENE, on one or more GAM545 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7968] It is yet further appreciated that specific functions, and accordingly utilities, of GAM545 correlate with, and may be deduced from, the identity of the target genes which GAM545 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7969] Nucleotide sequences of the GAM545 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM545 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM545 are further described hereinbelow with reference to Table Table1.

[7970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM545 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7971]

[7972] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 546 (GAM546) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7973] GAM546 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM546 was detected is described hereinabove with reference to Figs. 2-8.

[7974] GAM546 gene, herein designated GAM GENE, and GAM546 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7975] GAM546 gene, herein designated GAM GENE, encodes a GAM546 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM546 precursor RNA is designated SEQ ID:8687, and is provided hereinbelow with ref-

erence to the sequence listing part.

[7976] GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7977] An enzyme complex designated DICER COMPLEX, dices the GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM546 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of GAM546 RNA is designated SEQ ID:8609, and is provided hereinbelow with reference to the sequence listing part.

[7978] GAM546 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM546 target RNA, herein designated GAM TARGET RNA.

GAM546 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7979] GAM546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM546 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM546 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM546 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7980] The complementary binding of GAM546 RNA, herein designated GAM RNA, to target binding sites on GAM546 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM546 target RNA, herein designated GAM TARGET RNA, into GAM546 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7981] It is appreciated that GAM546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM546 target genes. The mRNA of each one of this plurality of GAM546 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM546 RNA, herein designated GAM RNA, and which when bound by GAM546 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM546 target proteins.

[7982] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM546 gene, herein designated GAM GENE, on one or more GAM546 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7983] It is yet further appreciated that specific functions, and accordingly utilities, of GAM546 correlate with, and may be deduced from, the identity of the target genes which GAM546 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7984] Nucleotide sequences of the GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM546 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM546 are further described hereinbelow with reference to Table Table1.

[7985] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM546 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7986]

[7987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 547 (GAM547) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7988] GAM547 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM547 was detected is described hereinabove with reference to Figs. 2-8.

[7989] GAM547 gene, herein designated GAM GENE, and GAM547 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[7990] GAM547 gene, herein designated GAM GENE, encodes a GAM547 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM547 precursor RNA is designated SEQ ID:8715, and is provided hereinbelow with reference to the sequence listing part.

[7991] GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7992] An enzyme complex designated DICER COMPLEX, dices the GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM547 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of GAM547 RNA is designated SEQ ID:8716, and is provided hereinbelow with reference to the sequence listing part.

[7993] GAM547 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM547 target RNA, herein designated GAM TARGET RNA. GAM547 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7994] GAM547 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM547 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM547 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM547 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM547 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7995] The complementary binding of GAM547 RNA, herein designated GAM RNA, to target binding sites on GAM547 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM547 target RNA, herein designated GAM TARGET RNA, into GAM547 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7996] It is appreciated that GAM547 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM547 target genes. The mRNA of each one of this plurality of GAM547 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM547 RNA, herein designated GAM RNA, and which when bound by GAM547 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM547 target proteins.

[7997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM547 gene, herein designated GAM GENE, on one or more GAM547 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM547 correlate with, and may be deduced from, the identity of the target genes which GAM547 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7999] Nucleotide sequences of the GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM547 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM547 are further described hereinbelow with reference to Table Table1.

[8000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM547 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8001]

[8002] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

548 (GAM548) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8003] GAM548 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM548 was detected is described hereinabove with reference to Figs. 2-8.

[8004] GAM548 gene, herein designated GAM GENE, and GAM548 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8005] GAM548 gene, herein designated GAM GENE, encodes a GAM548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM548 precursor RNA is designated SEQ ID:8724, and is provided hereinbelow with reference to the sequence listing part.

[8006] GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8007] An enzyme complex designated DICER COMPLEX, dices the GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM548 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of GAM548 RNA is designated SEQ ID:8725, and is provided hereinbelow with reference to the sequence listing part.

[8008] GAM548 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM548 target RNA, herein designated GAM TARGET RNA. GAM548 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8009] GAM548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM548 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM548 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM548 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM548 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8010] The complementary binding of GAM548 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM548 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM548 target RNA, herein designated GAM TARGET RNA, into GAM548 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8011] It is appreciated that GAM548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM548 target genes. The mRNA of each one of this plurality of GAM548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM548 RNA, herein designated GAM RNA, and which when bound by GAM548 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM548 target proteins.

[8012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM548 gene, herein designated GAM GENE, on one or more GAM548 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8013] It is yet further appreciated that specific functions, and accordingly utilities, of GAM548 correlate with, and may be deduced from, the identity of the target genes which GAM548 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8014] Nucleotide sequences of the GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM548 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM548 are further described hereinbelow with reference to Table Table1.

[8015] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM548 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8016]

[8017] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 549 (GAM549) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8018] GAM549 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM549 was detected is described hereinabove with reference to Figs. 2-8.

[8019] GAM549 gene, herein designated GAM GENE, and GAM549 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8020] GAM549 gene, herein designated GAM GENE, encodes a GAM549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM549 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM549 precursor RNA is designated SEQ ID:8728, and is provided hereinbelow with reference to the sequence listing part.

[8021] GAM549 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8022] An enzyme complex designated DICER COMPLEX, dices the GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM549 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 49%) nucleotide sequence of GAM549 RNA is designated SEQ ID:8729, and is provided hereinbelow with reference to the sequence listing part.

[8023] GAM549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM549 target RNA, herein designated GAM TARGET RNA. GAM549 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8024] GAM549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM549 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM549 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM549 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8025] The complementary binding of GAM549 RNA, herein designated GAM RNA, to target binding sites on GAM549 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM549 target RNA, herein designated GAM TARGET RNA, into GAM549 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8026] It is appreciated that GAM549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM549 target genes. The mRNA of each one of this plurality of GAM549 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM549 RNA, herein designated GAM RNA, and which when bound by

GAM549 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM549 target proteins.

[8027] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM549 gene, herein designated GAM GENE, on one or more GAM549 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8028] It is yet further appreciated that specific functions, and accordingly utilities, of GAM549 correlate with, and may be deduced from, the identity of the target genes which GAM549 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[8029] Nucleotide sequences of the GAM549 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM549 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM549 are further described hereinbelow with reference to Table Table1.

[8030] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM549 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8031]

[8032] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 550 (GAM550) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8033] GAM550 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM550 was detected is described hereinabove with reference to Figs. 2-8.

[8034] GAM550 gene, herein designated GAM GENE, and GAM550 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8035] GAM550 gene, herein designated GAM GENE, encodes a GAM550 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM550 precursor RNA is designated SEQ ID:8744, and is provided hereinbelow with reference to the sequence listing part.

[8036] GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[8037] An enzyme complex designated DICER COMPLEX, dices the GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM550 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of GAM550 RNA is designated SEQ ID:8745, and is provided hereinbelow with reference to the sequence listing part.

[8038] GAM550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM550 target RNA, herein designated GAM TARGET RNA. GAM550 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8039] GAM550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM550 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM550 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM550 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM550 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8040] The complementary binding of GAM550 RNA, herein designated GAM RNA, to target binding sites on GAM550 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM550 target RNA, herein designated GAM TARGET RNA, into GAM550 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8041] It is appreciated that GAM550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM550 target genes. The mRNA of each one of this plurality of GAM550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM550 RNA, herein designated GAM RNA, and which when bound by GAM550 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM550 target proteins.

[8042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM550 gene, herein designated GAM GENE, on one or more GAM550 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8043] It is yet further appreciated that specific functions, and accordingly utilities, of GAM550 correlate with, and may be deduced from, the identity of the target genes which GAM550 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8044] Nucleotide sequences of the GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM550 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM550 are further described hereinbelow with reference to Table Table1.

[8045] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM550 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8046]

[8047] Reference is now made to Fig. 11, which is a simplified diagram describing each of a plurality of novel bioinformatically detected regulatory genes, referred to here as Genomic Record(GR) genes, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8048] GR GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR GENE was detected is described hereinabove with reference to Figs. 6-15.

[8049] GR GENE encodes GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8050] GR PRECURSOR RNA folds spatially, forming GR FOLDED PRECURSOR RNA. It is appreciated that GR FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the sec-

ond half thereof, as is well known in the art.

[8051] GR FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into a plurality of separate GAM precursor RNAs, schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR, GAM4 PRECURSOR, GAM5 PRECURSOR, GAM6 PRECURSOR, GAM7 PRECURSOR and GAM8 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8052] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, schematically represented as GAM1 RNA, GAM2 RNA, GAM3 RNA, GAM4 RNA, GAM5 RNA, GAM6 RNA, GAM7 RNA and GAM8 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8053] GAM1 RNA binds complimentarily to a target binding site located in an untranslated region of GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM1 TARGET RNA into GAM1 TARGET PROTEIN, both of Fig. 10.

[8054] GAM2 RNA binds complimentarily to a target binding site

located in an untranslated region of GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM2 TARGET RNA into GAM2 TARGET PROTEIN, both of Fig. 10.

[8055] GAM3 RNA binds complimentarily to a target binding site located in an untranslated region of GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM3 TARGET RNA into GAM3 TARGET PROTEIN, both of Fig. 10.

[8056] GAM4 RNA binds complimentarily to a target binding site located in an untranslated region of GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM4 TARGET RNA into GAM4 TARGET PROTEIN, both of Fig. 10.

[8057] GAM5 RNA binds complimentarily to a target binding site located in an untranslated region of GAM5 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM5 TARGET RNA into GAM5 TARGET PROTEIN, both of Fig. 10.

[8058] GAM6 RNA binds complimentarily to a target binding site located in an untranslated region of GAM6 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM6 TARGET RNA into GAM6 TARGET PROTEIN, both of Fig. 10.

[8059] GAM7 RNA binds complimentarily to a target binding site located in an untranslated region of GAM7 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM7 TARGET RNA into GAM7 TARGET PROTEIN, both of Fig. 10.

[8060] GAM8 RNA binds complimentarily to a target binding site located in an untranslated region of GAM8 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 10, thereby inhibiting translation of GAM8 TARGET RNA into GAM8 TARGET PROTEIN, both of Fig. 10.

[8061] It is appreciated that specific functions, and accordingly utilities, of GR GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR GENE, schematically represented by GAM1 TARGET PRO-

TEIN through GAM8 TARGET PROTEIN.

[8062] Reference is now made to Fig. 551, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 551(GR551) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8063] GR551 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR551 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8064] GR551 GENE encodes GR551 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8065] GR551 PRECURSOR RNA folds spatially, forming GR551 FOLDED PRECURSOR RNA . It is appreciated that GR551 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR551 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[8066] GR551 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8067] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8068] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8069] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8070] It is appreciated that specific functions, and accordingly utilities, of GR551 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR551 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8071] Reference is now made to Fig. 552, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 552(GR552) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8072] GR552 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR552 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[8073] GR552 GENE encodes GR552 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8074] GR552 PRECURSOR RNA folds spatially, forming GR552 FOLDED PRECURSOR RNA . It is appreciated that GR552 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR552 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8075] GR552 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103 PRECURSOR and GAM312 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8076] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103 RNA and GAM312 RNA respectively, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

[8077] GAM103 RNA binds complimentarily to a target binding site located in an untranslated region of GAM103 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 103A, thereby inhibiting translation of GAM103 TARGET RNA into GAM103 TARGET PROTEIN, both of Fig. 103A.

[8078] GAM312 RNA binds complimentarily to a target binding site located in an untranslated region of GAM312 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 312A, thereby inhibiting translation of GAM312 TARGET RNA into GAM312 TARGET PROTEIN, both of Fig. 312A.

[8079] It is appreciated that specific functions, and accordingly utilities, of GR552 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR552 GENE: GAM103 TARGET PROTEIN and GAM312 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 103D and 312D

[8080] Reference is now made to Fig. 553, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 553(GR553) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8081] GR553 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR553 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8082] GR553 GENE encodes GR553 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8083] GR553 PRECURSOR RNA folds spatially, forming GR553 FOLDED PRECURSOR RNA . It is appreciated that GR553 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR553 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[8084] GR553 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM269 PRECURSOR and GAM372 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8085] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM269 RNA and GAM372 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8086] GAM269 RNA binds complimentarily to a target binding site located in an untranslated region of GAM269 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 269A, thereby inhibiting translation of GAM269 TARGET RNA into GAM269 TARGET PROTEIN, both of Fig. 269A.

[8087] GAM372 RNA binds complimentarily to a target binding site located in an untranslated region of GAM372 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 372A, thereby inhibiting translation of GAM372 TARGET RNA into GAM372 TARGET PROTEIN, both of Fig. 372A.

[8088] It is appreciated that specific functions, and accordingly utilities, of GR553 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR553 GENE: GAM269 TARGET PROTEIN and GAM372 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 269D and 372D

[8089] Reference is now made to Fig. 554, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 554(GR554) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8090] GR554 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR554 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8091] GR554 GENE encodes GR554 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8092] GR554 PRECURSOR RNA folds spatially, forming GR554 FOLDED PRECURSOR RNA . It is appreciated that GR554 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR554 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8093] GR554 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM150 PRECURSOR and GAM542 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8094] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM150 RNA and GAM542 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8095] GAM150 RNA binds complimentarily to a target binding site located in an untranslated region of GAM150 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 150A, thereby inhibiting translation of GAM150 TARGET RNA into GAM150 TARGET PROTEIN, both of Fig. 150A.

[8096] GAM542 RNA binds complimentarily to a target binding site located in an untranslated region of GAM542 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 542A, thereby inhibiting translation of GAM542 TARGET RNA into GAM542 TARGET PROTEIN, both of Fig. 542A.

[8097] It is appreciated that specific functions, and accordingly utilities, of GR554 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR554 GENE: GAM150 TARGET PROTEIN and GAM542 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 150D and 542D

[8098] Reference is now made to Fig. 555, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 555(GR555) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8099] GR555 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR555 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8100] GR555 GENE encodes GR555 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8101] GR555 PRECURSOR RNA folds spatially, forming GR555 FOLDED PRECURSOR RNA . It is appreciated that GR555 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR555 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8102] GR555 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM293 PRECURSOR and GAM368 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8103] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM293 RNA and GAM368 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8104] GAM293 RNA binds complimentarily to a target binding site located in an untranslated region of GAM293 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 293A, thereby inhibiting translation of GAM293 TARGET RNA into GAM293 TARGET PROTEIN, both of Fig. 293A.

[8105] GAM368 RNA binds complimentarily to a target binding site located in an untranslated region of GAM368 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 368A, thereby inhibiting transla-

tion of GAM368 TARGET RNA into GAM368 TARGET PROTEIN, both of Fig. 368A.

[8106] It is appreciated that specific functions, and accordingly utilities, of GR555 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR555 GENE: GAM293 TARGET PROTEIN and GAM368 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 293D and 368D

[8107] Reference is now made to Fig. 556, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 556(GR556) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8108] GR556 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR556 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8109] GR556 GENE encodes GR556 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[8110] GR556 PRECURSOR RNA folds spatially, forming GR556 FOLDED PRECURSOR RNA . It is appreciated that GR556 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR556 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8111] GR556 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM515 PRECURSOR and GAM516 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8112] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM515 RNA and GAM516 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8113] GAM515 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM515 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 515A, thereby inhibiting translation of GAM515 TARGET RNA into GAM515 TARGET PROTEIN, both of Fig. 515A.

[8114] GAM516 RNA binds complimentarily to a target binding site located in an untranslated region of GAM516 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 516A, thereby inhibiting translation of GAM516 TARGET RNA into GAM516 TARGET PROTEIN, both of Fig. 516A.

[8115] It is appreciated that specific functions, and accordingly utilities, of GR556 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR556 GENE: GAM515 TARGET PROTEIN and GAM516 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 515D and 516D

[8116] Reference is now made to Fig. 557, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 557(GR557) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8117] GR557 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR557 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8118] GR557 GENE encodes GR557 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8119] GR557 PRECURSOR RNA folds spatially, forming GR557 FOLDED PRECURSOR RNA . It is appreciated that GR557 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR557 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8120] GR557 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85 PRECURSOR and GAM121 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8121] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85 RNA and GAM121 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8122] GAM85 RNA binds complimentarily to a target binding site located in an untranslated region of GAM85 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 85A, thereby inhibiting translation of GAM85 TARGET RNA into GAM85 TARGET PROTEIN, both of Fig. 85A.

[8123] GAM121 RNA binds complimentarily to a target binding site located in an untranslated region of GAM121 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 121A, thereby inhibiting translation of GAM121 TARGET RNA into GAM121 TARGET PRO-

TEIN, both of Fig. 121A.

[8124] It is appreciated that specific functions, and accordingly utilities, of GR557 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR557 GENE: GAM85 TARGET PROTEIN and GAM121 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 85D and 121D

[8125] Reference is now made to Fig. 558, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 558(GR558) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8126] GR558 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR558 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8127] GR558 GENE encodes GR558 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8128] GR558 PRECURSOR RNA folds spatially, forming GR558 FOLDED PRECURSOR RNA . It is appreciated that GR558 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR558 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8129] GR558 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM266 PRECURSOR, GAM357 PRECURSOR and GAM504 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8130] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM266 RNA, GAM357 RNA and GAM504 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8131] GAM266 RNA binds complimentarily to a target binding site located in an untranslated region of GAM266 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 266A, thereby inhibiting translation of GAM266 TARGET RNA into GAM266 TARGET PROTEIN, both of Fig. 266A.

[8132] GAM357 RNA binds complimentarily to a target binding site located in an untranslated region of GAM357 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 357A, thereby inhibiting translation of GAM357 TARGET RNA into GAM357 TARGET PROTEIN, both of Fig. 357A.

[8133] GAM504 RNA binds complimentarily to a target binding site located in an untranslated region of GAM504 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 504A, thereby inhibiting translation of GAM504 TARGET RNA into GAM504 TARGET PROTEIN, both of Fig. 504A.

[8134] It is appreciated that specific functions, and accordingly utilities, of GR558 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR558 GENE: GAM266 TARGET PROTEIN, GAM357 TARGET PROTEIN and GAM504 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 266D, 357D and 504D

[8135] Reference is now made to Fig. 559, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 559(GR559) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8136] GR559 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR559 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8137] GR559 GENE encodes GR559 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8138] GR559 PRECURSOR RNA folds spatially, forming GR559 FOLDED PRECURSOR RNA . It is appreciated that GR559 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR559 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8139] GR559 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM41 PRECURSOR, GAM45 PRECURSOR and GAM179 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8140] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41 RNA, GAM45 RNA and GAM179 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8141] GAM41 RNA binds complimentarily to a target binding site located in an untranslated region of GAM41 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 41A, thereby inhibiting translation of GAM41 TARGET RNA into GAM41 TARGET PROTEIN, both of Fig. 41A.

[8142] GAM45 RNA binds complimentarily to a target binding site located in an untranslated region of GAM45 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 45A, thereby inhibiting translation of GAM45 TARGET RNA into GAM45 TARGET PROTEIN, both of Fig. 45A.

[8143] GAM179 RNA binds complimentarily to a target binding site located in an untranslated region of GAM179 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 179A, thereby inhibiting translation of GAM179 TARGET RNA into GAM179 TARGET PROTEIN, both of Fig. 179A.

[8144] It is appreciated that specific functions, and accordingly utilities, of GR559 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR559 GENE: GAM41 TARGET PROTEIN, GAM45 TARGET PROTEIN and GAM179 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 41D, 45D and 179D

[8145] Reference is now made to Fig. 560, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 560(GR560) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8146] GR560 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR560 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8147] GR560 GENE encodes GR560 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8148] GR560 PRECURSOR RNA folds spatially, forming GR560 FOLDED PRECURSOR RNA . It is appreciated that GR560 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR560 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8149] GR560 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8150] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8151] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8152] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting transla-

tion of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8153] It is appreciated that specific functions, and accordingly utilities, of GR560 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR560 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8154] Reference is now made to Fig. 561, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 561(GR561) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8155] GR561 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR561 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8156] GR561 GENE encodes GR561 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[8157] GR561 PRECURSOR RNA folds spatially, forming GR561 FOLDED PRECURSOR RNA . It is appreciated that GR561 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR561 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8158] GR561 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM212 PRECURSOR and GAM493 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8159] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212 RNA and GAM493 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8160] GAM212 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM212 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 212A, thereby inhibiting translation of GAM212 TARGET RNA into GAM212 TARGET PROTEIN, both of Fig. 212A.

[8161] GAM493 RNA binds complimentarily to a target binding site located in an untranslated region of GAM493 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 493A, thereby inhibiting translation of GAM493 TARGET RNA into GAM493 TARGET PROTEIN, both of Fig. 493A.

[8162] It is appreciated that specific functions, and accordingly utilities, of GR561 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR561 GENE: GAM212 TARGET PROTEIN and GAM493 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 212D and 493D

[8163] Reference is now made to Fig. 562, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 562(GR562) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8164] GR562 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR562 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8165] GR562 GENE encodes GR562 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8166] GR562 PRECURSOR RNA folds spatially, forming GR562 FOLDED PRECURSOR RNA . It is appreciated that GR562 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR562 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8167] GR562 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35 PRECURSOR and GAM513 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8168] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35 RNA and GAM513 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8169] GAM35 RNA binds complimentarily to a target binding site located in an untranslated region of GAM35 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 35A, thereby inhibiting translation of GAM35 TARGET RNA into GAM35 TARGET PROTEIN, both of Fig. 35A.

[8170] GAM513 RNA binds complimentarily to a target binding site located in an untranslated region of GAM513 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 513A, thereby inhibiting translation of GAM513 TARGET RNA into GAM513 TARGET PROTEIN, both of Fig. 513A.

[8171] It is appreciated that specific functions, and accordingly utilities, of GR562 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR562 GENE: GAM35 TARGET PROTEIN and GAM513 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 35D and 513D

[8172] Reference is now made to Fig. 563, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 563(GR563) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8173] GR563 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR563 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8174] GR563 GENE encodes GR563 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8175] GR563 PRECURSOR RNA folds spatially, forming GR563 FOLDED PRECURSOR RNA . It is appreciated that GR563 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR563 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8176] GR563 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM224 PRECURSOR and GAM262 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8177] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM224 RNA and GAM262 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8178] GAM224 RNA binds complimentarily to a target binding site located in an untranslated region of GAM224 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 224A, thereby inhibiting translation of GAM224 TARGET RNA into GAM224 TARGET PROTEIN, both of Fig. 224A.

[8179] GAM262 RNA binds complimentarily to a target binding site located in an untranslated region of GAM262 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 262A, thereby inhibiting translation of GAM262 TARGET RNA into GAM262 TARGET PROTEIN, both of Fig. 262A.

[8180] It is appreciated that specific functions, and accordingly utilities, of GR563 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR563 GENE: GAM224 TARGET PROTEIN and GAM262 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 224D and 262D

[8181] Reference is now made to Fig. 564, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 564(GR564) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8182] GR564 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR564 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8183] GR564 GENE encodes GR564 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8184] GR564 PRECURSOR RNA folds spatially, forming GR564 FOLDED PRECURSOR RNA . It is appreciated that GR564 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR564 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8185] GR564 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM263 PRECURSOR and GAM385 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8186] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM263 RNA and GAM385 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8187] GAM263 RNA binds complimentarily to a target binding site located in an untranslated region of GAM263 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 263A, thereby inhibiting translation of GAM263 TARGET RNA into GAM263 TARGET PROTEIN, both of Fig. 263A.

[8188] GAM385 RNA binds complimentarily to a target binding site located in an untranslated region of GAM385 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 385A, thereby inhibiting translation of GAM385 TARGET RNA into GAM385 TARGET PROTEIN, both of Fig. 385A.

[8189] It is appreciated that specific functions, and accordingly utilities, of GR564 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR564 GENE: GAM263 TARGET PROTEIN and GAM385

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 263D and 385D

[8190] Reference is now made to Fig. 565, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 565(GR565) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8191] GR565 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR565 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8192] GR565 GENE encodes GR565 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8193] GR565 PRECURSOR RNA folds spatially, forming GR565 FOLDED PRECURSOR RNA . It is appreciated that GR565 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR565 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8194] GR565 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM431 PRECURSOR and GAM531 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8195] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM431 RNA and GAM531 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8196] GAM431 RNA binds complimentarily to a target binding site located in an untranslated region of GAM431 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 431A, thereby inhibiting translation of GAM431 TARGET RNA into GAM431 TARGET PROTEIN, both of Fig. 431A.

[8197] GAM531 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM531 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 531A, thereby inhibiting translation of GAM531 TARGET RNA into GAM531 TARGET PROTEIN, both of Fig. 531A.

[8198] It is appreciated that specific functions, and accordingly utilities, of GR565 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR565 GENE: GAM431 TARGET PROTEIN and GAM531 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 431D and 531D

[8199] Reference is now made to Fig. 566, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 566(GR566) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8200] GR566 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR566 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8201] GR566 GENE encodes GR566 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8202] GR566 PRECURSOR RNA folds spatially, forming GR566 FOLDED PRECURSOR RNA . It is appreciated that GR566 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR566 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8203] GR566 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM473 PRECURSOR and GAM477 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8204] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM473 RNA and GAM477 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8205] GAM473 RNA binds complimentarily to a target binding site located in an untranslated region of GAM473 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 473A, thereby inhibiting translation of GAM473 TARGET RNA into GAM473 TARGET PROTEIN, both of Fig. 473A.

[8206] GAM477 RNA binds complimentarily to a target binding site located in an untranslated region of GAM477 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 477A, thereby inhibiting translation of GAM477 TARGET RNA into GAM477 TARGET PROTEIN, both of Fig. 477A.

[8207] It is appreciated that specific functions, and accordingly utilities, of GR566 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR566 GENE: GAM473 TARGET PROTEIN and GAM477 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 473D and 477D

[8208] Reference is now made to Fig. 567, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 567(GR567) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8209] GR567 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR567 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8210] GR567 GENE encodes GR567 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8211] GR567 PRECURSOR RNA folds spatially, forming GR567 FOLDED PRECURSOR RNA . It is appreciated that GR567 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR567 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8212] GR567 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM480 PRECURSOR and GAM508 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8213] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM480 RNA and GAM508 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8214] GAM480 RNA binds complimentarily to a target binding site located in an untranslated region of GAM480 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 480A, thereby inhibiting translation of GAM480 TARGET RNA into GAM480 TARGET PROTEIN, both of Fig. 480A.

[8215] GAM508 RNA binds complimentarily to a target binding site located in an untranslated region of GAM508 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 508A, thereby inhibiting translation of GAM508 TARGET RNA into GAM508 TARGET PROTEIN, both of Fig. 508A.

[8216] It is appreciated that specific functions, and accordingly utilities, of GR567 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR567 GENE: GAM480 TARGET PROTEIN and GAM508 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 480D and 508D

[8217] Reference is now made to Fig. 568, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 568(GR568) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8218] GR568 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR568 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8219] GR568 GENE encodes GR568 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8220] GR568 PRECURSOR RNA folds spatially, forming GR568 FOLDED PRECURSOR RNA . It is appreciated that GR568 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR568 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8221] GR568 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM163 PRECURSOR and GAM369 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8222] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM163 RNA

and GAM369 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8223] GAM163 RNA binds complimentarily to a target binding site located in an untranslated region of GAM163 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 163A, thereby inhibiting translation of GAM163 TARGET RNA into GAM163 TARGET PROTEIN, both of Fig. 163A.

[8224] GAM369 RNA binds complimentarily to a target binding site located in an untranslated region of GAM369 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 369A, thereby inhibiting translation of GAM369 TARGET RNA into GAM369 TARGET PROTEIN, both of Fig. 369A.

[8225] It is appreciated that specific functions, and accordingly utilities, of GR568 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR568 GENE: GAM163 TARGET PROTEIN and GAM369 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 163D and

[8226] Reference is now made to Fig. 569, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 569(GR569) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8227] GR569 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR569 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8228] GR569 GENE encodes GR569 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8229] GR569 PRECURSOR RNA folds spatially, forming GR569 FOLDED PRECURSOR RNA . It is appreciated that GR569 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR569 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[8230] GR569 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM167 PRECURSOR and GAM499 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8231] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167 RNA and GAM499 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8232] GAM167 RNA binds complimentarily to a target binding site located in an untranslated region of GAM167 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 167A, thereby inhibiting translation of GAM167 TARGET RNA into GAM167 TARGET PROTEIN, both of Fig. 167A.

[8233] GAM499 RNA binds complimentarily to a target binding site located in an untranslated region of GAM499 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 499A, thereby inhibiting translation of GAM499 TARGET RNA into GAM499 TARGET PROTEIN, both of Fig. 499A.

[8234] It is appreciated that specific functions, and accordingly utilities, of GR569 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR569 GENE: GAM167 TARGET PROTEIN and GAM499 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 167D and 499D

[8235] Reference is now made to Fig. 570, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 570(GR570) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8236] GR570 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR570 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[8237] GR570 GENE encodes GR570 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8238] GR570 PRECURSOR RNA folds spatially, forming GR570 FOLDED PRECURSOR RNA . It is appreciated that GR570 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR570 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8239] GR570 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8240] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

[8241] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8242] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8243] It is appreciated that specific functions, and accordingly utilities, of GR570 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR570 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8244] Reference is now made to Fig. 571, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 571(GR571) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8245] GR571 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR571 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8246] GR571 GENE encodes GR571 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8247] GR571 PRECURSOR RNA folds spatially, forming GR571 FOLDED PRECURSOR RNA . It is appreciated that GR571 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR571 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[8248] GR571 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM318 PRECURSOR and GAM320 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8249] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM318 RNA and GAM320 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8250] GAM318 RNA binds complimentarily to a target binding site located in an untranslated region of GAM318 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 318A, thereby inhibiting translation of GAM318 TARGET RNA into GAM318 TARGET PROTEIN, both of Fig. 318A.

[8251] GAM320 RNA binds complimentarily to a target binding site located in an untranslated region of GAM320 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 320A, thereby inhibiting translation of GAM320 TARGET RNA into GAM320 TARGET PROTEIN, both of Fig. 320A.

[8252] It is appreciated that specific functions, and accordingly utilities, of GR571 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR571 GENE: GAM318 TARGET PROTEIN and GAM320 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 318D and 320D

[8253] Reference is now made to Fig. 572, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 572(GR572) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8254] GR572 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR572 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8255] GR572 GENE encodes GR572 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8256] GR572 PRECURSOR RNA folds spatially, forming GR572 FOLDED PRECURSOR RNA . It is appreciated that GR572 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR572 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8257] GR572 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM166 PRECURSOR, GAM255 PRECURSOR and GAM438 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8258] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM166 RNA, GAM255 RNA and GAM438 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8259] GAM166 RNA binds complimentarily to a target binding site located in an untranslated region of GAM166 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 166A, thereby inhibiting translation of GAM166 TARGET RNA into GAM166 TARGET PROTEIN, both of Fig. 166A.

[8260] GAM255 RNA binds complimentarily to a target binding site located in an untranslated region of GAM255 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 255A, thereby inhibiting translation of GAM255 TARGET RNA into GAM255 TARGET PROTEIN, both of Fig. 255A.

[8261] GAM438 RNA binds complimentarily to a target binding site located in an untranslated region of GAM438 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 438A, thereby inhibiting translation of GAM438 TARGET RNA into GAM438 TARGET PROTEIN, both of Fig. 438A.

[8262] It is appreciated that specific functions, and accordingly utilities, of GR572 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR572 GENE: GAM166 TARGET PROTEIN, GAM255 TARGET PROTEIN and GAM438 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 166D, 255D and 438D

[8263] Reference is now made to Fig. 573, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 573(GR573) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8264] GR573 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR573 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8265] GR573 GENE encodes GR573 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8266] GR573 PRECURSOR RNA folds spatially, forming GR573 FOLDED PRECURSOR RNA . It is appreciated that GR573 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR573 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8267] GR573 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM182 PRECURSOR and GAM287 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8268] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM182 RNA and GAM287 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8269] GAM182 RNA binds complimentarily to a target binding site located in an untranslated region of GAM182 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 182A, thereby inhibiting transla-

tion of GAM182 TARGET RNA into GAM182 TARGET PROTEIN, both of Fig. 182A.

[8270] GAM287 RNA binds complimentarily to a target binding site located in an untranslated region of GAM287 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 287A, thereby inhibiting translation of GAM287 TARGET RNA into GAM287 TARGET PROTEIN, both of Fig. 287A.

[8271] It is appreciated that specific functions, and accordingly utilities, of GR573 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR573 GENE: GAM182 TARGET PROTEIN and GAM287 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 182D and 287D

[8272] Reference is now made to Fig. 574, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 574(GR574) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art.

[8273] GR574 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR574 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8274] GR574 GENE encodes GR574 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8275] GR574 PRECURSOR RNA folds spatially, forming GR574 FOLDED PRECURSOR RNA . It is appreciated that GR574 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR574 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8276] GR574 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM305 PRECURSOR and GAM329 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECUR-

SOR RNA of Fig. 8.

[8277] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM305 RNA and GAM329 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8278] GAM305 RNA binds complimentarily to a target binding site located in an untranslated region of GAM305 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 305A, thereby inhibiting translation of GAM305 TARGET RNA into GAM305 TARGET PROTEIN, both of Fig. 305A.

[8279] GAM329 RNA binds complimentarily to a target binding site located in an untranslated region of GAM329 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 329A, thereby inhibiting translation of GAM329 TARGET RNA into GAM329 TARGET PROTEIN, both of Fig. 329A.

[8280] It is appreciated that specific functions, and accordingly utilities, of GR574 GENE correlate with, and may be deduced from, the identity of the target genes, which are in-

hibited by GAM RNAs comprised in the operon-like cluster of GR574 GENE: GAM305 TARGET PROTEIN and GAM329 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 305D and 329D

[8281] Reference is now made to Fig. 575, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 575(GR575) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8282] GR575 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR575 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8283] GR575 GENE encodes GR575 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8284] GR575 PRECURSOR RNA folds spatially, forming GR575 FOLDED PRECURSOR RNA . It is appreciated that GR575 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin

structures are due to the fact that the nucleotide sequence of GR575 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8285] GR575 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM165 PRECURSOR and GAM506 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8286] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165 RNA and GAM506 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8287] GAM165 RNA binds complimentarily to a target binding site located in an untranslated region of GAM165 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 165A, thereby inhibiting translation of GAM165 TARGET RNA into GAM165 TARGET PRO-

TEIN, both of Fig. 165A.

[8288] GAM506 RNA binds complimentarily to a target binding site located in an untranslated region of GAM506 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 506A, thereby inhibiting translation of GAM506 TARGET RNA into GAM506 TARGET PROTEIN, both of Fig. 506A.

[8289] It is appreciated that specific functions, and accordingly utilities, of GR575 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR575 GENE: GAM165 TARGET PROTEIN and GAM506 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 165D and 506D

[8290] Reference is now made to Fig. 576, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 576(GR576) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[8291] GR576 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR576 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8292] GR576 GENE encodes GR576 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8293] GR576 PRECURSOR RNA folds spatially, forming GR576 FOLDED PRECURSOR RNA . It is appreciated that GR576 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR576 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8294] GR576 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181 PRECURSOR and GAM392 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8295] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181 RNA and GAM392 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8296] GAM181 RNA binds complimentarily to a target binding site located in an untranslated region of GAM181 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 181A, thereby inhibiting translation of GAM181 TARGET RNA into GAM181 TARGET PROTEIN, both of Fig. 181A.

[8297] GAM392 RNA binds complimentarily to a target binding site located in an untranslated region of GAM392 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 392A, thereby inhibiting translation of GAM392 TARGET RNA into GAM392 TARGET PROTEIN, both of Fig. 392A.

[8298] It is appreciated that specific functions, and accordingly utilities, of GR576 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR576 GENE: GAM181 TARGET PROTEIN and GAM392 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 181D and 392D

[8299] Reference is now made to Fig. 577, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 577(GR577) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8300] GR577 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR577 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8301] GR577 GENE encodes GR577 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8302] GR577 PRECURSOR RNA folds spatially, forming GR577 FOLDED PRECURSOR RNA . It is appreciated that GR577 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR577 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8303] GR577 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM249 PRECURSOR and GAM384 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8304] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM249 RNA and GAM384 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8305] GAM249 RNA binds complimentarily to a target binding site located in an untranslated region of GAM249 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 249A, thereby inhibiting translation of GAM249 TARGET RNA into GAM249 TARGET PROTEIN, both of Fig. 249A.

[8306] GAM384 RNA binds complimentarily to a target binding site located in an untranslated region of GAM384 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 384A, thereby inhibiting translation of GAM384 TARGET RNA into GAM384 TARGET PROTEIN, both of Fig. 384A.

[8307] It is appreciated that specific functions, and accordingly utilities, of GR577 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR577 GENE: GAM249 TARGET PROTEIN and GAM384 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 249D and 384D

[8308] Reference is now made to Fig. 578, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 578(GR578) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8309] GR578 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR578 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8310] GR578 GENE encodes GR578 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8311] GR578 PRECURSOR RNA folds spatially, forming GR578 FOLDED PRECURSOR RNA . It is appreciated that GR578 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR578 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8312] GR578 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM526 PRECURSOR and GAM541 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8313] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM526 RNA and GAM541 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8314] GAM526 RNA binds complimentarily to a target binding site located in an untranslated region of GAM526 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 526A, thereby inhibiting translation of GAM526 TARGET RNA into GAM526 TARGET PROTEIN, both of Fig. 526A.

[8315] GAM541 RNA binds complimentarily to a target binding site located in an untranslated region of GAM541 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 541A, thereby inhibiting translation of GAM541 TARGET RNA into GAM541 TARGET PROTEIN, both of Fig. 541A.

[8316] It is appreciated that specific functions, and accordingly utilities, of GR578 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR578 GENE: GAM526 TARGET PROTEIN and GAM541

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 526D and 541D

[8317] Reference is now made to Fig. 579, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 579(GR579) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8318] GR579 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR579 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8319] GR579 GENE encodes GR579 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8320] GR579 PRECURSOR RNA folds spatially, forming GR579 FOLDED PRECURSOR RNA . It is appreciated that GR579 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR579 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8321] GR579 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM323 PRECURSOR and GAM529 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8322] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM323 RNA and GAM529 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8323] GAM323 RNA binds complimentarily to a target binding site located in an untranslated region of GAM323 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 323A, thereby inhibiting translation of GAM323 TARGET RNA into GAM323 TARGET PROTEIN, both of Fig. 323A.

[8324] GAM529 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM529 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 529A, thereby inhibiting translation of GAM529 TARGET RNA into GAM529 TARGET PROTEIN, both of Fig. 529A.

[8325] It is appreciated that specific functions, and accordingly utilities, of GR579 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR579 GENE: GAM323 TARGET PROTEIN and GAM529 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 323D and 529D

[8326] Reference is now made to Fig. 580, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 580(GR580) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8327] GR580 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR580 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8328] GR580 GENE encodes GR580 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8329] GR580 PRECURSOR RNA folds spatially, forming GR580 FOLDED PRECURSOR RNA . It is appreciated that GR580 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR580 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8330] GR580 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM91 PRECURSOR and GAM465 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8331] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM91 RNA and GAM465 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8332] GAM91 RNA binds complimentarily to a target binding site located in an untranslated region of GAM91 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 91A, thereby inhibiting translation of GAM91 TARGET RNA into GAM91 TARGET PROTEIN, both of Fig. 91A.

[8333] GAM465 RNA binds complimentarily to a target binding site located in an untranslated region of GAM465 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 465A, thereby inhibiting translation of GAM465 TARGET RNA into GAM465 TARGET PROTEIN, both of Fig. 465A.

[8334] It is appreciated that specific functions, and accordingly utilities, of GR580 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR580 GENE: GAM91 TARGET PROTEIN and GAM465 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 91D and 465D

[8335] Reference is now made to Fig. 581, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 581(GR581) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8336] GR581 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR581 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8337] GR581 GENE encodes GR581 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8338] GR581 PRECURSOR RNA folds spatially, forming GR581 FOLDED PRECURSOR RNA . It is appreciated that GR581 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR581 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8339] GR581 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44 PRECURSOR and GAM403 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8340] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44 RNA and GAM403 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8341] GAM44 RNA binds complimentarily to a target binding site located in an untranslated region of GAM44 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 44A, thereby inhibiting translation of GAM44 TARGET RNA into GAM44 TARGET PROTEIN, both of Fig. 44A.

[8342] GAM403 RNA binds complimentarily to a target binding site located in an untranslated region of GAM403 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 403A, thereby inhibiting translation of GAM403 TARGET RNA into GAM403 TARGET PROTEIN, both of Fig. 403A.

[8343] It is appreciated that specific functions, and accordingly utilities, of GR581 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR581 GENE: GAM44 TARGET PROTEIN and GAM403 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 44D and 403D

[8344] Reference is now made to Fig. 582, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 582(GR582) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8345] GR582 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR582 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8346] GR582 GENE encodes GR582 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8347] GR582 PRECURSOR RNA folds spatially, forming GR582 FOLDED PRECURSOR RNA . It is appreciated that GR582 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR582 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8348] GR582 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM67 PRECURSOR, GAM295 PRECURSOR and GAM331 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8349] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM67 RNA,

GAM295 RNA and GAM331 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8350] GAM67 RNA binds complimentarily to a target binding site located in an untranslated region of GAM67 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 67A, thereby inhibiting translation of GAM67 TARGET RNA into GAM67 TARGET PROTEIN, both of Fig. 67A.

[8351] GAM295 RNA binds complimentarily to a target binding site located in an untranslated region of GAM295 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 295A, thereby inhibiting translation of GAM295 TARGET RNA into GAM295 TARGET PROTEIN, both of Fig. 295A.

[8352] GAM331 RNA binds complimentarily to a target binding site located in an untranslated region of GAM331 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 331A, thereby inhibiting translation of GAM331 TARGET RNA into GAM331 TARGET PROTEIN, both of Fig. 331A.

[8353] It is appreciated that specific functions, and accordingly utilities, of GR582 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR582 GENE: GAM67 TARGET PROTEIN, GAM295 TARGET PROTEIN and GAM331 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 67D, 295D and 331D

[8354] Reference is now made to Fig. 583, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 583(GR583) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8355] GR583 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR583 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8356] GR583 GENE encodes GR583 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8357] GR583 PRECURSOR RNA folds spatially, forming GR583

FOLDED PRECURSOR RNA . It is appreciated that GR583 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR583 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8358] GR583 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM189 PRECURSOR and GAM251 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8359] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM189 RNA and GAM251 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8360] GAM189 RNA binds complimentarily to a target binding site located in an untranslated region of GAM189 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 189A, thereby inhibiting translation of GAM189 TARGET RNA into GAM189 TARGET PROTEIN, both of Fig. 189A.

[8361] GAM251 RNA binds complimentarily to a target binding site located in an untranslated region of GAM251 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 251A, thereby inhibiting translation of GAM251 TARGET RNA into GAM251 TARGET PROTEIN, both of Fig. 251A.

[8362] It is appreciated that specific functions, and accordingly utilities, of GR583 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR583 GENE: GAM189 TARGET PROTEIN and GAM251 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 189D and 251D

[8363] Reference is now made to Fig. 584, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 584(GR584) gene, which encodes an operon-like cluster

of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8364] GR584 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR584 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8365] GR584 GENE encodes GR584 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8366] GR584 PRECURSOR RNA folds spatially, forming GR584 FOLDED PRECURSOR RNA . It is appreciated that GR584 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR584 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8367] GR584 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53 PRECURSOR and GAM442 PRE-

CURSOR, each of which GAM precursor RNAs being a hair-pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8368] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53 RNA and GAM442 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8369] GAM53 RNA binds complimentarily to a target binding site located in an untranslated region of GAM53 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 53A, thereby inhibiting translation of GAM53 TARGET RNA into GAM53 TARGET PROTEIN, both of Fig. 53A.

[8370] GAM442 RNA binds complimentarily to a target binding site located in an untranslated region of GAM442 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 442A, thereby inhibiting translation of GAM442 TARGET RNA into GAM442 TARGET PROTEIN, both of Fig. 442A.

[8371] It is appreciated that specific functions, and accordingly

utilities, of GR584 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR584 GENE: GAM53 TARGET PROTEIN and GAM442 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 53D and 442D

[8372] Reference is now made to Fig. 585, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 585(GR585) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8373] GR585 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR585 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8374] GR585 GENE encodes GR585 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8375] GR585 PRECURSOR RNA folds spatially, forming GR585 FOLDED PRECURSOR RNA . It is appreciated that GR585

FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR585 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8376] GR585 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44 PRECURSOR and GAM403 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8377] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44 RNA and GAM403 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8378] GAM44 RNA binds complimentarily to a target binding site located in an untranslated region of GAM44 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 44A, thereby inhibiting translation of GAM44 TARGET RNA into GAM44 TARGET PROTEIN, both of Fig. 44A.

[8379] GAM403 RNA binds complimentarily to a target binding site located in an untranslated region of GAM403 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 403A, thereby inhibiting translation of GAM403 TARGET RNA into GAM403 TARGET PROTEIN, both of Fig. 403A.

[8380] It is appreciated that specific functions, and accordingly utilities, of GR585 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR585 GENE: GAM44 TARGET PROTEIN and GAM403 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 44D and 403D

[8381] Reference is now made to Fig. 586, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 586(GR586) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn

modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8382] GR586 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR586 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8383] GR586 GENE encodes GR586 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8384] GR586 PRECURSOR RNA folds spatially, forming GR586 FOLDED PRECURSOR RNA . It is appreciated that GR586 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR586 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8385] GR586 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110 PRECURSOR and GAM207 PRECURSOR, each of which GAM precursor RNAs being a hair-

pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8386] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110 RNA and GAM207 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8387] GAM110 RNA binds complimentarily to a target binding site located in an untranslated region of GAM110 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 110A, thereby inhibiting translation of GAM110 TARGET RNA into GAM110 TARGET PROTEIN, both of Fig. 110A.

[8388] GAM207 RNA binds complimentarily to a target binding site located in an untranslated region of GAM207 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 207A, thereby inhibiting translation of GAM207 TARGET RNA into GAM207 TARGET PROTEIN, both of Fig. 207A.

[8389] It is appreciated that specific functions, and accordingly utilities, of GR586 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR586 GENE: GAM110 TARGET PROTEIN and GAM207 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 110D and 207D

[8390] Reference is now made to Fig. 587, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 587(GR587) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8391] GR587 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR587 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8392] GR587 GENE encodes GR587 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8393] GR587 PRECURSOR RNA folds spatially, forming GR587 FOLDED PRECURSOR RNA . It is appreciated that GR587 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR587 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8394] GR587 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM109 PRECURSOR, GAM215 PRECURSOR and GAM418 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8395] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109 RNA, GAM215 RNA and GAM418 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8396] GAM109 RNA binds complimentarily to a target binding site located in an untranslated region of GAM109 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 109A, thereby inhibiting transla-

tion of GAM109 TARGET RNA into GAM109 TARGET PROTEIN, both of Fig. 109A.

[8397] GAM215 RNA binds complimentarily to a target binding site located in an untranslated region of GAM215 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 215A, thereby inhibiting translation of GAM215 TARGET RNA into GAM215 TARGET PROTEIN, both of Fig. 215A.

[8398] GAM418 RNA binds complimentarily to a target binding site located in an untranslated region of GAM418 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 418A, thereby inhibiting translation of GAM418 TARGET RNA into GAM418 TARGET PROTEIN, both of Fig. 418A.

[8399] It is appreciated that specific functions, and accordingly utilities, of GR587 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR587 GENE: GAM109 TARGET PROTEIN, GAM215 TARGET PROTEIN and GAM418 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with ref-

erence to Figs. 109D, 215D and 418D

[8400] Reference is now made to Fig. 588, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 588(GR588) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8401] GR588 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR588 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8402] GR588 GENE encodes GR588 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8403] GR588 PRECURSOR RNA folds spatially, forming GR588 FOLDED PRECURSOR RNA . It is appreciated that GR588 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR588 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[8404] GR588 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120 PRECURSOR and GAM205 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8405] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120 RNA and GAM205 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8406] GAM120 RNA binds complimentarily to a target binding site located in an untranslated region of GAM120 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 120A, thereby inhibiting translation of GAM120 TARGET RNA into GAM120 TARGET PROTEIN, both of Fig. 120A.

[8407] GAM205 RNA binds complimentarily to a target binding site located in an untranslated region of GAM205 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 205A, thereby inhibiting translation of GAM205 TARGET RNA into GAM205 TARGET PROTEIN, both of Fig. 205A.

[8408] It is appreciated that specific functions, and accordingly utilities, of GR588 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR588 GENE: GAM120 TARGET PROTEIN and GAM205 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 120D and 205D

[8409] Reference is now made to Fig. 589, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 589(GR589) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8410] GR589 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR589 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[8411] GR589 GENE encodes GR589 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8412] GR589 PRECURSOR RNA folds spatially, forming GR589 FOLDED PRECURSOR RNA . It is appreciated that GR589 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR589 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8413] GR589 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM31 PRECURSOR, GAM78 PRECURSOR and GAM177 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8414] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31 RNA, GAM78 RNA and GAM177 RNA respectively, each of which

GAM RNAs corresponding to GAM RNA of Fig. 8.

[8415] GAM31 RNA binds complimentarily to a target binding site located in an untranslated region of GAM31 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 31A, thereby inhibiting translation of GAM31 TARGET RNA into GAM31 TARGET PROTEIN, both of Fig. 31A.

[8416] GAM78 RNA binds complimentarily to a target binding site located in an untranslated region of GAM78 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 78A, thereby inhibiting translation of GAM78 TARGET RNA into GAM78 TARGET PROTEIN, both of Fig. 78A.

[8417] GAM177 RNA binds complimentarily to a target binding site located in an untranslated region of GAM177 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 177A, thereby inhibiting translation of GAM177 TARGET RNA into GAM177 TARGET PROTEIN, both of Fig. 177A.

[8418] It is appreciated that specific functions, and accordingly

utilities, of GR589 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR589 GENE: GAM31 TARGET PROTEIN, GAM78 TARGET PROTEIN and GAM177 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 31D, 78D and 177D

[8419] Reference is now made to Fig. 590, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 590(GR590) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8420] GR590 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR590 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8421] GR590 GENE encodes GR590 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8422] GR590 PRECURSOR RNA folds spatially, forming GR590 FOLDED PRECURSOR RNA . It is appreciated that GR590

FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR590 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8423] GR590 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM258 PRECURSOR, GAM439 PRECURSOR and GAM537 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8424] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM258 RNA, GAM439 RNA and GAM537 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8425] GAM258 RNA binds complimentarily to a target binding site located in an untranslated region of GAM258 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 258A, thereby inhibiting translation of GAM258 TARGET RNA into GAM258 TARGET PROTEIN, both of Fig. 258A.

[8426] GAM439 RNA binds complimentarily to a target binding site located in an untranslated region of GAM439 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 439A, thereby inhibiting translation of GAM439 TARGET RNA into GAM439 TARGET PROTEIN, both of Fig. 439A.

[8427] GAM537 RNA binds complimentarily to a target binding site located in an untranslated region of GAM537 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 537A, thereby inhibiting translation of GAM537 TARGET RNA into GAM537 TARGET PROTEIN, both of Fig. 537A.

[8428] It is appreciated that specific functions, and accordingly utilities, of GR590 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR590 GENE: GAM258 TARGET PROTEIN, GAM439 TARGET PROTEIN and GAM537 TARGET PROTEIN. The function

of these target genes is elaborated hereinabove with reference to Figs. 258D, 439D and 537D

[8429] Reference is now made to Fig. 591, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 591(GR591) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8430] GR591 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR591 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8431] GR591 GENE encodes GR591 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8432] GR591 PRECURSOR RNA folds spatially, forming GR591 FOLDED PRECURSOR RNA . It is appreciated that GR591 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR591 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8433] GR591 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM209 PRECURSOR and GAM525 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8434] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM209 RNA and GAM525 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8435] GAM209 RNA binds complimentarily to a target binding site located in an untranslated region of GAM209 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 209A, thereby inhibiting translation of GAM209 TARGET RNA into GAM209 TARGET PROTEIN, both of Fig. 209A.

[8436] GAM525 RNA binds complimentarily to a target binding site located in an untranslated region of GAM525 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 525A, thereby inhibiting translation of GAM525 TARGET RNA into GAM525 TARGET PROTEIN, both of Fig. 525A.

[8437] It is appreciated that specific functions, and accordingly utilities, of GR591 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR591 GENE: GAM209 TARGET PROTEIN and GAM525 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 209D and 525D

[8438] Reference is now made to Fig. 592, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 592(GR592) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8439] GR592 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR592 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8440] GR592 GENE encodes GR592 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8441] GR592 PRECURSOR RNA folds spatially, forming GR592 FOLDED PRECURSOR RNA . It is appreciated that GR592 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR592 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8442] GR592 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM27 PRECURSOR, GAM423 PRECURSOR, GAM449 PRECURSOR and GAM459 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8443] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM27 RNA, GAM423 RNA, GAM449 RNA and GAM459 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8444] GAM27 RNA binds complimentarily to a target binding site located in an untranslated region of GAM27 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 27A, thereby inhibiting translation of GAM27 TARGET RNA into GAM27 TARGET PROTEIN, both of Fig. 27A.

[8445] GAM423 RNA binds complimentarily to a target binding site located in an untranslated region of GAM423 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 423A, thereby inhibiting translation of GAM423 TARGET RNA into GAM423 TARGET PROTEIN, both of Fig. 423A.

[8446] GAM449 RNA binds complimentarily to a target binding site located in an untranslated region of GAM449 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 449A, thereby inhibiting transla-

tion of GAM449 TARGET RNA into GAM449 TARGET PROTEIN, both of Fig. 449A.

[8447] GAM459 RNA binds complimentarily to a target binding site located in an untranslated region of GAM459 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 459A, thereby inhibiting translation of GAM459 TARGET RNA into GAM459 TARGET PROTEIN, both of Fig. 459A.

[8448] It is appreciated that specific functions, and accordingly utilities, of GR592 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR592 GENE: GAM27 TARGET PROTEIN, GAM423 TARGET PROTEIN, GAM449 TARGET PROTEIN and GAM459 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 27D, 423D, 449D and 459D

[8449] Reference is now made to Fig. 593, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 593(GR593) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn

modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8450] GR593 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR593 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8451] GR593 GENE encodes GR593 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8452] GR593 PRECURSOR RNA folds spatially, forming GR593 FOLDED PRECURSOR RNA . It is appreciated that GR593 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR593 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8453] GR593 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32 PRECURSOR and GAM359 PRECURSOR, each of which GAM precursor RNAs being a hair-

pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8454] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32 RNA and GAM359 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8455] GAM32 RNA binds complimentarily to a target binding site located in an untranslated region of GAM32 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 32A, thereby inhibiting translation of GAM32 TARGET RNA into GAM32 TARGET PROTEIN, both of Fig. 32A.

[8456] GAM359 RNA binds complimentarily to a target binding site located in an untranslated region of GAM359 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 359A, thereby inhibiting translation of GAM359 TARGET RNA into GAM359 TARGET PROTEIN, both of Fig. 359A.

[8457] It is appreciated that specific functions, and accordingly utilities, of GR593 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR593 GENE: GAM32 TARGET PROTEIN and GAM359 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 32D and 359D

[8458] Reference is now made to Fig. 594, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 594(GR594) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8459] GR594 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR594 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8460] GR594 GENE encodes GR594 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8461] GR594 PRECURSOR RNA folds spatially, forming GR594 FOLDED PRECURSOR RNA . It is appreciated that GR594 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR594 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8462] GR594 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM285 PRECURSOR, GAM326 PRECURSOR, GAM436 PRECURSOR and GAM498 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8463] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM285 RNA, GAM326 RNA, GAM436 RNA and GAM498 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8464] GAM285 RNA binds complimentarily to a target binding site located in an untranslated region of GAM285 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 285A, thereby inhibiting translation of GAM285 TARGET RNA into GAM285 TARGET PROTEIN, both of Fig. 285A.

[8465] GAM326 RNA binds complimentarily to a target binding site located in an untranslated region of GAM326 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 326A, thereby inhibiting translation of GAM326 TARGET RNA into GAM326 TARGET PROTEIN, both of Fig. 326A.

[8466] GAM436 RNA binds complimentarily to a target binding site located in an untranslated region of GAM436 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 436A, thereby inhibiting translation of GAM436 TARGET RNA into GAM436 TARGET PROTEIN, both of Fig. 436A.

[8467] GAM498 RNA binds complimentarily to a target binding site located in an untranslated region of GAM498 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 498A, thereby inhibiting transla-

tion of GAM498 TARGET RNA into GAM498 TARGET PROTEIN, both of Fig. 498A.

[8468] It is appreciated that specific functions, and accordingly utilities, of GR594 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR594 GENE: GAM285 TARGET PROTEIN, GAM326 TARGET PROTEIN, GAM436 TARGET PROTEIN and GAM498 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 285D, 326D, 436D and 498D

[8469] Reference is now made to Fig. 595, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 595(GR595) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8470] GR595 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR595 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8471] GR595 GENE encodes GR595 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8472] GR595 PRECURSOR RNA folds spatially, forming GR595 FOLDED PRECURSOR RNA . It is appreciated that GR595 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR595 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8473] GR595 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM101 PRECURSOR, GAM125 PRECURSOR and GAM183 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8474] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM101 RNA, GAM125 RNA and GAM183 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8475] GAM101 RNA binds complimentarily to a target binding site located in an untranslated region of GAM101 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 101A, thereby inhibiting translation of GAM101 TARGET RNA into GAM101 TARGET PROTEIN, both of Fig. 101A.

[8476] GAM125 RNA binds complimentarily to a target binding site located in an untranslated region of GAM125 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 125A, thereby inhibiting translation of GAM125 TARGET RNA into GAM125 TARGET PROTEIN, both of Fig. 125A.

[8477] GAM183 RNA binds complimentarily to a target binding site located in an untranslated region of GAM183 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 183A, thereby inhibiting translation of GAM183 TARGET RNA into GAM183 TARGET PROTEIN, both of Fig. 183A.

[8478] It is appreciated that specific functions, and accordingly utilities, of GR595 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR595 GENE: GAM101 TARGET PROTEIN, GAM125 TARGET PROTEIN and GAM183 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 101D, 125D and 183D

[8479] Reference is now made to Fig. 596, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 596(GR596) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8480] GR596 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR596 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8481] GR596 GENE encodes GR596 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8482] GR596 PRECURSOR RNA folds spatially, forming GR596 FOLDED PRECURSOR RNA . It is appreciated that GR596 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR596 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8483] GR596 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8484] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8485] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting transla-

tion of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8486] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8487] It is appreciated that specific functions, and accordingly utilities, of GR596 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR596 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8488] Reference is now made to Fig. 597, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 597(GR597) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art.

[8489] GR597 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR597 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8490] GR597 GENE encodes GR597 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8491] GR597 PRECURSOR RNA folds spatially, forming GR597 FOLDED PRECURSOR RNA . It is appreciated that GR597 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR597 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8492] GR597 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM155 PRECURSOR and GAM413 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECUR-

SOR RNA of Fig. 8.

[8493] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM155 RNA and GAM413 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8494] GAM155 RNA binds complimentarily to a target binding site located in an untranslated region of GAM155 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 155A, thereby inhibiting translation of GAM155 TARGET RNA into GAM155 TARGET PROTEIN, both of Fig. 155A.

[8495] GAM413 RNA binds complimentarily to a target binding site located in an untranslated region of GAM413 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 413A, thereby inhibiting translation of GAM413 TARGET RNA into GAM413 TARGET PROTEIN, both of Fig. 413A.

[8496] It is appreciated that specific functions, and accordingly utilities, of GR597 GENE correlate with, and may be deduced from, the identity of the target genes, which are in-

hibited by GAM RNAs comprised in the operon-like cluster of GR597 GENE: GAM155 TARGET PROTEIN and GAM413 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 155D and 413D

[8497] Reference is now made to Fig. 598, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 598(GR598) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8498] GR598 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR598 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8499] GR598 GENE encodes GR598 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8500] GR598 PRECURSOR RNA folds spatially, forming GR598 FOLDED PRECURSOR RNA . It is appreciated that GR598 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin

structures are due to the fact that the nucleotide sequence of GR598 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8501] GR598 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39 PRECURSOR and GAM416 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8502] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39 RNA and GAM416 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8503] GAM39 RNA binds complimentarily to a target binding site located in an untranslated region of GAM39 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 39A, thereby inhibiting translation of GAM39 TARGET RNA into GAM39 TARGET PROTEIN, both

of Fig. 39A.

[8504] GAM416 RNA binds complimentarily to a target binding site located in an untranslated region of GAM416 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 416A, thereby inhibiting translation of GAM416 TARGET RNA into GAM416 TARGET PROTEIN, both of Fig. 416A.

[8505] It is appreciated that specific functions, and accordingly utilities, of GR598 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR598 GENE: GAM39 TARGET PROTEIN and GAM416 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 39D and 416D

[8506] Reference is now made to Fig. 599, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 599(GR599) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[8507] GR599 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR599 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8508] GR599 GENE encodes GR599 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8509] GR599 PRECURSOR RNA folds spatially, forming GR599 FOLDED PRECURSOR RNA . It is appreciated that GR599 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR599 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8510] GR599 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM441 PRECURSOR and GAM527 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8511] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM441 RNA and GAM527 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8512] GAM441 RNA binds complimentarily to a target binding site located in an untranslated region of GAM441 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 441A, thereby inhibiting translation of GAM441 TARGET RNA into GAM441 TARGET PROTEIN, both of Fig. 441A.

[8513] GAM527 RNA binds complimentarily to a target binding site located in an untranslated region of GAM527 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 527A, thereby inhibiting translation of GAM527 TARGET RNA into GAM527 TARGET PROTEIN, both of Fig. 527A.

[8514] It is appreciated that specific functions, and accordingly utilities, of GR599 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR599 GENE: GAM441 TARGET PROTEIN and GAM527 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 441D and 527D

[8515] Reference is now made to Fig. 600, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 600(GR600) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8516] GR600 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR600 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8517] GR600 GENE encodes GR600 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8518] GR600 PRECURSOR RNA folds spatially, forming GR600 FOLDED PRECURSOR RNA . It is appreciated that GR600 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR600 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8519] GR600 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM254 PRECURSOR and GAM495 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8520] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM254 RNA and GAM495 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8521] GAM254 RNA binds complimentarily to a target binding site located in an untranslated region of GAM254 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 254A, thereby inhibiting translation of GAM254 TARGET RNA into GAM254 TARGET PROTEIN, both of Fig. 254A.

[8522] GAM495 RNA binds complimentarily to a target binding site located in an untranslated region of GAM495 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 495A, thereby inhibiting translation of GAM495 TARGET RNA into GAM495 TARGET PROTEIN, both of Fig. 495A.

[8523] It is appreciated that specific functions, and accordingly utilities, of GR600 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR600 GENE: GAM254 TARGET PROTEIN and GAM495 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 254D and 495D

[8524] Reference is now made to Fig. 601, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 601(GR601) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8525] GR601 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR601 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8526] GR601 GENE encodes GR601 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8527] GR601 PRECURSOR RNA folds spatially, forming GR601 FOLDED PRECURSOR RNA . It is appreciated that GR601 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR601 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8528] GR601 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM51 PRECURSOR and GAM298 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8529] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51 RNA and GAM298 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8530] GAM51 RNA binds complimentarily to a target binding site located in an untranslated region of GAM51 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 51A, thereby inhibiting translation of GAM51 TARGET RNA into GAM51 TARGET PROTEIN, both of Fig. 51A.

[8531] GAM298 RNA binds complimentarily to a target binding site located in an untranslated region of GAM298 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 298A, thereby inhibiting translation of GAM298 TARGET RNA into GAM298 TARGET PROTEIN, both of Fig. 298A.

[8532] It is appreciated that specific functions, and accordingly utilities, of GR601 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR601 GENE: GAM51 TARGET PROTEIN and GAM298

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 51D and 298D

[8533] Reference is now made to Fig. 602, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 602(GR602) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8534] GR602 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR602 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8535] GR602 GENE encodes GR602 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8536] GR602 PRECURSOR RNA folds spatially, forming GR602 FOLDED PRECURSOR RNA . It is appreciated that GR602 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR602 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8537] GR602 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM222 PRECURSOR, GAM341 PRECURSOR and GAM484 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8538] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM222 RNA, GAM341 RNA and GAM484 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8539] GAM222 RNA binds complimentarily to a target binding site located in an untranslated region of GAM222 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 222A, thereby inhibiting translation of GAM222 TARGET RNA into GAM222 TARGET PROTEIN, both of Fig. 222A.

[8540] GAM341 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM341 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 341A, thereby inhibiting translation of GAM341 TARGET RNA into GAM341 TARGET PROTEIN, both of Fig. 341A.

[8541] GAM484 RNA binds complimentarily to a target binding site located in an untranslated region of GAM484 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 484A, thereby inhibiting translation of GAM484 TARGET RNA into GAM484 TARGET PROTEIN, both of Fig. 484A.

[8542] It is appreciated that specific functions, and accordingly utilities, of GR602 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR602 GENE: GAM222 TARGET PROTEIN, GAM341 TARGET PROTEIN and GAM484 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 222D, 341D and 484D

[8543] Reference is now made to Fig. 603, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 603(GR603) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8544] GR603 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR603 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8545] GR603 GENE encodes GR603 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8546] GR603 PRECURSOR RNA folds spatially, forming GR603 FOLDED PRECURSOR RNA . It is appreciated that GR603 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR603 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8547] GR603 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM314 PRECURSOR and GAM433 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8548] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM314 RNA and GAM433 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8549] GAM314 RNA binds complimentarily to a target binding site located in an untranslated region of GAM314 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 314A, thereby inhibiting translation of GAM314 TARGET RNA into GAM314 TARGET PROTEIN, both of Fig. 314A.

[8550] GAM433 RNA binds complimentarily to a target binding site located in an untranslated region of GAM433 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 433A, thereby inhibiting translation of GAM433 TARGET RNA into GAM433 TARGET PRO-

TEIN, both of Fig. 433A.

[8551] It is appreciated that specific functions, and accordingly utilities, of GR603 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR603 GENE: GAM314 TARGET PROTEIN and GAM433 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 314D and 433D

[8552] Reference is now made to Fig. 604, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 604(GR604) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8553] GR604 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR604 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8554] GR604 GENE encodes GR604 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8555] GR604 PRECURSOR RNA folds spatially, forming GR604 FOLDED PRECURSOR RNA . It is appreciated that GR604 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR604 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8556] GR604 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM109 PRECURSOR, GAM215 PRECURSOR and GAM418 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8557] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109 RNA, GAM215 RNA and GAM418 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8558] GAM109 RNA binds complimentarily to a target binding site located in an untranslated region of GAM109 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 109A, thereby inhibiting translation of GAM109 TARGET RNA into GAM109 TARGET PROTEIN, both of Fig. 109A.

[8559] GAM215 RNA binds complimentarily to a target binding site located in an untranslated region of GAM215 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 215A, thereby inhibiting translation of GAM215 TARGET RNA into GAM215 TARGET PROTEIN, both of Fig. 215A.

[8560] GAM418 RNA binds complimentarily to a target binding site located in an untranslated region of GAM418 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 418A, thereby inhibiting translation of GAM418 TARGET RNA into GAM418 TARGET PROTEIN, both of Fig. 418A.

[8561] It is appreciated that specific functions, and accordingly utilities, of GR604 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR604 GENE: GAM109 TARGET PROTEIN, GAM215 TARGET PROTEIN and GAM418 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 109D, 215D and 418D

[8562] Reference is now made to Fig. 605, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 605(GR605) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8563] GR605 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR605 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8564] GR605 GENE encodes GR605 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8565] GR605 PRECURSOR RNA folds spatially, forming GR605 FOLDED PRECURSOR RNA . It is appreciated that GR605 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR605 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8566] GR605 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM46 PRECURSOR, GAM77 PRECURSOR and GAM382 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8567] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46 RNA, GAM77 RNA and GAM382 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8568] GAM46 RNA binds complimentarily to a target binding site located in an untranslated region of GAM46 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 46A, thereby inhibiting translation of GAM46 TARGET RNA into GAM46 TARGET PROTEIN, both of Fig. 46A.

[8569] GAM77 RNA binds complimentarily to a target binding site located in an untranslated region of GAM77 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 77A, thereby inhibiting translation of GAM77 TARGET RNA into GAM77 TARGET PROTEIN, both of Fig. 77A.

[8570] GAM382 RNA binds complimentarily to a target binding site located in an untranslated region of GAM382 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 382A, thereby inhibiting translation of GAM382 TARGET RNA into GAM382 TARGET PROTEIN, both of Fig. 382A.

[8571] It is appreciated that specific functions, and accordingly utilities, of GR605 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR605 GENE: GAM46 TARGET PROTEIN, GAM77 TARGET PROTEIN and GAM382 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 46D, 77D and 382D

[8572] Reference is now made to Fig. 606, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 606(GR606) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8573] GR606 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR606 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8574] GR606 GENE encodes GR606 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8575] GR606 PRECURSOR RNA folds spatially, forming GR606 FOLDED PRECURSOR RNA . It is appreciated that GR606 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR606 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8576] GR606 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM447 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8577] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM447 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8578] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8579] GAM447 RNA binds complimentarily to a target binding site located in an untranslated region of GAM447 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 447A, thereby inhibiting transla-

tion of GAM447 TARGET RNA into GAM447 TARGET PROTEIN, both of Fig. 447A.

[8580] It is appreciated that specific functions, and accordingly utilities, of GR606 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR606 GENE: GAM218 TARGET PROTEIN and GAM447 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 447D

[8581] Reference is now made to Fig. 607, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 607(GR607) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8582] GR607 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR607 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8583] GR607 GENE encodes GR607 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[8584] GR607 PRECURSOR RNA folds spatially, forming GR607 FOLDED PRECURSOR RNA . It is appreciated that GR607 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR607 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8585] GR607 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM283 PRECURSOR and GAM297 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8586] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM283 RNA and GAM297 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8587] GAM283 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM283 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 283A, thereby inhibiting translation of GAM283 TARGET RNA into GAM283 TARGET PROTEIN, both of Fig. 283A.

[8588] GAM297 RNA binds complimentarily to a target binding site located in an untranslated region of GAM297 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 297A, thereby inhibiting translation of GAM297 TARGET RNA into GAM297 TARGET PROTEIN, both of Fig. 297A.

[8589] It is appreciated that specific functions, and accordingly utilities, of GR607 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR607 GENE: GAM283 TARGET PROTEIN and GAM297 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 283D and 297D

[8590] Reference is now made to Fig. 608, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 608(GR608) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8591] GR608 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR608 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8592] GR608 GENE encodes GR608 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8593] GR608 PRECURSOR RNA folds spatially, forming GR608 FOLDED PRECURSOR RNA . It is appreciated that GR608 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR608 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8594] GR608 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM38 PRECURSOR and GAM333 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8595] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38 RNA and GAM333 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8596] GAM38 RNA binds complimentarily to a target binding site located in an untranslated region of GAM38 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 38A, thereby inhibiting translation of GAM38 TARGET RNA into GAM38 TARGET PROTEIN, both of Fig. 38A.

[8597] GAM333 RNA binds complimentarily to a target binding site located in an untranslated region of GAM333 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 333A, thereby inhibiting translation of GAM333 TARGET RNA into GAM333 TARGET PRO-

TEIN, both of Fig. 333A.

[8598] It is appreciated that specific functions, and accordingly utilities, of GR608 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR608 GENE: GAM38 TARGET PROTEIN and GAM333 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 38D and 333D

[8599] Reference is now made to Fig. 609, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 609(GR609) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8600] GR609 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR609 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8601] GR609 GENE encodes GR609 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8602] GR609 PRECURSOR RNA folds spatially, forming GR609 FOLDED PRECURSOR RNA . It is appreciated that GR609 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR609 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8603] GR609 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM265 PRECURSOR and GAM276 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8604] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM265 RNA and GAM276 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8605] GAM265 RNA binds complimentarily to a target binding site located in an untranslated region of GAM265 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 265A, thereby inhibiting translation of GAM265 TARGET RNA into GAM265 TARGET PROTEIN, both of Fig. 265A.

[8606] GAM276 RNA binds complimentarily to a target binding site located in an untranslated region of GAM276 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 276A, thereby inhibiting translation of GAM276 TARGET RNA into GAM276 TARGET PROTEIN, both of Fig. 276A.

[8607] It is appreciated that specific functions, and accordingly utilities, of GR609 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR609 GENE: GAM265 TARGET PROTEIN and GAM276 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 265D and 276D

[8608] Reference is now made to Fig. 610, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

610(GR610) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8609] GR610 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR610 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8610] GR610 GENE encodes GR610 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8611] GR610 PRECURSOR RNA folds spatially, forming GR610 FOLDED PRECURSOR RNA . It is appreciated that GR610 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR610 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8612] GR610 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM

precursor RNAs, GAM251 PRECURSOR, GAM306 PRECURSOR and GAM510 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8613] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM251 RNA, GAM306 RNA and GAM510 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8614] GAM251 RNA binds complimentarily to a target binding site located in an untranslated region of GAM251 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 251A, thereby inhibiting translation of GAM251 TARGET RNA into GAM251 TARGET PROTEIN, both of Fig. 251A.

[8615] GAM306 RNA binds complimentarily to a target binding site located in an untranslated region of GAM306 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 306A, thereby inhibiting translation of GAM306 TARGET RNA into GAM306 TARGET PROTEIN, both of Fig. 306A.

[8616] GAM510 RNA binds complimentarily to a target binding site located in an untranslated region of GAM510 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 510A, thereby inhibiting translation of GAM510 TARGET RNA into GAM510 TARGET PROTEIN, both of Fig. 510A.

[8617] It is appreciated that specific functions, and accordingly utilities, of GR610 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR610 GENE: GAM251 TARGET PROTEIN, GAM306 TARGET PROTEIN and GAM510 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 251D, 306D and 510D

[8618] Reference is now made to Fig. 611, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 611(GR611) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8619] GR611 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR611 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8620] GR611 GENE encodes GR611 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8621] GR611 PRECURSOR RNA folds spatially, forming GR611 FOLDED PRECURSOR RNA . It is appreciated that GR611 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR611 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8622] GR611 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM230 PRECURSOR and GAM307 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8623] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM230 RNA and GAM307 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8624] GAM230 RNA binds complimentarily to a target binding site located in an untranslated region of GAM230 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 230A, thereby inhibiting translation of GAM230 TARGET RNA into GAM230 TARGET PROTEIN, both of Fig. 230A.

[8625] GAM307 RNA binds complimentarily to a target binding site located in an untranslated region of GAM307 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 307A, thereby inhibiting translation of GAM307 TARGET RNA into GAM307 TARGET PROTEIN, both of Fig. 307A.

[8626] It is appreciated that specific functions, and accordingly utilities, of GR611 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR611 GENE: GAM230 TARGET PROTEIN and GAM307

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 230D and 307D

[8627] Reference is now made to Fig. 612, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 612(GR612) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8628] GR612 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR612 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8629] GR612 GENE encodes GR612 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8630] GR612 PRECURSOR RNA folds spatially, forming GR612 FOLDED PRECURSOR RNA . It is appreciated that GR612 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR612 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8631] GR612 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM296 PRECURSOR and GAM303 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8632] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM296 RNA and GAM303 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8633] GAM296 RNA binds complimentarily to a target binding site located in an untranslated region of GAM296 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 296A, thereby inhibiting translation of GAM296 TARGET RNA into GAM296 TARGET PROTEIN, both of Fig. 296A.

[8634] GAM303 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM303 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 303A, thereby inhibiting translation of GAM303 TARGET RNA into GAM303 TARGET PROTEIN, both of Fig. 303A.

[8635] It is appreciated that specific functions, and accordingly utilities, of GR612 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR612 GENE: GAM296 TARGET PROTEIN and GAM303 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 296D and 303D

[8636] Reference is now made to Fig. 613, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 613(GR613) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8637] GR613 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR613 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8638] GR613 GENE encodes GR613 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8639] GR613 PRECURSOR RNA folds spatially, forming GR613 FOLDED PRECURSOR RNA . It is appreciated that GR613 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR613 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8640] GR613 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM199 PRECURSOR, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8641] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM199 RNA, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8642] GAM199 RNA binds complimentarily to a target binding site located in an untranslated region of GAM199 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 199A, thereby inhibiting translation of GAM199 TARGET RNA into GAM199 TARGET PROTEIN, both of Fig. 199A.

[8643] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8644] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PRO-

TEIN, both of Fig. 448A.

[8645] It is appreciated that specific functions, and accordingly utilities, of GR613 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR613 GENE: GAM199 TARGET PROTEIN, GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 199D, 218D and 448D

[8646] Reference is now made to Fig. 614, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 614(GR614) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8647] GR614 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR614 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8648] GR614 GENE encodes GR614 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8649] GR614 PRECURSOR RNA folds spatially, forming GR614 FOLDED PRECURSOR RNA . It is appreciated that GR614 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR614 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8650] GR614 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM526 PRECURSOR and GAM541 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8651] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM526 RNA and GAM541 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8652] GAM526 RNA binds complimentarily to a target binding site located in an untranslated region of GAM526 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 526A, thereby inhibiting translation of GAM526 TARGET RNA into GAM526 TARGET PROTEIN, both of Fig. 526A.

[8653] GAM541 RNA binds complimentarily to a target binding site located in an untranslated region of GAM541 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 541A, thereby inhibiting translation of GAM541 TARGET RNA into GAM541 TARGET PROTEIN, both of Fig. 541A.

[8654] It is appreciated that specific functions, and accordingly utilities, of GR614 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR614 GENE: GAM526 TARGET PROTEIN and GAM541 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 526D and 541D

[8655] Reference is now made to Fig. 615, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

615(GR615) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8656] GR615 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR615 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8657] GR615 GENE encodes GR615 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8658] GR615 PRECURSOR RNA folds spatially, forming GR615 FOLDED PRECURSOR RNA . It is appreciated that GR615 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR615 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8659] GR615 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM

precursor RNAs, GAM113 PRECURSOR and GAM221 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8660] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113 RNA and GAM221 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8661] GAM113 RNA binds complimentarily to a target binding site located in an untranslated region of GAM113 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 113A, thereby inhibiting translation of GAM113 TARGET RNA into GAM113 TARGET PROTEIN, both of Fig. 113A.

[8662] GAM221 RNA binds complimentarily to a target binding site located in an untranslated region of GAM221 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 221A, thereby inhibiting translation of GAM221 TARGET RNA into GAM221 TARGET PROTEIN, both of Fig. 221A.

[8663] It is appreciated that specific functions, and accordingly utilities, of GR615 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR615 GENE: GAM113 TARGET PROTEIN and GAM221 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 113D and 221D

[8664] Reference is now made to Fig. 616, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 616(GR616) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8665] GR616 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR616 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8666] GR616 GENE encodes GR616 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8667] GR616 PRECURSOR RNA folds spatially, forming GR616

FOLDED PRECURSOR RNA . It is appreciated that GR616 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR616 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8668] GR616 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94 PRECURSOR and GAM175 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8669] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94 RNA and GAM175 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8670] GAM94 RNA binds complimentarily to a target binding site located in an untranslated region of GAM94 TARGET RNA, which target binding site corresponds to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 94A, thereby inhibiting translation of GAM94 TARGET RNA into GAM94 TARGET PROTEIN, both of Fig. 94A.

[8671] GAM175 RNA binds complimentarily to a target binding site located in an untranslated region of GAM175 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 175A, thereby inhibiting translation of GAM175 TARGET RNA into GAM175 TARGET PROTEIN, both of Fig. 175A.

[8672] It is appreciated that specific functions, and accordingly utilities, of GR616 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR616 GENE: GAM94 TARGET PROTEIN and GAM175 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 94D and 175D

[8673] Reference is now made to Fig. 617, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 617(GR617) gene, which encodes an operon-like cluster

of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8674] GR617 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR617 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8675] GR617 GENE encodes GR617 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8676] GR617 PRECURSOR RNA folds spatially, forming GR617 FOLDED PRECURSOR RNA . It is appreciated that GR617 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR617 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8677] GR617 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28 PRECURSOR and GAM274 PRE-

CURSOR, each of which GAM precursor RNAs being a hair-pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8678] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28 RNA and GAM274 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8679] GAM28 RNA binds complimentarily to a target binding site located in an untranslated region of GAM28 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 28A, thereby inhibiting translation of GAM28 TARGET RNA into GAM28 TARGET PROTEIN, both of Fig. 28A.

[8680] GAM274 RNA binds complimentarily to a target binding site located in an untranslated region of GAM274 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 274A, thereby inhibiting translation of GAM274 TARGET RNA into GAM274 TARGET PROTEIN, both of Fig. 274A.

[8681] It is appreciated that specific functions, and accordingly

utilities, of GR617 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR617 GENE: GAM28 TARGET PROTEIN and GAM274 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 28D and 274D

[8682] Reference is now made to Fig. 618, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 618(GR618) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8683] GR618 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR618 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8684] GR618 GENE encodes GR618 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8685] GR618 PRECURSOR RNA folds spatially, forming GR618 FOLDED PRECURSOR RNA . It is appreciated that GR618

FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR618 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8686] GR618 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM174 PRECURSOR and GAM259 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8687] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM174 RNA and GAM259 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8688] GAM174 RNA binds complimentarily to a target binding site located in an untranslated region of GAM174 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 174A, thereby inhibiting translation of GAM174 TARGET RNA into GAM174 TARGET PROTEIN, both of Fig. 174A.

[8689] GAM259 RNA binds complimentarily to a target binding site located in an untranslated region of GAM259 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 259A, thereby inhibiting translation of GAM259 TARGET RNA into GAM259 TARGET PROTEIN, both of Fig. 259A.

[8690] It is appreciated that specific functions, and accordingly utilities, of GR618 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR618 GENE: GAM174 TARGET PROTEIN and GAM259 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 174D and 259D

[8691] Reference is now made to Fig. 619, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 619(GR619) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn

modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8692] GR619 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR619 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8693] GR619 GENE encodes GR619 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8694] GR619 PRECURSOR RNA folds spatially, forming GR619 FOLDED PRECURSOR RNA . It is appreciated that GR619 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR619 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8695] GR619 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM526 PRECURSOR and GAM541 PRECURSOR, each of which GAM precursor RNAs being a hair-

pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8696] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM526 RNA and GAM541 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8697] GAM526 RNA binds complimentarily to a target binding site located in an untranslated region of GAM526 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 526A, thereby inhibiting translation of GAM526 TARGET RNA into GAM526 TARGET PROTEIN, both of Fig. 526A.

[8698] GAM541 RNA binds complimentarily to a target binding site located in an untranslated region of GAM541 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 541A, thereby inhibiting translation of GAM541 TARGET RNA into GAM541 TARGET PROTEIN, both of Fig. 541A.

[8699] It is appreciated that specific functions, and accordingly utilities, of GR619 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR619 GENE: GAM526 TARGET PROTEIN and GAM541 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 526D and 541D

[8700] Reference is now made to Fig. 620, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 620(GR620) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8701] GR620 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR620 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8702] GR620 GENE encodes GR620 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8703] GR620 PRECURSOR RNA folds spatially, forming GR620 FOLDED PRECURSOR RNA . It is appreciated that GR620 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR620 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8704] GR620 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM172 PRECURSOR and GAM462 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8705] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172 RNA and GAM462 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8706] GAM172 RNA binds complimentarily to a target binding site located in an untranslated region of GAM172 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 172A, thereby inhibiting transla-

tion of GAM172 TARGET RNA into GAM172 TARGET PROTEIN, both of Fig. 172A.

[8707] GAM462 RNA binds complimentarily to a target binding site located in an untranslated region of GAM462 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 462A, thereby inhibiting translation of GAM462 TARGET RNA into GAM462 TARGET PROTEIN, both of Fig. 462A.

[8708] It is appreciated that specific functions, and accordingly utilities, of GR620 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR620 GENE: GAM172 TARGET PROTEIN and GAM462 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 172D and 462D

[8709] Reference is now made to Fig. 621, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 621(GR621) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art.

[8710] GR621 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR621 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8711] GR621 GENE encodes GR621 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8712] GR621 PRECURSOR RNA folds spatially, forming GR621 FOLDED PRECURSOR RNA . It is appreciated that GR621 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR621 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8713] GR621 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM391 PRECURSOR and GAM500 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECUR-

SOR RNA of Fig. 8.

[8714] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM391 RNA and GAM500 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8715] GAM391 RNA binds complimentarily to a target binding site located in an untranslated region of GAM391 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 391A, thereby inhibiting translation of GAM391 TARGET RNA into GAM391 TARGET PROTEIN, both of Fig. 391A.

[8716] GAM500 RNA binds complimentarily to a target binding site located in an untranslated region of GAM500 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 500A, thereby inhibiting translation of GAM500 TARGET RNA into GAM500 TARGET PROTEIN, both of Fig. 500A.

[8717] It is appreciated that specific functions, and accordingly utilities, of GR621 GENE correlate with, and may be deduced from, the identity of the target genes, which are in-

hibited by GAM RNAs comprised in the operon-like cluster of GR621 GENE: GAM391 TARGET PROTEIN and GAM500 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 391D and 500D

[8718] Reference is now made to Fig. 622, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 622(GR622) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8719] GR622 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR622 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8720] GR622 GENE encodes GR622 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8721] GR622 PRECURSOR RNA folds spatially, forming GR622 FOLDED PRECURSOR RNA . It is appreciated that GR622 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin

structures are due to the fact that the nucleotide sequence of GR622 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8722] GR622 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM139 PRECURSOR, GAM159 PRECURSOR and GAM377 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8723] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139 RNA, GAM159 RNA and GAM377 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8724] GAM139 RNA binds complimentarily to a target binding site located in an untranslated region of GAM139 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 139A, thereby inhibiting translation of GAM139 TARGET RNA into GAM139 TARGET PRO-

TEIN, both of Fig. 139A.

[8725] GAM159 RNA binds complimentarily to a target binding site located in an untranslated region of GAM159 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 159A, thereby inhibiting translation of GAM159 TARGET RNA into GAM159 TARGET PROTEIN, both of Fig. 159A.

[8726] GAM377 RNA binds complimentarily to a target binding site located in an untranslated region of GAM377 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 377A, thereby inhibiting translation of GAM377 TARGET RNA into GAM377 TARGET PROTEIN, both of Fig. 377A.

[8727] It is appreciated that specific functions, and accordingly utilities, of GR622 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR622 GENE: GAM139 TARGET PROTEIN, GAM159 TARGET PROTEIN and GAM377 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 139D, 159D and 377D

[8728] Reference is now made to Fig. 623, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 623(GR623) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8729] GR623 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR623 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8730] GR623 GENE encodes GR623 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8731] GR623 PRECURSOR RNA folds spatially, forming GR623 FOLDED PRECURSOR RNA . It is appreciated that GR623 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR623 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[8732] GR623 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM236 PRECURSOR and GAM360 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8733] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM236 RNA and GAM360 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8734] GAM236 RNA binds complimentarily to a target binding site located in an untranslated region of GAM236 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 236A, thereby inhibiting translation of GAM236 TARGET RNA into GAM236 TARGET PROTEIN, both of Fig. 236A.

[8735] GAM360 RNA binds complimentarily to a target binding site located in an untranslated region of GAM360 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 360A, thereby inhibiting translation of GAM360 TARGET RNA into GAM360 TARGET PROTEIN, both of Fig. 360A.

[8736] It is appreciated that specific functions, and accordingly utilities, of GR623 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR623 GENE: GAM236 TARGET PROTEIN and GAM360 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 236D and 360D

[8737] Reference is now made to Fig. 624, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 624(GR624) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8738] GR624 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR624 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8739] GR624 GENE encodes GR624 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8740] GR624 PRECURSOR RNA folds spatially, forming GR624 FOLDED PRECURSOR RNA . It is appreciated that GR624 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR624 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8741] GR624 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM66 PRECURSOR and GAM474 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8742] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66 RNA and GAM474 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8743] GAM66 RNA binds complimentarily to a target binding site located in an untranslated region of GAM66 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 66A, thereby inhibiting translation of GAM66 TARGET RNA into GAM66 TARGET PROTEIN, both of Fig. 66A.

[8744] GAM474 RNA binds complimentarily to a target binding site located in an untranslated region of GAM474 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 474A, thereby inhibiting translation of GAM474 TARGET RNA into GAM474 TARGET PROTEIN, both of Fig. 474A.

[8745] It is appreciated that specific functions, and accordingly utilities, of GR624 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR624 GENE: GAM66 TARGET PROTEIN and GAM474 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 66D and 474D

[8746] Reference is now made to Fig. 625, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 625(GR625) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8747] GR625 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR625 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8748] GR625 GENE encodes GR625 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8749] GR625 PRECURSOR RNA folds spatially, forming GR625 FOLDED PRECURSOR RNA . It is appreciated that GR625 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR625 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8750] GR625 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM291 PRECURSOR and GAM419 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8751] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM291 RNA and GAM419 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8752] GAM291 RNA binds complimentarily to a target binding site located in an untranslated region of GAM291 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 291A, thereby inhibiting translation of GAM291 TARGET RNA into GAM291 TARGET PROTEIN, both of Fig. 291A.

[8753] GAM419 RNA binds complimentarily to a target binding site located in an untranslated region of GAM419 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 419A, thereby inhibiting transla-

tion of GAM419 TARGET RNA into GAM419 TARGET PROTEIN, both of Fig. 419A.

[8754] It is appreciated that specific functions, and accordingly utilities, of GR625 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR625 GENE: GAM291 TARGET PROTEIN and GAM419 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 291D and 419D

[8755] Reference is now made to Fig. 626, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 626(GR626) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8756] GR626 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR626 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8757] GR626 GENE encodes GR626 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[8758] GR626 PRECURSOR RNA folds spatially, forming GR626 FOLDED PRECURSOR RNA . It is appreciated that GR626 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR626 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8759] GR626 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM30 PRECURSOR and GAM227 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8760] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30 RNA and GAM227 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8761] GAM30 RNA binds complimentarily to a target binding site

located in an untranslated region of GAM30 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 30A, thereby inhibiting translation of GAM30 TARGET RNA into GAM30 TARGET PROTEIN, both of Fig. 30A.

[8762] GAM227 RNA binds complimentarily to a target binding site located in an untranslated region of GAM227 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 227A, thereby inhibiting translation of GAM227 TARGET RNA into GAM227 TARGET PROTEIN, both of Fig. 227A.

[8763] It is appreciated that specific functions, and accordingly utilities, of GR626 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR626 GENE: GAM30 TARGET PROTEIN and GAM227 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 30D and 227D

[8764] Reference is now made to Fig. 627, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 627(GR627) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8765] GR627 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR627 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8766] GR627 GENE encodes GR627 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8767] GR627 PRECURSOR RNA folds spatially, forming GR627 FOLDED PRECURSOR RNA . It is appreciated that GR627 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR627 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8768] GR627 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM196 PRECURSOR, GAM411 PRECURSOR and GAM468 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8769] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196 RNA, GAM411 RNA and GAM468 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8770] GAM196 RNA binds complimentarily to a target binding site located in an untranslated region of GAM196 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 196A, thereby inhibiting translation of GAM196 TARGET RNA into GAM196 TARGET PROTEIN, both of Fig. 196A.

[8771] GAM411 RNA binds complimentarily to a target binding site located in an untranslated region of GAM411 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 411A, thereby inhibiting translation of GAM411 TARGET RNA into GAM411 TARGET PRO-

TEIN, both of Fig. 411A.

[8772] GAM468 RNA binds complimentarily to a target binding site located in an untranslated region of GAM468 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 468A, thereby inhibiting translation of GAM468 TARGET RNA into GAM468 TARGET PROTEIN, both of Fig. 468A.

[8773] It is appreciated that specific functions, and accordingly utilities, of GR627 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR627 GENE: GAM196 TARGET PROTEIN, GAM411 TARGET PROTEIN and GAM468 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 196D, 411D and 468D

[8774] Reference is now made to Fig. 628, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 628(GR628) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[8775] GR628 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR628 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8776] GR628 GENE encodes GR628 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8777] GR628 PRECURSOR RNA folds spatially, forming GR628 FOLDED PRECURSOR RNA . It is appreciated that GR628 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR628 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8778] GR628 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM146 PRECURSOR and GAM410 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8779] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM146 RNA and GAM410 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8780] GAM146 RNA binds complimentarily to a target binding site located in an untranslated region of GAM146 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 146A, thereby inhibiting translation of GAM146 TARGET RNA into GAM146 TARGET PROTEIN, both of Fig. 146A.

[8781] GAM410 RNA binds complimentarily to a target binding site located in an untranslated region of GAM410 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 410A, thereby inhibiting translation of GAM410 TARGET RNA into GAM410 TARGET PROTEIN, both of Fig. 410A.

[8782] It is appreciated that specific functions, and accordingly utilities, of GR628 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR628 GENE: GAM146 TARGET PROTEIN and GAM410 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 146D and 410D

[8783] Reference is now made to Fig. 629, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 629(GR629) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8784] GR629 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR629 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8785] GR629 GENE encodes GR629 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8786] GR629 PRECURSOR RNA folds spatially, forming GR629 FOLDED PRECURSOR RNA . It is appreciated that GR629 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR629 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8787] GR629 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM223 PRECURSOR and GAM356 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8788] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM223 RNA and GAM356 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8789] GAM223 RNA binds complimentarily to a target binding site located in an untranslated region of GAM223 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 223A, thereby inhibiting translation of GAM223 TARGET RNA into GAM223 TARGET PROTEIN, both of Fig. 223A.

[8790] GAM356 RNA binds complimentarily to a target binding site located in an untranslated region of GAM356 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 356A, thereby inhibiting translation of GAM356 TARGET RNA into GAM356 TARGET PROTEIN, both of Fig. 356A.

[8791] It is appreciated that specific functions, and accordingly utilities, of GR629 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR629 GENE: GAM223 TARGET PROTEIN and GAM356 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 223D and 356D

[8792] Reference is now made to Fig. 630, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 630(GR630) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8793] GR630 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR630 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8794] GR630 GENE encodes GR630 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8795] GR630 PRECURSOR RNA folds spatially, forming GR630 FOLDED PRECURSOR RNA . It is appreciated that GR630 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR630 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8796] GR630 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM173 PRECURSOR and GAM351 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8797] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM173 RNA and GAM351 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8798] GAM173 RNA binds complimentarily to a target binding site located in an untranslated region of GAM173 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 173A, thereby inhibiting translation of GAM173 TARGET RNA into GAM173 TARGET PROTEIN, both of Fig. 173A.

[8799] GAM351 RNA binds complimentarily to a target binding site located in an untranslated region of GAM351 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 351A, thereby inhibiting translation of GAM351 TARGET RNA into GAM351 TARGET PROTEIN, both of Fig. 351A.

[8800] It is appreciated that specific functions, and accordingly utilities, of GR630 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR630 GENE: GAM173 TARGET PROTEIN and GAM351

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 173D and 351D

[8801] Reference is now made to Fig. 631, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 631(GR631) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8802] GR631 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR631 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8803] GR631 GENE encodes GR631 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8804] GR631 PRECURSOR RNA folds spatially, forming GR631 FOLDED PRECURSOR RNA . It is appreciated that GR631 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR631 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8805] GR631 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8806] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8807] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8808] GAM448 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8809] It is appreciated that specific functions, and accordingly utilities, of GR631 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR631 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8810] Reference is now made to Fig. 632, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 632(GR632) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8811] GR632 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR632 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8812] GR632 GENE encodes GR632 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8813] GR632 PRECURSOR RNA folds spatially, forming GR632 FOLDED PRECURSOR RNA . It is appreciated that GR632 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR632 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8814] GR632 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM104 PRECURSOR, GAM162 PRECURSOR and GAM497 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8815] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM104 RNA, GAM162 RNA and GAM497 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8816] GAM104 RNA binds complimentarily to a target binding site located in an untranslated region of GAM104 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 104A, thereby inhibiting translation of GAM104 TARGET RNA into GAM104 TARGET PROTEIN, both of Fig. 104A.

[8817] GAM162 RNA binds complimentarily to a target binding site located in an untranslated region of GAM162 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 162A, thereby inhibiting translation of GAM162 TARGET RNA into GAM162 TARGET PROTEIN, both of Fig. 162A.

[8818] GAM497 RNA binds complimentarily to a target binding site located in an untranslated region of GAM497 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 497A, thereby inhibiting translation of GAM497 TARGET RNA into GAM497 TARGET PRO-

TEIN, both of Fig. 497A.

[8819] It is appreciated that specific functions, and accordingly utilities, of GR632 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR632 GENE: GAM104 TARGET PROTEIN, GAM162 TARGET PROTEIN and GAM497 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 104D, 162D and 497D

[8820] Reference is now made to Fig. 633, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 633(GR633) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8821] GR633 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR633 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8822] GR633 GENE encodes GR633 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8823] GR633 PRECURSOR RNA folds spatially, forming GR633 FOLDED PRECURSOR RNA . It is appreciated that GR633 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR633 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8824] GR633 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8825] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8826] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8827] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8828] It is appreciated that specific functions, and accordingly utilities, of GR633 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR633 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8829] Reference is now made to Fig. 634, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

634(GR634) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8830] GR634 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR634 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8831] GR634 GENE encodes GR634 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8832] GR634 PRECURSOR RNA folds spatially, forming GR634 FOLDED PRECURSOR RNA . It is appreciated that GR634 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR634 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8833] GR634 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM

precursor RNAs, GAM52 PRECURSOR, GAM367 PRECURSOR and GAM395 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8834] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52 RNA, GAM367 RNA and GAM395 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8835] GAM52 RNA binds complimentarily to a target binding site located in an untranslated region of GAM52 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 52A, thereby inhibiting translation of GAM52 TARGET RNA into GAM52 TARGET PROTEIN, both of Fig. 52A.

[8836] GAM367 RNA binds complimentarily to a target binding site located in an untranslated region of GAM367 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 367A, thereby inhibiting translation of GAM367 TARGET RNA into GAM367 TARGET PROTEIN, both of Fig. 367A.

[8837] GAM395 RNA binds complimentarily to a target binding site located in an untranslated region of GAM395 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 395A, thereby inhibiting translation of GAM395 TARGET RNA into GAM395 TARGET PROTEIN, both of Fig. 395A.

[8838] It is appreciated that specific functions, and accordingly utilities, of GR634 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR634 GENE: GAM52 TARGET PROTEIN, GAM367 TARGET PROTEIN and GAM395 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 52D, 367D and 395D

[8839] Reference is now made to Fig. 635, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 635(GR635) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8840] GR635 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR635 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8841] GR635 GENE encodes GR635 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8842] GR635 PRECURSOR RNA folds spatially, forming GR635 FOLDED PRECURSOR RNA . It is appreciated that GR635 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR635 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8843] GR635 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM216 PRECURSOR and GAM286 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8844] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM216 RNA and GAM286 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8845] GAM216 RNA binds complimentarily to a target binding site located in an untranslated region of GAM216 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 216A, thereby inhibiting translation of GAM216 TARGET RNA into GAM216 TARGET PROTEIN, both of Fig. 216A.

[8846] GAM286 RNA binds complimentarily to a target binding site located in an untranslated region of GAM286 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 286A, thereby inhibiting translation of GAM286 TARGET RNA into GAM286 TARGET PROTEIN, both of Fig. 286A.

[8847] It is appreciated that specific functions, and accordingly utilities, of GR635 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR635 GENE: GAM216 TARGET PROTEIN and GAM286

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 216D and 286D

[8848] Reference is now made to Fig. 636, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 636(GR636) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8849] GR636 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR636 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8850] GR636 GENE encodes GR636 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8851] GR636 PRECURSOR RNA folds spatially, forming GR636 FOLDED PRECURSOR RNA . It is appreciated that GR636 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR636 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8852] GR636 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8853] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8854] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8855] GAM448 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8856] It is appreciated that specific functions, and accordingly utilities, of GR636 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR636 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8857] Reference is now made to Fig. 637, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 637(GR637) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8858] GR637 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR637 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8859] GR637 GENE encodes GR637 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8860] GR637 PRECURSOR RNA folds spatially, forming GR637 FOLDED PRECURSOR RNA . It is appreciated that GR637 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR637 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8861] GR637 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM188 PRECURSOR and GAM234 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8862] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM188 RNA and GAM234 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8863] GAM188 RNA binds complimentarily to a target binding site located in an untranslated region of GAM188 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 188A, thereby inhibiting translation of GAM188 TARGET RNA into GAM188 TARGET PROTEIN, both of Fig. 188A.

[8864] GAM234 RNA binds complimentarily to a target binding site located in an untranslated region of GAM234 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 234A, thereby inhibiting translation of GAM234 TARGET RNA into GAM234 TARGET PROTEIN, both of Fig. 234A.

[8865] It is appreciated that specific functions, and accordingly utilities, of GR637 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR637 GENE: GAM188 TARGET PROTEIN and GAM234 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 188D and 234D

[8866] Reference is now made to Fig. 638, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 638(GR638) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8867] GR638 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR638 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8868] GR638 GENE encodes GR638 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8869] GR638 PRECURSOR RNA folds spatially, forming GR638 FOLDED PRECURSOR RNA . It is appreciated that GR638 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR638 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8870] GR638 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8871] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8872] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8873] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[8874] It is appreciated that specific functions, and accordingly utilities, of GR638 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR638 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[8875] Reference is now made to Fig. 639, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 639(GR639) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8876] GR639 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR639 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8877] GR639 GENE encodes GR639 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8878] GR639 PRECURSOR RNA folds spatially, forming GR639 FOLDED PRECURSOR RNA . It is appreciated that GR639 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR639 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8879] GR639 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102 PRECURSOR and GAM128 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8880] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102 RNA

and GAM128 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8881] GAM102 RNA binds complimentarily to a target binding site located in an untranslated region of GAM102 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 102A, thereby inhibiting translation of GAM102 TARGET RNA into GAM102 TARGET PROTEIN, both of Fig. 102A.

[8882] GAM128 RNA binds complimentarily to a target binding site located in an untranslated region of GAM128 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 128A, thereby inhibiting translation of GAM128 TARGET RNA into GAM128 TARGET PROTEIN, both of Fig. 128A.

[8883] It is appreciated that specific functions, and accordingly utilities, of GR639 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR639 GENE: GAM102 TARGET PROTEIN and GAM128 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 102D and

[8884] Reference is now made to Fig. 640, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 640(GR640) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8885] GR640 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR640 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8886] GR640 GENE encodes GR640 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8887] GR640 PRECURSOR RNA folds spatially, forming GR640 FOLDED PRECURSOR RNA . It is appreciated that GR640 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR640 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[8888] GR640 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM197 PRECURSOR and GAM475 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8889] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM197 RNA and GAM475 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8890] GAM197 RNA binds complimentarily to a target binding site located in an untranslated region of GAM197 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 197A, thereby inhibiting translation of GAM197 TARGET RNA into GAM197 TARGET PROTEIN, both of Fig. 197A.

[8891] GAM475 RNA binds complimentarily to a target binding site located in an untranslated region of GAM475 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 475A, thereby inhibiting translation of GAM475 TARGET RNA into GAM475 TARGET PROTEIN, both of Fig. 475A.

[8892] It is appreciated that specific functions, and accordingly utilities, of GR640 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR640 GENE: GAM197 TARGET PROTEIN and GAM475 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 197D and 475D

[8893] Reference is now made to Fig. 641, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 641(GR641) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8894] GR641 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR641 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[8895] GR641 GENE encodes GR641 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8896] GR641 PRECURSOR RNA folds spatially, forming GR641 FOLDED PRECURSOR RNA . It is appreciated that GR641 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR641 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8897] GR641 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM515 PRECURSOR and GAM516 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8898] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM515 RNA and GAM516 RNA respectively, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

[8899] GAM515 RNA binds complimentarily to a target binding site located in an untranslated region of GAM515 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 515A, thereby inhibiting translation of GAM515 TARGET RNA into GAM515 TARGET PROTEIN, both of Fig. 515A.

[8900] GAM516 RNA binds complimentarily to a target binding site located in an untranslated region of GAM516 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 516A, thereby inhibiting translation of GAM516 TARGET RNA into GAM516 TARGET PROTEIN, both of Fig. 516A.

[8901] It is appreciated that specific functions, and accordingly utilities, of GR641 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR641 GENE: GAM515 TARGET PROTEIN and GAM516 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 515D and 516D

[8902] Reference is now made to Fig. 642, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 642(GR642) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8903] GR642 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR642 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8904] GR642 GENE encodes GR642 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8905] GR642 PRECURSOR RNA folds spatially, forming GR642 FOLDED PRECURSOR RNA . It is appreciated that GR642 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR642 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[8906] GR642 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM81 PRECURSOR and GAM490 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8907] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM81 RNA and GAM490 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8908] GAM81 RNA binds complimentarily to a target binding site located in an untranslated region of GAM81 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 81A, thereby inhibiting translation of GAM81 TARGET RNA into GAM81 TARGET PROTEIN, both of Fig. 81A.

[8909] GAM490 RNA binds complimentarily to a target binding site located in an untranslated region of GAM490 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 490A, thereby inhibiting translation of GAM490 TARGET RNA into GAM490 TARGET PROTEIN, both of Fig. 490A.

[8910] It is appreciated that specific functions, and accordingly utilities, of GR642 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR642 GENE: GAM81 TARGET PROTEIN and GAM490 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 81D and 490D

[8911] Reference is now made to Fig. 643, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 643(GR643) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8912] GR643 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR643 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8913] GR643 GENE encodes GR643 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8914] GR643 PRECURSOR RNA folds spatially, forming GR643 FOLDED PRECURSOR RNA . It is appreciated that GR643 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR643 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8915] GR643 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM364 PRECURSOR and GAM538 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8916] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM364 RNA and GAM538 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8917] GAM364 RNA binds complimentarily to a target binding site located in an untranslated region of GAM364 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 364A, thereby inhibiting translation of GAM364 TARGET RNA into GAM364 TARGET PROTEIN, both of Fig. 364A.

[8918] GAM538 RNA binds complimentarily to a target binding site located in an untranslated region of GAM538 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 538A, thereby inhibiting translation of GAM538 TARGET RNA into GAM538 TARGET PROTEIN, both of Fig. 538A.

[8919] It is appreciated that specific functions, and accordingly utilities, of GR643 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR643 GENE: GAM364 TARGET PROTEIN and GAM538 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 364D and 538D

[8920] Reference is now made to Fig. 644, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 644(GR644) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8921] GR644 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR644 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8922] GR644 GENE encodes GR644 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8923] GR644 PRECURSOR RNA folds spatially, forming GR644 FOLDED PRECURSOR RNA . It is appreciated that GR644 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR644 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8924] GR644 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM321 PRECURSOR and GAM422 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8925] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM321 RNA and GAM422 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8926] GAM321 RNA binds complimentarily to a target binding site located in an untranslated region of GAM321 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 321A, thereby inhibiting translation of GAM321 TARGET RNA into GAM321 TARGET PROTEIN, both of Fig. 321A.

[8927] GAM422 RNA binds complimentarily to a target binding site located in an untranslated region of GAM422 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 422A, thereby inhibiting transla-

tion of GAM422 TARGET RNA into GAM422 TARGET PROTEIN, both of Fig. 422A.

[8928] It is appreciated that specific functions, and accordingly utilities, of GR644 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR644 GENE: GAM321 TARGET PROTEIN and GAM422 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 321D and 422D

[8929] Reference is now made to Fig. 645, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 645(GR645) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8930] GR645 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR645 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8931] GR645 GENE encodes GR645 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[8932] GR645 PRECURSOR RNA folds spatially, forming GR645 FOLDED PRECURSOR RNA . It is appreciated that GR645 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR645 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8933] GR645 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM147 PRECURSOR and GAM361 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8934] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM147 RNA and GAM361 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8935] GAM147 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM147 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 147A, thereby inhibiting translation of GAM147 TARGET RNA into GAM147 TARGET PROTEIN, both of Fig. 147A.

[8936] GAM361 RNA binds complimentarily to a target binding site located in an untranslated region of GAM361 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 361A, thereby inhibiting translation of GAM361 TARGET RNA into GAM361 TARGET PROTEIN, both of Fig. 361A.

[8937] It is appreciated that specific functions, and accordingly utilities, of GR645 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR645 GENE: GAM147 TARGET PROTEIN and GAM361 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 147D and 361D

[8938] Reference is now made to Fig. 646, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 646(GR646) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8939] GR646 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR646 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8940] GR646 GENE encodes GR646 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8941] GR646 PRECURSOR RNA folds spatially, forming GR646 FOLDED PRECURSOR RNA . It is appreciated that GR646 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR646 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8942] GR646 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM230 PRECURSOR and GAM307 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8943] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM230 RNA and GAM307 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8944] GAM230 RNA binds complimentarily to a target binding site located in an untranslated region of GAM230 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 230A, thereby inhibiting translation of GAM230 TARGET RNA into GAM230 TARGET PROTEIN, both of Fig. 230A.

[8945] GAM307 RNA binds complimentarily to a target binding site located in an untranslated region of GAM307 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 307A, thereby inhibiting translation of GAM307 TARGET RNA into GAM307 TARGET PRO-

TEIN, both of Fig. 307A.

[8946] It is appreciated that specific functions, and accordingly utilities, of GR646 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR646 GENE: GAM230 TARGET PROTEIN and GAM307 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 230D and 307D

[8947] Reference is now made to Fig. 647, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 647(GR647) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8948] GR647 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR647 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8949] GR647 GENE encodes GR647 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8950] GR647 PRECURSOR RNA folds spatially, forming GR647 FOLDED PRECURSOR RNA . It is appreciated that GR647 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR647 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8951] GR647 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM60 PRECURSOR and GAM414 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8952] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60 RNA and GAM414 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8953] GAM60 RNA binds complimentarily to a target binding site located in an untranslated region of GAM60 TARGET RNA,

which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 60A, thereby inhibiting translation of GAM60 TARGET RNA into GAM60 TARGET PROTEIN, both of Fig. 60A.

[8954] GAM414 RNA binds complimentarily to a target binding site located in an untranslated region of GAM414 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 414A, thereby inhibiting translation of GAM414 TARGET RNA into GAM414 TARGET PROTEIN, both of Fig. 414A.

[8955] It is appreciated that specific functions, and accordingly utilities, of GR647 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR647 GENE: GAM60 TARGET PROTEIN and GAM414 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 60D and 414D

[8956] Reference is now made to Fig. 648, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

648(GR648) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8957] GR648 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR648 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8958] GR648 GENE encodes GR648 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8959] GR648 PRECURSOR RNA folds spatially, forming GR648 FOLDED PRECURSOR RNA . It is appreciated that GR648 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR648 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8960] GR648 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM

precursor RNAs, GAM218 PRECURSOR and GAM447 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8961] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM447 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8962] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[8963] GAM447 RNA binds complimentarily to a target binding site located in an untranslated region of GAM447 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 447A, thereby inhibiting translation of GAM447 TARGET RNA into GAM447 TARGET PROTEIN, both of Fig. 447A.

[8964] It is appreciated that specific functions, and accordingly utilities, of GR648 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR648 GENE: GAM218 TARGET PROTEIN and GAM447 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 447D

[8965] Reference is now made to Fig. 649, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 649(GR649) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8966] GR649 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR649 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8967] GR649 GENE encodes GR649 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8968] GR649 PRECURSOR RNA folds spatially, forming GR649

FOLDED PRECURSOR RNA . It is appreciated that GR649 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR649 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8969] GR649 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM88 PRECURSOR and GAM363 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8970] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88 RNA and GAM363 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8971] GAM88 RNA binds complimentarily to a target binding site located in an untranslated region of GAM88 TARGET RNA, which target binding site corresponds to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 88A, thereby inhibiting translation of GAM88 TARGET RNA into GAM88 TARGET PROTEIN, both of Fig. 88A.

[8972] GAM363 RNA binds complimentarily to a target binding site located in an untranslated region of GAM363 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 363A, thereby inhibiting translation of GAM363 TARGET RNA into GAM363 TARGET PROTEIN, both of Fig. 363A.

[8973] It is appreciated that specific functions, and accordingly utilities, of GR649 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR649 GENE: GAM88 TARGET PROTEIN and GAM363 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 88D and 363D

[8974] Reference is now made to Fig. 650, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 650(GR650) gene, which encodes an operon-like cluster

of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8975] GR650 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR650 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8976] GR650 GENE encodes GR650 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8977] GR650 PRECURSOR RNA folds spatially, forming GR650 FOLDED PRECURSOR RNA . It is appreciated that GR650 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR650 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8978] GR650 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM99 PRECURSOR, GAM434 PRECUR-

SOR and GAM492 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8979] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99 RNA, GAM434 RNA and GAM492 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8980] GAM99 RNA binds complimentarily to a target binding site located in an untranslated region of GAM99 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 99A, thereby inhibiting translation of GAM99 TARGET RNA into GAM99 TARGET PROTEIN, both of Fig. 99A.

[8981] GAM434 RNA binds complimentarily to a target binding site located in an untranslated region of GAM434 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 434A, thereby inhibiting translation of GAM434 TARGET RNA into GAM434 TARGET PROTEIN, both of Fig. 434A.

[8982] GAM492 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM492 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 492A, thereby inhibiting translation of GAM492 TARGET RNA into GAM492 TARGET PROTEIN, both of Fig. 492A.

[8983] It is appreciated that specific functions, and accordingly utilities, of GR650 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR650 GENE: GAM99 TARGET PROTEIN, GAM434 TARGET PROTEIN and GAM492 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 99D, 434D and 492D

[8984] Reference is now made to Fig. 651, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 651(GR651) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8985] GR651 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR651 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8986] GR651 GENE encodes GR651 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8987] GR651 PRECURSOR RNA folds spatially, forming GR651 FOLDED PRECURSOR RNA . It is appreciated that GR651 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR651 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8988] GR651 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM83 PRECURSOR and GAM132 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8989] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM83 RNA and GAM132 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8990] GAM83 RNA binds complimentarily to a target binding site located in an untranslated region of GAM83 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 83A, thereby inhibiting translation of GAM83 TARGET RNA into GAM83 TARGET PROTEIN, both of Fig. 83A.

[8991] GAM132 RNA binds complimentarily to a target binding site located in an untranslated region of GAM132 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 132A, thereby inhibiting translation of GAM132 TARGET RNA into GAM132 TARGET PROTEIN, both of Fig. 132A.

[8992] It is appreciated that specific functions, and accordingly utilities, of GR651 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR651 GENE: GAM83 TARGET PROTEIN and GAM132 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 83D and 132D

[8993] Reference is now made to Fig. 652, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 652(GR652) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[8994] GR652 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR652 GENE was detected is described hereinabove with reference to Figs. 6-15.

[8995] GR652 GENE encodes GR652 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[8996] GR652 PRECURSOR RNA folds spatially, forming GR652 FOLDED PRECURSOR RNA . It is appreciated that GR652 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR652 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[8997] GR652 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM50 PRECURSOR and GAM300 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[8998] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50 RNA and GAM300 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[8999] GAM50 RNA binds complimentarily to a target binding site located in an untranslated region of GAM50 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 50A, thereby inhibiting translation of GAM50 TARGET RNA into GAM50 TARGET PROTEIN, both of Fig. 50A.

[9000] GAM300 RNA binds complimentarily to a target binding site located in an untranslated region of GAM300 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 300A, thereby inhibiting translation of GAM300 TARGET RNA into GAM300 TARGET PROTEIN, both of Fig. 300A.

[9001] It is appreciated that specific functions, and accordingly utilities, of GR652 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR652 GENE: GAM50 TARGET PROTEIN and GAM300 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 50D and 300D

[9002] Reference is now made to Fig. 653, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 653(GR653) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9003] GR653 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR653 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9004] GR653 GENE encodes GR653 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9005] GR653 PRECURSOR RNA folds spatially, forming GR653 FOLDED PRECURSOR RNA . It is appreciated that GR653 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR653 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9006] GR653 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64 PRECURSOR and GAM169 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9007] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64 RNA

and GAM169 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9008] GAM64 RNA binds complimentarily to a target binding site located in an untranslated region of GAM64 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 64A, thereby inhibiting translation of GAM64 TARGET RNA into GAM64 TARGET PROTEIN, both of Fig. 64A.

[9009] GAM169 RNA binds complimentarily to a target binding site located in an untranslated region of GAM169 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 169A, thereby inhibiting translation of GAM169 TARGET RNA into GAM169 TARGET PROTEIN, both of Fig. 169A.

[9010] It is appreciated that specific functions, and accordingly utilities, of GR653 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR653 GENE: GAM64 TARGET PROTEIN and GAM169 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 64D and

[9011] Reference is now made to Fig. 654, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 654(GR654) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9012] GR654 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR654 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9013] GR654 GENE encodes GR654 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9014] GR654 PRECURSOR RNA folds spatially, forming GR654 FOLDED PRECURSOR RNA . It is appreciated that GR654 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR654 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[9015] GR654 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM133 PRECURSOR and GAM284 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9016] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM133 RNA and GAM284 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9017] GAM133 RNA binds complimentarily to a target binding site located in an untranslated region of GAM133 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 133A, thereby inhibiting translation of GAM133 TARGET RNA into GAM133 TARGET PROTEIN, both of Fig. 133A.

[9018] GAM284 RNA binds complimentarily to a target binding site located in an untranslated region of GAM284 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 284A, thereby inhibiting translation of GAM284 TARGET RNA into GAM284 TARGET PROTEIN, both of Fig. 284A.

[9019] It is appreciated that specific functions, and accordingly utilities, of GR654 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR654 GENE: GAM133 TARGET PROTEIN and GAM284 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 133D and 284D

[9020] Reference is now made to Fig. 655, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 655(GR655) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9021] GR655 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR655 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[9022] GR655 GENE encodes GR655 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9023] GR655 PRECURSOR RNA folds spatially, forming GR655 FOLDED PRECURSOR RNA . It is appreciated that GR655 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR655 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9024] GR655 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM447 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9025] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM447 RNA respectively, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

[9026] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[9027] GAM447 RNA binds complimentarily to a target binding site located in an untranslated region of GAM447 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 447A, thereby inhibiting translation of GAM447 TARGET RNA into GAM447 TARGET PROTEIN, both of Fig. 447A.

[9028] It is appreciated that specific functions, and accordingly utilities, of GR655 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR655 GENE: GAM218 TARGET PROTEIN and GAM447 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 447D

[9029] Reference is now made to Fig. 656, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 656(GR656) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9030] GR656 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR656 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9031] GR656 GENE encodes GR656 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9032] GR656 PRECURSOR RNA folds spatially, forming GR656 FOLDED PRECURSOR RNA . It is appreciated that GR656 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR656 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[9033] GR656 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47 PRECURSOR and GAM430 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9034] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47 RNA and GAM430 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9035] GAM47 RNA binds complimentarily to a target binding site located in an untranslated region of GAM47 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 47A, thereby inhibiting translation of GAM47 TARGET RNA into GAM47 TARGET PROTEIN, both of Fig. 47A.

[9036] GAM430 RNA binds complimentarily to a target binding site located in an untranslated region of GAM430 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 430A, thereby inhibiting translation of GAM430 TARGET RNA into GAM430 TARGET PROTEIN, both of Fig. 430A.

[9037] It is appreciated that specific functions, and accordingly utilities, of GR656 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR656 GENE: GAM47 TARGET PROTEIN and GAM430 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 47D and 430D

[9038] Reference is now made to Fig. 657, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 657(GR657) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9039] GR657 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR657 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9040] GR657 GENE encodes GR657 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9041] GR657 PRECURSOR RNA folds spatially, forming GR657 FOLDED PRECURSOR RNA . It is appreciated that GR657 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR657 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9042] GR657 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM282 PRECURSOR and GAM290 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9043] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM282 RNA and GAM290 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9044] GAM282 RNA binds complimentarily to a target binding site located in an untranslated region of GAM282 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 282A, thereby inhibiting translation of GAM282 TARGET RNA into GAM282 TARGET PROTEIN, both of Fig. 282A.

[9045] GAM290 RNA binds complimentarily to a target binding site located in an untranslated region of GAM290 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 290A, thereby inhibiting translation of GAM290 TARGET RNA into GAM290 TARGET PROTEIN, both of Fig. 290A.

[9046] It is appreciated that specific functions, and accordingly utilities, of GR657 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR657 GENE: GAM282 TARGET PROTEIN and GAM290 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 282D and 290D

[9047] Reference is now made to Fig. 658, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 658(GR658) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9048] GR658 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR658 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9049] GR658 GENE encodes GR658 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9050] GR658 PRECURSOR RNA folds spatially, forming GR658 FOLDED PRECURSOR RNA . It is appreciated that GR658 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR658 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9051] GR658 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM80 PRECURSOR, GAM424 PRECURSOR and GAM505 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9052] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80 RNA, GAM424 RNA and GAM505 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9053] GAM80 RNA binds complimentarily to a target binding site located in an untranslated region of GAM80 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 80A, thereby inhibiting translation of GAM80 TARGET RNA into GAM80 TARGET PROTEIN, both of Fig. 80A.

[9054] GAM424 RNA binds complimentarily to a target binding site located in an untranslated region of GAM424 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 424A, thereby inhibiting transla-

tion of GAM424 TARGET RNA into GAM424 TARGET PROTEIN, both of Fig. 424A.

[9055] GAM505 RNA binds complimentarily to a target binding site located in an untranslated region of GAM505 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 505A, thereby inhibiting translation of GAM505 TARGET RNA into GAM505 TARGET PROTEIN, both of Fig. 505A.

[9056] It is appreciated that specific functions, and accordingly utilities, of GR658 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR658 GENE: GAM80 TARGET PROTEIN, GAM424 TARGET PROTEIN and GAM505 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 80D, 424D and 505D

[9057] Reference is now made to Fig. 659, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 659(GR659) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art.

[9058] GR659 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR659 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9059] GR659 GENE encodes GR659 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9060] GR659 PRECURSOR RNA folds spatially, forming GR659 FOLDED PRECURSOR RNA . It is appreciated that GR659 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR659 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9061] GR659 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218 PRECURSOR and GAM448 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECUR-

SOR RNA of Fig. 8.

[9062] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218 RNA and GAM448 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9063] GAM218 RNA binds complimentarily to a target binding site located in an untranslated region of GAM218 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 218A, thereby inhibiting translation of GAM218 TARGET RNA into GAM218 TARGET PROTEIN, both of Fig. 218A.

[9064] GAM448 RNA binds complimentarily to a target binding site located in an untranslated region of GAM448 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 448A, thereby inhibiting translation of GAM448 TARGET RNA into GAM448 TARGET PROTEIN, both of Fig. 448A.

[9065] It is appreciated that specific functions, and accordingly utilities, of GR659 GENE correlate with, and may be deduced from, the identity of the target genes, which are in-

hibited by GAM RNAs comprised in the operon-like cluster of GR659 GENE: GAM218 TARGET PROTEIN and GAM448 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 218D and 448D

[9066] Reference is now made to Fig. 660, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 660(GR660) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9067] GR660 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR660 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9068] GR660 GENE encodes GR660 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9069] GR660 PRECURSOR RNA folds spatially, forming GR660 FOLDED PRECURSOR RNA . It is appreciated that GR660 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin

structures are due to the fact that the nucleotide sequence of GR660 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9070] GR660 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM420 PRECURSOR and GAM550 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9071] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM420 RNA and GAM550 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9072] GAM420 RNA binds complimentarily to a target binding site located in an untranslated region of GAM420 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 420A, thereby inhibiting translation of GAM420 TARGET RNA into GAM420 TARGET PRO-

TEIN, both of Fig. 420A.

[9073] GAM550 RNA binds complimentarily to a target binding site located in an untranslated region of GAM550 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 550A, thereby inhibiting translation of GAM550 TARGET RNA into GAM550 TARGET PROTEIN, both of Fig. 550A.

[9074] It is appreciated that specific functions, and accordingly utilities, of GR660 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR660 GENE: GAM420 TARGET PROTEIN and GAM550 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 420D and 550D

[9075] Reference is now made to Fig. 661, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 661(GR661) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[9076] GR661 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR661 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9077] GR661 GENE encodes GR661 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9078] GR661 PRECURSOR RNA folds spatially, forming GR661 FOLDED PRECURSOR RNA . It is appreciated that GR661 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR661 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9079] GR661 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM317 PRECURSOR and GAM501 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9080] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM317 RNA and GAM501 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9081] GAM317 RNA binds complimentarily to a target binding site located in an untranslated region of GAM317 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 317A, thereby inhibiting translation of GAM317 TARGET RNA into GAM317 TARGET PROTEIN, both of Fig. 317A.

[9082] GAM501 RNA binds complimentarily to a target binding site located in an untranslated region of GAM501 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 501A, thereby inhibiting translation of GAM501 TARGET RNA into GAM501 TARGET PROTEIN, both of Fig. 501A.

[9083] It is appreciated that specific functions, and accordingly utilities, of GR661 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR661 GENE: GAM317 TARGET PROTEIN and GAM501 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 317D and 501D

[9084] Reference is now made to Fig. 662, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 662(GR662) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9085] GR662 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR662 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9086] GR662 GENE encodes GR662 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9087] GR662 PRECURSOR RNA folds spatially, forming GR662 FOLDED PRECURSOR RNA . It is appreciated that GR662 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR662 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9088] GR662 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111 PRECURSOR and GAM242 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9089] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111 RNA and GAM242 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9090] GAM111 RNA binds complimentarily to a target binding site located in an untranslated region of GAM111 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 111A, thereby inhibiting translation of GAM111 TARGET RNA into GAM111 TARGET PROTEIN, both of Fig. 111A.

[9091] GAM242 RNA binds complimentarily to a target binding site located in an untranslated region of GAM242 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 242A, thereby inhibiting translation of GAM242 TARGET RNA into GAM242 TARGET PROTEIN, both of Fig. 242A.

[9092] It is appreciated that specific functions, and accordingly utilities, of GR662 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR662 GENE: GAM111 TARGET PROTEIN and GAM242 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 111D and 242D

[9093] Reference is now made to Fig. 663, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 663(GR663) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9094] GR663 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR663 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9095] GR663 GENE encodes GR663 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9096] GR663 PRECURSOR RNA folds spatially, forming GR663 FOLDED PRECURSOR RNA . It is appreciated that GR663 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR663 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9097] GR663 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM135 PRECURSOR and GAM309 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9098] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM135 RNA and GAM309 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9099] GAM135 RNA binds complimentarily to a target binding site located in an untranslated region of GAM135 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 135A, thereby inhibiting translation of GAM135 TARGET RNA into GAM135 TARGET PROTEIN, both of Fig. 135A.

[9100] GAM309 RNA binds complimentarily to a target binding site located in an untranslated region of GAM309 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 309A, thereby inhibiting translation of GAM309 TARGET RNA into GAM309 TARGET PROTEIN, both of Fig. 309A.

[9101] It is appreciated that specific functions, and accordingly utilities, of GR663 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR663 GENE: GAM135 TARGET PROTEIN and GAM309

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 135D and 309D

[9102] Reference is now made to Fig. 664, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 664(GR664) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9103] GR664 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR664 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9104] GR664 GENE encodes GR664 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9105] GR664 PRECURSOR RNA folds spatially, forming GR664 FOLDED PRECURSOR RNA . It is appreciated that GR664 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR664 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9106] GR664 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM119 PRECURSOR, GAM248 PRECURSOR and GAM257 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9107] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119 RNA, GAM248 RNA and GAM257 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9108] GAM119 RNA binds complimentarily to a target binding site located in an untranslated region of GAM119 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 119A, thereby inhibiting translation of GAM119 TARGET RNA into GAM119 TARGET PROTEIN, both of Fig. 119A.

[9109] GAM248 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM248 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 248A, thereby inhibiting translation of GAM248 TARGET RNA into GAM248 TARGET PROTEIN, both of Fig. 248A.

[9110] GAM257 RNA binds complimentarily to a target binding site located in an untranslated region of GAM257 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 257A, thereby inhibiting translation of GAM257 TARGET RNA into GAM257 TARGET PROTEIN, both of Fig. 257A.

[9111] It is appreciated that specific functions, and accordingly utilities, of GR664 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR664 GENE: GAM119 TARGET PROTEIN, GAM248 TARGET PROTEIN and GAM257 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 119D, 248D and 257D

[9112] Reference is now made to Fig. 665, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 665(GR665) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9113] GR665 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR665 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9114] GR665 GENE encodes GR665 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9115] GR665 PRECURSOR RNA folds spatially, forming GR665 FOLDED PRECURSOR RNA . It is appreciated that GR665 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR665 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9116] GR665 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM115 PRECURSOR and GAM452 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9117] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM115 RNA and GAM452 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9118] GAM115 RNA binds complimentarily to a target binding site located in an untranslated region of GAM115 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 115A, thereby inhibiting translation of GAM115 TARGET RNA into GAM115 TARGET PROTEIN, both of Fig. 115A.

[9119] GAM452 RNA binds complimentarily to a target binding site located in an untranslated region of GAM452 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 452A, thereby inhibiting translation of GAM452 TARGET RNA into GAM452 TARGET PRO-

TEIN, both of Fig. 452A.

[9120] It is appreciated that specific functions, and accordingly utilities, of GR665 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR665 GENE: GAM115 TARGET PROTEIN and GAM452 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 115D and 452D

[9121] Reference is now made to Fig. 666, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 666(GR666) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9122] GR666 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR666 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9123] GR666 GENE encodes GR666 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9124] GR666 PRECURSOR RNA folds spatially, forming GR666 FOLDED PRECURSOR RNA . It is appreciated that GR666 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR666 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9125] GR666 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156 PRECURSOR and GAM346 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9126] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156 RNA and GAM346 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9127] GAM156 RNA binds complimentarily to a target binding site located in an untranslated region of GAM156 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 156A, thereby inhibiting translation of GAM156 TARGET RNA into GAM156 TARGET PROTEIN, both of Fig. 156A.

[9128] GAM346 RNA binds complimentarily to a target binding site located in an untranslated region of GAM346 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 346A, thereby inhibiting translation of GAM346 TARGET RNA into GAM346 TARGET PROTEIN, both of Fig. 346A.

[9129] It is appreciated that specific functions, and accordingly utilities, of GR666 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR666 GENE: GAM156 TARGET PROTEIN and GAM346 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 156D and 346D

[9130] Reference is now made to Fig. 667, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

667(GR667) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9131] GR667 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR667 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9132] GR667 GENE encodes GR667 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9133] GR667 PRECURSOR RNA folds spatially, forming GR667 FOLDED PRECURSOR RNA . It is appreciated that GR667 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR667 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9134] GR667 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM

precursor RNAs, GAM288 PRECURSOR and GAM405 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9135] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM288 RNA and GAM405 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9136] GAM288 RNA binds complimentarily to a target binding site located in an untranslated region of GAM288 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 288A, thereby inhibiting translation of GAM288 TARGET RNA into GAM288 TARGET PROTEIN, both of Fig. 288A.

[9137] GAM405 RNA binds complimentarily to a target binding site located in an untranslated region of GAM405 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 405A, thereby inhibiting translation of GAM405 TARGET RNA into GAM405 TARGET PROTEIN, both of Fig. 405A.

[9138] It is appreciated that specific functions, and accordingly utilities, of GR667 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR667 GENE: GAM288 TARGET PROTEIN and GAM405 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 288D and 405D

[9139] Reference is now made to Fig. 668, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 668(GR668) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9140] GR668 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR668 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9141] GR668 GENE encodes GR668 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9142] GR668 PRECURSOR RNA folds spatially, forming GR668

FOLDED PRECURSOR RNA . It is appreciated that GR668 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR668 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9143] GR668 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM259 PRECURSOR and GAM379 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9144] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM259 RNA and GAM379 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9145] GAM259 RNA binds complimentarily to a target binding site located in an untranslated region of GAM259 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 259A, thereby inhibiting translation of GAM259 TARGET RNA into GAM259 TARGET PROTEIN, both of Fig. 259A.

[9146] GAM379 RNA binds complimentarily to a target binding site located in an untranslated region of GAM379 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 379A, thereby inhibiting translation of GAM379 TARGET RNA into GAM379 TARGET PROTEIN, both of Fig. 379A.

[9147] It is appreciated that specific functions, and accordingly utilities, of GR668 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR668 GENE: GAM259 TARGET PROTEIN and GAM379 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 259D and 379D

[9148] Reference is now made to Fig. 669, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 669(GR669) gene, which encodes an operon-like cluster

of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9149] GR669 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR669 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9150] GR669 GENE encodes GR669 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9151] GR669 PRECURSOR RNA folds spatially, forming GR669 FOLDED PRECURSOR RNA . It is appreciated that GR669 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR669 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9152] GR669 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM68 PRECURSOR and GAM365 PRE-

CURSOR, each of which GAM precursor RNAs being a hair-pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9153] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM68 RNA and GAM365 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9154] GAM68 RNA binds complimentarily to a target binding site located in an untranslated region of GAM68 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 68A, thereby inhibiting translation of GAM68 TARGET RNA into GAM68 TARGET PROTEIN, both of Fig. 68A.

[9155] GAM365 RNA binds complimentarily to a target binding site located in an untranslated region of GAM365 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 365A, thereby inhibiting translation of GAM365 TARGET RNA into GAM365 TARGET PROTEIN, both of Fig. 365A.

[9156] It is appreciated that specific functions, and accordingly

utilities, of GR669 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR669 GENE: GAM68 TARGET PROTEIN and GAM365 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 68D and 365D

[9157] Reference is now made to Fig. 670, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 670(GR670) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9158] GR670 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR670 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9159] GR670 GENE encodes GR670 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9160] GR670 PRECURSOR RNA folds spatially, forming GR670 FOLDED PRECURSOR RNA . It is appreciated that GR670

FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR670 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9161] GR670 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97 PRECURSOR and GAM316 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9162] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97 RNA and GAM316 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9163] GAM97 RNA binds complimentarily to a target binding site located in an untranslated region of GAM97 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 97A, thereby inhibiting translation of GAM97 TARGET RNA into GAM97 TARGET PROTEIN, both of Fig. 97A.

[9164] GAM316 RNA binds complimentarily to a target binding site located in an untranslated region of GAM316 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 316A, thereby inhibiting translation of GAM316 TARGET RNA into GAM316 TARGET PROTEIN, both of Fig. 316A.

[9165] It is appreciated that specific functions, and accordingly utilities, of GR670 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR670 GENE: GAM97 TARGET PROTEIN and GAM316 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 97D and 316D

[9166] Reference is now made to Fig. 671, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 671(GR671) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn

modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9167] GR671 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR671 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9168] GR671 GENE encodes GR671 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9169] GR671 PRECURSOR RNA folds spatially, forming GR671 FOLDED PRECURSOR RNA . It is appreciated that GR671 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR671 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9170] GR671 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214 PRECURSOR and GAM450 PRECURSOR, each of which GAM precursor RNAs being a hair-

pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9171] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214 RNA and GAM450 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9172] GAM214 RNA binds complimentarily to a target binding site located in an untranslated region of GAM214 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 214A, thereby inhibiting translation of GAM214 TARGET RNA into GAM214 TARGET PROTEIN, both of Fig. 214A.

[9173] GAM450 RNA binds complimentarily to a target binding site located in an untranslated region of GAM450 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 450A, thereby inhibiting translation of GAM450 TARGET RNA into GAM450 TARGET PROTEIN, both of Fig. 450A.

[9174] It is appreciated that specific functions, and accordingly utilities, of GR671 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR671 GENE: GAM214 TARGET PROTEIN and GAM450 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 214D and 450D

[9175] Reference is now made to Fig. 672, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 672(GR672) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9176] GR672 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR672 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9177] GR672 GENE encodes GR672 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9178] GR672 PRECURSOR RNA folds spatially, forming GR672 FOLDED PRECURSOR RNA . It is appreciated that GR672 FOLDED PRECURSOR RNA comprises a plurality of what is

known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR672 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9179] GR672 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM334 PRECURSOR and GAM390 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9180] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM334 RNA and GAM390 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9181] GAM334 RNA binds complimentarily to a target binding site located in an untranslated region of GAM334 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 334A, thereby inhibiting transla-

tion of GAM334 TARGET RNA into GAM334 TARGET PROTEIN, both of Fig. 334A.

[9182] GAM390 RNA binds complimentarily to a target binding site located in an untranslated region of GAM390 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 390A, thereby inhibiting translation of GAM390 TARGET RNA into GAM390 TARGET PROTEIN, both of Fig. 390A.

[9183] It is appreciated that specific functions, and accordingly utilities, of GR672 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR672 GENE: GAM334 TARGET PROTEIN and GAM390 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 334D and 390D

[9184] Reference is now made to Fig. 673, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 673(GR673) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art.

[9185] GR673 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR673 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9186] GR673 GENE encodes GR673 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9187] GR673 PRECURSOR RNA folds spatially, forming GR673 FOLDED PRECURSOR RNA . It is appreciated that GR673 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR673 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9188] GR673 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM275 PRECURSOR and GAM415 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9189] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM275 RNA and GAM415 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9190] GAM275 RNA binds complimentarily to a target binding site located in an untranslated region of GAM275 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 275A, thereby inhibiting translation of GAM275 TARGET RNA into GAM275 TARGET PROTEIN, both of Fig. 275A.

[9191] GAM415 RNA binds complimentarily to a target binding site located in an untranslated region of GAM415 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 415A, thereby inhibiting translation of GAM415 TARGET RNA into GAM415 TARGET PROTEIN, both of Fig. 415A.

[9192] It is appreciated that specific functions, and accordingly utilities, of GR673 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR673 GENE: GAM275 TARGET PROTEIN and GAM415 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 275D and 415D

[9193] Reference is now made to Fig. 674, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record

674(GR674) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9194] GR674 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR674 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9195] GR674 GENE encodes GR674 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9196] GR674 PRECURSOR RNA folds spatially, forming GR674 FOLDED PRECURSOR RNA . It is appreciated that GR674 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR674 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9197] GR674 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM

precursor RNAs, GAM44 PRECURSOR, GAM403 PRECURSOR and GAM520 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9198] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44 RNA, GAM403 RNA and GAM520 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9199] GAM44 RNA binds complimentarily to a target binding site located in an untranslated region of GAM44 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 44A, thereby inhibiting translation of GAM44 TARGET RNA into GAM44 TARGET PROTEIN, both of Fig. 44A.

[9200] GAM403 RNA binds complimentarily to a target binding site located in an untranslated region of GAM403 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 403A, thereby inhibiting translation of GAM403 TARGET RNA into GAM403 TARGET PROTEIN, both of Fig. 403A.

[9201] GAM520 RNA binds complimentarily to a target binding site located in an untranslated region of GAM520 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 520A, thereby inhibiting translation of GAM520 TARGET RNA into GAM520 TARGET PROTEIN, both of Fig. 520A.

[9202] It is appreciated that specific functions, and accordingly utilities, of GR674 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR674 GENE: GAM44 TARGET PROTEIN, GAM403 TARGET PROTEIN and GAM520 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 44D, 403D and 520D

[9203] Reference is now made to Fig. 675, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 675(GR675) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9204] GR675 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR675 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9205] GR675 GENE encodes GR675 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9206] GR675 PRECURSOR RNA folds spatially, forming GR675 FOLDED PRECURSOR RNA . It is appreciated that GR675 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR675 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9207] GR675 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM95 PRECURSOR and GAM261 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9208] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM95 RNA and GAM261 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9209] GAM95 RNA binds complimentarily to a target binding site located in an untranslated region of GAM95 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 95A, thereby inhibiting translation of GAM95 TARGET RNA into GAM95 TARGET PROTEIN, both of Fig. 95A.

[9210] GAM261 RNA binds complimentarily to a target binding site located in an untranslated region of GAM261 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 261A, thereby inhibiting translation of GAM261 TARGET RNA into GAM261 TARGET PROTEIN, both of Fig. 261A.

[9211] It is appreciated that specific functions, and accordingly utilities, of GR675 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR675 GENE: GAM95 TARGET PROTEIN and GAM261

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 95D and 261D

[9212] Reference is now made to Fig. 676, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 676(GR676) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9213] GR676 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR676 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9214] GR676 GENE encodes GR676 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9215] GR676 PRECURSOR RNA folds spatially, forming GR676 FOLDED PRECURSOR RNA . It is appreciated that GR676 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR676 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9216] GR676 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM229 PRECURSOR and GAM370 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9217] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM229 RNA and GAM370 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9218] GAM229 RNA binds complimentarily to a target binding site located in an untranslated region of GAM229 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 229A, thereby inhibiting translation of GAM229 TARGET RNA into GAM229 TARGET PROTEIN, both of Fig. 229A.

[9219] GAM370 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM370 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 370A, thereby inhibiting translation of GAM370 TARGET RNA into GAM370 TARGET PROTEIN, both of Fig. 370A.

[9220] It is appreciated that specific functions, and accordingly utilities, of GR676 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR676 GENE: GAM229 TARGET PROTEIN and GAM370 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 229D and 370D

[9221] Reference is now made to Fig. 677, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 677(GR677) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9222] GR677 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR677 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9223] GR677 GENE encodes GR677 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9224] GR677 PRECURSOR RNA folds spatially, forming GR677 FOLDED PRECURSOR RNA . It is appreciated that GR677 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR677 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9225] GR677 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM158 PRECURSOR and GAM466 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9226] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM158 RNA and GAM466 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9227] GAM158 RNA binds complimentarily to a target binding site located in an untranslated region of GAM158 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 158A, thereby inhibiting translation of GAM158 TARGET RNA into GAM158 TARGET PROTEIN, both of Fig. 158A.

[9228] GAM466 RNA binds complimentarily to a target binding site located in an untranslated region of GAM466 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 466A, thereby inhibiting translation of GAM466 TARGET RNA into GAM466 TARGET PROTEIN, both of Fig. 466A.

[9229] It is appreciated that specific functions, and accordingly utilities, of GR677 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR677 GENE: GAM158 TARGET PROTEIN and GAM466 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 158D and 466D

[9230] Reference is now made to Fig. 678, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 678(GR678) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9231] GR678 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR678 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9232] GR678 GENE encodes GR678 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9233] GR678 PRECURSOR RNA folds spatially, forming GR678 FOLDED PRECURSOR RNA . It is appreciated that GR678 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR678 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9234] GR678 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM350 PRECURSOR and GAM470 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9235] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM350 RNA and GAM470 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9236] GAM350 RNA binds complimentarily to a target binding site located in an untranslated region of GAM350 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 350A, thereby inhibiting translation of GAM350 TARGET RNA into GAM350 TARGET PROTEIN, both of Fig. 350A.

[9237] GAM470 RNA binds complimentarily to a target binding site located in an untranslated region of GAM470 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 470A, thereby inhibiting translation of GAM470 TARGET RNA into GAM470 TARGET PROTEIN, both of Fig. 470A.

[9238] It is appreciated that specific functions, and accordingly utilities, of GR678 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR678 GENE: GAM350 TARGET PROTEIN and GAM470 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 350D and 470D

[9239] Reference is now made to Fig. 679, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 679(GR679) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9240] GR679 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR679 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9241] GR679 GENE encodes GR679 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9242] GR679 PRECURSOR RNA folds spatially, forming GR679 FOLDED PRECURSOR RNA . It is appreciated that GR679 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR679 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9243] GR679 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM143 PRECURSOR and GAM398 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9244] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM143 RNA

and GAM398 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9245] GAM143 RNA binds complimentarily to a target binding site located in an untranslated region of GAM143 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 143A, thereby inhibiting translation of GAM143 TARGET RNA into GAM143 TARGET PROTEIN, both of Fig. 143A.

[9246] GAM398 RNA binds complimentarily to a target binding site located in an untranslated region of GAM398 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 398A, thereby inhibiting translation of GAM398 TARGET RNA into GAM398 TARGET PROTEIN, both of Fig. 398A.

[9247] It is appreciated that specific functions, and accordingly utilities, of GR679 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR679 GENE: GAM143 TARGET PROTEIN and GAM398 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 143D and

[9248] Reference is now made to Fig. 680, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 680(GR680) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9249] GR680 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR680 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9250] GR680 GENE encodes GR680 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9251] GR680 PRECURSOR RNA folds spatially, forming GR680 FOLDED PRECURSOR RNA . It is appreciated that GR680 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR680 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[9252] GR680 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM526 PRECURSOR and GAM541 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9253] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM526 RNA and GAM541 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9254] GAM526 RNA binds complimentarily to a target binding site located in an untranslated region of GAM526 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 526A, thereby inhibiting translation of GAM526 TARGET RNA into GAM526 TARGET PROTEIN, both of Fig. 526A.

[9255] GAM541 RNA binds complimentarily to a target binding site located in an untranslated region of GAM541 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 541A, thereby inhibiting translation of GAM541 TARGET RNA into GAM541 TARGET PROTEIN, both of Fig. 541A.

[9256] It is appreciated that specific functions, and accordingly utilities, of GR680 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR680 GENE: GAM526 TARGET PROTEIN and GAM541 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 526D and 541D

[9257] Reference is now made to Fig. 681, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 681(GR681) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9258] GR681 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR681 GENE was detected is described hereinabove with

reference to Figs. 6-15.

[9259] GR681 GENE encodes GR681 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9260] GR681 PRECURSOR RNA folds spatially, forming GR681 FOLDED PRECURSOR RNA . It is appreciated that GR681 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR681 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9261] GR681 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107 PRECURSOR and GAM264 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9262] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107 RNA and GAM264 RNA respectively, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

[9263] GAM107 RNA binds complimentarily to a target binding site located in an untranslated region of GAM107 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 107A, thereby inhibiting translation of GAM107 TARGET RNA into GAM107 TARGET PROTEIN, both of Fig. 107A.

[9264] GAM264 RNA binds complimentarily to a target binding site located in an untranslated region of GAM264 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 264A, thereby inhibiting translation of GAM264 TARGET RNA into GAM264 TARGET PROTEIN, both of Fig. 264A.

[9265] It is appreciated that specific functions, and accordingly utilities, of GR681 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR681 GENE: GAM107 TARGET PROTEIN and GAM264 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 107D and 264D

[9266] Reference is now made to Fig. 682, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 682(GR682) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9267] GR682 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR682 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9268] GR682 GENE encodes GR682 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9269] GR682 PRECURSOR RNA folds spatially, forming GR682 FOLDED PRECURSOR RNA . It is appreciated that GR682 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR682 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[9270] GR682 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM431 PRECURSOR and GAM532 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9271] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM431 RNA and GAM532 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9272] GAM431 RNA binds complimentarily to a target binding site located in an untranslated region of GAM431 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 431A, thereby inhibiting translation of GAM431 TARGET RNA into GAM431 TARGET PROTEIN, both of Fig. 431A.

[9273] GAM532 RNA binds complimentarily to a target binding site located in an untranslated region of GAM532 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 532A, thereby inhibiting translation of GAM532 TARGET RNA into GAM532 TARGET PROTEIN, both of Fig. 532A.

[9274] It is appreciated that specific functions, and accordingly utilities, of GR682 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR682 GENE: GAM431 TARGET PROTEIN and GAM532 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 431D and 532D

[9275] Reference is now made to Fig. 683, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 683(GR683) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9276] GR683 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR683 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9277] GR683 GENE encodes GR683 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9278] GR683 PRECURSOR RNA folds spatially, forming GR683 FOLDED PRECURSOR RNA . It is appreciated that GR683 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR683 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9279] GR683 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM332 PRECURSOR and GAM432 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9280] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM332 RNA and GAM432 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9281] GAM332 RNA binds complimentarily to a target binding site located in an untranslated region of GAM332 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 332A, thereby inhibiting translation of GAM332 TARGET RNA into GAM332 TARGET PROTEIN, both of Fig. 332A.

[9282] GAM432 RNA binds complimentarily to a target binding site located in an untranslated region of GAM432 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 432A, thereby inhibiting translation of GAM432 TARGET RNA into GAM432 TARGET PROTEIN, both of Fig. 432A.

[9283] It is appreciated that specific functions, and accordingly utilities, of GR683 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR683 GENE: GAM332 TARGET PROTEIN and GAM432 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 332D and 432D

[9284] Reference is now made to Fig. 684, which is a simplified

diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 684(GR684) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9285] GR684 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR684 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9286] GR684 GENE encodes GR684 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9287] GR684 PRECURSOR RNA folds spatially, forming GR684 FOLDED PRECURSOR RNA . It is appreciated that GR684 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR684 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9288] GR684 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM352 PRECURSOR and GAM488 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9289] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM352 RNA and GAM488 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9290] GAM352 RNA binds complimentarily to a target binding site located in an untranslated region of GAM352 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 352A, thereby inhibiting translation of GAM352 TARGET RNA into GAM352 TARGET PROTEIN, both of Fig. 352A.

[9291] GAM488 RNA binds complimentarily to a target binding site located in an untranslated region of GAM488 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 488A, thereby inhibiting transla-

tion of GAM488 TARGET RNA into GAM488 TARGET PROTEIN, both of Fig. 488A.

[9292] It is appreciated that specific functions, and accordingly utilities, of GR684 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR684 GENE: GAM352 TARGET PROTEIN and GAM488 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 352D and 488D

[9293] Reference is now made to Fig. 685, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 685(GR685) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9294] GR685 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR685 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9295] GR685 GENE encodes GR685 PRECURSOR RNA, an RNA

molecule, typically several hundred nucleotides long.

[9296] GR685 PRECURSOR RNA folds spatially, forming GR685 FOLDED PRECURSOR RNA . It is appreciated that GR685 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR685 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9297] GR685 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM310 PRECURSOR and GAM507 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9298] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM310 RNA and GAM507 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9299] GAM310 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM310 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 310A, thereby inhibiting translation of GAM310 TARGET RNA into GAM310 TARGET PROTEIN, both of Fig. 310A.

[9300] GAM507 RNA binds complimentarily to a target binding site located in an untranslated region of GAM507 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 507A, thereby inhibiting translation of GAM507 TARGET RNA into GAM507 TARGET PROTEIN, both of Fig. 507A.

[9301] It is appreciated that specific functions, and accordingly utilities, of GR685 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR685 GENE: GAM310 TARGET PROTEIN and GAM507 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 310D and 507D

[9302] Reference is now made to Fig. 686, which is a simplified diagram describing a novel bioinformatically detected

regulatory gene, referred to here as Genomic Record 686(GR686) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9303] GR686 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR686 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9304] GR686 GENE encodes GR686 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9305] GR686 PRECURSOR RNA folds spatially, forming GR686 FOLDED PRECURSOR RNA . It is appreciated that GR686 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR686 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9306] GR686 FOLDED PRECURSOR RNA is naturally processed by

cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM171 PRECURSOR, GAM347 PRECURSOR and GAM457 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9307] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM171 RNA, GAM347 RNA and GAM457 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9308] GAM171 RNA binds complimentarily to a target binding site located in an untranslated region of GAM171 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 171A, thereby inhibiting translation of GAM171 TARGET RNA into GAM171 TARGET PROTEIN, both of Fig. 171A.

[9309] GAM347 RNA binds complimentarily to a target binding site located in an untranslated region of GAM347 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 347A, thereby inhibiting translation of GAM347 TARGET RNA into GAM347 TARGET PRO-

TEIN, both of Fig. 347A.

[9310] GAM457 RNA binds complimentarily to a target binding site located in an untranslated region of GAM457 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 457A, thereby inhibiting translation of GAM457 TARGET RNA into GAM457 TARGET PROTEIN, both of Fig. 457A.

[9311] It is appreciated that specific functions, and accordingly utilities, of GR686 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR686 GENE: GAM171 TARGET PROTEIN, GAM347 TARGET PROTEIN and GAM457 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 171D, 347D and 457D

[9312] Reference is now made to Fig. 687, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 687(GR687) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[9313] GR687 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR687 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9314] GR687 GENE encodes GR687 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9315] GR687 PRECURSOR RNA folds spatially, forming GR687 FOLDED PRECURSOR RNA . It is appreciated that GR687 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR687 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9316] GR687 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM96 PRECURSOR and GAM277 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9317] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96 RNA and GAM277 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9318] GAM96 RNA binds complimentarily to a target binding site located in an untranslated region of GAM96 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 96A, thereby inhibiting translation of GAM96 TARGET RNA into GAM96 TARGET PROTEIN, both of Fig. 96A.

[9319] GAM277 RNA binds complimentarily to a target binding site located in an untranslated region of GAM277 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 277A, thereby inhibiting translation of GAM277 TARGET RNA into GAM277 TARGET PROTEIN, both of Fig. 277A.

[9320] It is appreciated that specific functions, and accordingly utilities, of GR687 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster

of GR687 GENE: GAM96 TARGET PROTEIN and GAM277 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 96D and 277D

[9321] Reference is now made to Fig. 688, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 688(GR688) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9322] GR688 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR688 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9323] GR688 GENE encodes GR688 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9324] GR688 PRECURSOR RNA folds spatially, forming GR688 FOLDED PRECURSOR RNA . It is appreciated that GR688 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence

of GR688 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9325] GR688 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM86 PRECURSOR and GAM202 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9326] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86 RNA and GAM202 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9327] GAM86 RNA binds complimentarily to a target binding site located in an untranslated region of GAM86 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 86A, thereby inhibiting translation of GAM86 TARGET RNA into GAM86 TARGET PROTEIN, both of Fig. 86A.

[9328] GAM202 RNA binds complimentarily to a target binding site located in an untranslated region of GAM202 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 202A, thereby inhibiting translation of GAM202 TARGET RNA into GAM202 TARGET PROTEIN, both of Fig. 202A.

[9329] It is appreciated that specific functions, and accordingly utilities, of GR688 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR688 GENE: GAM86 TARGET PROTEIN and GAM202 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 86D and 202D

[9330] Reference is now made to Fig. 689, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 689(GR689) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9331] GR689 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR689 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9332] GR689 GENE encodes GR689 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9333] GR689 PRECURSOR RNA folds spatially, forming GR689 FOLDED PRECURSOR RNA . It is appreciated that GR689 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR689 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9334] GR689 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM29 PRECURSOR and GAM180 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9335] The above mentioned GAM precursor RNAs are diced by

DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM29 RNA and GAM180 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9336] GAM29 RNA binds complimentarily to a target binding site located in an untranslated region of GAM29 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 29A, thereby inhibiting translation of GAM29 TARGET RNA into GAM29 TARGET PROTEIN, both of Fig. 29A.

[9337] GAM180 RNA binds complimentarily to a target binding site located in an untranslated region of GAM180 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 180A, thereby inhibiting translation of GAM180 TARGET RNA into GAM180 TARGET PROTEIN, both of Fig. 180A.

[9338] It is appreciated that specific functions, and accordingly utilities, of GR689 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR689 GENE: GAM29 TARGET PROTEIN and GAM180

TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 29D and 180D

[9339] Reference is now made to Fig. 690, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 690(GR690) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9340] GR690 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR690 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9341] GR690 GENE encodes GR690 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9342] GR690 PRECURSOR RNA folds spatially, forming GR690 FOLDED PRECURSOR RNA . It is appreciated that GR690 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR690 PRECURSOR RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9343] GR690 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47 PRECURSOR and GAM430 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9344] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47 RNA and GAM430 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9345] GAM47 RNA binds complimentarily to a target binding site located in an untranslated region of GAM47 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 47A, thereby inhibiting translation of GAM47 TARGET RNA into GAM47 TARGET PROTEIN, both of Fig. 47A.

[9346] GAM430 RNA binds complimentarily to a target binding

site located in an untranslated region of GAM430 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 430A, thereby inhibiting translation of GAM430 TARGET RNA into GAM430 TARGET PROTEIN, both of Fig. 430A.

[9347] It is appreciated that specific functions, and accordingly utilities, of GR690 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR690 GENE: GAM47 TARGET PROTEIN and GAM430 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 47D and 430D

[9348] Reference is now made to Fig. 691, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 691(GR691) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9349] GR691 GENE is a novel bioinformatically detected regula-

tory, non protein coding, RNA gene. The method by which GR691 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9350] GR691 GENE encodes GR691 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9351] GR691 PRECURSOR RNA folds spatially, forming GR691 FOLDED PRECURSOR RNA . It is appreciated that GR691 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR691 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9352] GR691 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM281 PRECURSOR and GAM517 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9353] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA

segments of about 22 nucleotides in length, GAM281 RNA and GAM517 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9354] GAM281 RNA binds complimentarily to a target binding site located in an untranslated region of GAM281 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 281A, thereby inhibiting translation of GAM281 TARGET RNA into GAM281 TARGET PROTEIN, both of Fig. 281A.

[9355] GAM517 RNA binds complimentarily to a target binding site located in an untranslated region of GAM517 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 517A, thereby inhibiting translation of GAM517 TARGET RNA into GAM517 TARGET PROTEIN, both of Fig. 517A.

[9356] It is appreciated that specific functions, and accordingly utilities, of GR691 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR691 GENE: GAM281 TARGET PROTEIN and GAM517 TARGET PROTEIN. The function of these target genes is

elaborated hereinabove with reference to Figs. 281D and 517D

[9357] Reference is now made to Fig. 692, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 692(GR692) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9358] GR692 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR692 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9359] GR692 GENE encodes GR692 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9360] GR692 PRECURSOR RNA folds spatially, forming GR692 FOLDED PRECURSOR RNA . It is appreciated that GR692 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR692 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9361] GR692 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM98 PRECURSOR and GAM455 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9362] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM98 RNA and GAM455 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9363] GAM98 RNA binds complimentarily to a target binding site located in an untranslated region of GAM98 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 98A, thereby inhibiting translation of GAM98 TARGET RNA into GAM98 TARGET PROTEIN, both of Fig. 98A.

[9364] GAM455 RNA binds complimentarily to a target binding site located in an untranslated region of GAM455 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 455A, thereby inhibiting translation of GAM455 TARGET RNA into GAM455 TARGET PROTEIN, both of Fig. 455A.

[9365] It is appreciated that specific functions, and accordingly utilities, of GR692 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR692 GENE: GAM98 TARGET PROTEIN and GAM455 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 98D and 455D

[9366] Reference is now made to Fig. 693, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 693(GR693) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9367] GR693 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR693 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9368] GR693 GENE encodes GR693 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9369] GR693 PRECURSOR RNA folds spatially, forming GR693 FOLDED PRECURSOR RNA . It is appreciated that GR693 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR693 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9370] GR693 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM74 PRECURSOR, GAM200 PRECURSOR and GAM243 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9371] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM74 RNA,

GAM200 RNA and GAM243 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9372] GAM74 RNA binds complimentarily to a target binding site located in an untranslated region of GAM74 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 74A, thereby inhibiting translation of GAM74 TARGET RNA into GAM74 TARGET PROTEIN, both of Fig. 74A.

[9373] GAM200 RNA binds complimentarily to a target binding site located in an untranslated region of GAM200 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 200A, thereby inhibiting translation of GAM200 TARGET RNA into GAM200 TARGET PROTEIN, both of Fig. 200A.

[9374] GAM243 RNA binds complimentarily to a target binding site located in an untranslated region of GAM243 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 243A, thereby inhibiting translation of GAM243 TARGET RNA into GAM243 TARGET PROTEIN, both of Fig. 243A.

[9375] It is appreciated that specific functions, and accordingly utilities, of GR693 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR693 GENE: GAM74 TARGET PROTEIN, GAM200 TARGET PROTEIN and GAM243 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 74D, 200D and 243D

[9376] Reference is now made to Fig. 694, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 694(GR694) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9377] GR694 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR694 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9378] GR694 GENE encodes GR694 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9379] GR694 PRECURSOR RNA folds spatially, forming GR694

FOLDED PRECURSOR RNA . It is appreciated that GR694 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR694 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9380] GR694 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM129 PRECURSOR and GAM154 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9381] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM129 RNA and GAM154 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9382] GAM129 RNA binds complimentarily to a target binding site located in an untranslated region of GAM129 TARGET RNA, which target binding site corresponds to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 129A, thereby inhibiting translation of GAM129 TARGET RNA into GAM129 TARGET PROTEIN, both of Fig. 129A.

[9383] GAM154 RNA binds complimentarily to a target binding site located in an untranslated region of GAM154 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 154A, thereby inhibiting translation of GAM154 TARGET RNA into GAM154 TARGET PROTEIN, both of Fig. 154A.

[9384] It is appreciated that specific functions, and accordingly utilities, of GR694 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR694 GENE: GAM129 TARGET PROTEIN and GAM154 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 129D and 154D

[9385] Reference is now made to Fig. 695, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 695(GR695) gene, which encodes an operon-like cluster

of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9386] GR695 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR695 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9387] GR695 GENE encodes GR695 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9388] GR695 PRECURSOR RNA folds spatially, forming GR695 FOLDED PRECURSOR RNA . It is appreciated that GR695 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR695 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9389] GR695 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM336 PRECURSOR and GAM549 PRE-

CURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9390] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM336 RNA and GAM549 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9391] GAM336 RNA binds complimentarily to a target binding site located in an untranslated region of GAM336 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 336A, thereby inhibiting translation of GAM336 TARGET RNA into GAM336 TARGET PROTEIN, both of Fig. 336A.

[9392] GAM549 RNA binds complimentarily to a target binding site located in an untranslated region of GAM549 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 549A, thereby inhibiting translation of GAM549 TARGET RNA into GAM549 TARGET PROTEIN, both of Fig. 549A.

[9393] It is appreciated that specific functions, and accordingly

utilities, of GR695 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR695 GENE: GAM336 TARGET PROTEIN and GAM549 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 336D and 549D

[9394] Reference is now made to Fig. 696, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 696(GR696) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9395] GR696 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR696 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9396] GR696 GENE encodes GR696 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9397] GR696 PRECURSOR RNA folds spatially, forming GR696 FOLDED PRECURSOR RNA . It is appreciated that GR696

FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR696 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9398] GR696 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM426 PRECURSOR and GAM496 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9399] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM426 RNA and GAM496 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9400] GAM426 RNA binds complimentarily to a target binding site located in an untranslated region of GAM426 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig. 426A, thereby inhibiting translation of GAM426 TARGET RNA into GAM426 TARGET PROTEIN, both of Fig. 426A.

[9401] GAM496 RNA binds complimentarily to a target binding site located in an untranslated region of GAM496 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 496A, thereby inhibiting translation of GAM496 TARGET RNA into GAM496 TARGET PROTEIN, both of Fig. 496A.

[9402] It is appreciated that specific functions, and accordingly utilities, of GR696 GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR696 GENE: GAM426 TARGET PROTEIN and GAM496 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 426D and 496D

[9403] Reference is now made to Fig. 697, which is a simplified diagram describing a novel bioinformatically detected regulatory gene, referred to here as Genomic Record 697(GR697) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn

modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[9404] GR697 GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR697 GENE was detected is described hereinabove with reference to Figs. 6-15.

[9405] GR697 GENE encodes GR697 PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[9406] GR697 PRECURSOR RNA folds spatially, forming GR697 FOLDED PRECURSOR RNA . It is appreciated that GR697 FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR697 PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[9407] GR697 FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM201 PRECURSOR and GAM325 PRECURSOR, each of which GAM precursor RNAs being a hair-

pin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[9408] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM201 RNA and GAM325 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[9409] GAM201 RNA binds complimentarily to a target binding site located in an untranslated region of GAM201 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 201A, thereby inhibiting translation of GAM201 TARGET RNA into GAM201 TARGET PROTEIN, both of Fig. 201A.

[9410] GAM325 RNA binds complimentarily to a target binding site located in an untranslated region of GAM325 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 325A, thereby inhibiting translation of GAM325 TARGET RNA into GAM325 TARGET PROTEIN, both of Fig. 325A.

[9411] It is appreciated that specific functions, and accordingly utilities, of GR697 GENE correlate with, and may be de-

duced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR697 GENE: GAM201 TARGET PROTEIN and GAM325 TARGET PROTEIN. The function of these target genes is elaborated hereinabove with reference to Figs. 201D and 325D

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